

## SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 70%

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

---

091  
904  
296

*This Page Blank (uspto)*



GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 15, 2006, 14:59:58 ; Search time 0.001 Seconds  
(without alignments)  
119.944 Million cell updates/sec

Title: US-09-904-968A-3-COPY  
Perfect score: 29  
Sequence: 1 ccaccacctgctgtgacctggtgtaaat 29

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 177 seqs, 2068 residues

Total number of hits satisfying chosen parameters: 354

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 177 summaries

Database : issdb.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description                           |
|------------|-------|-------------|--------|----|---------------------------------------|
| C 1        | 15.2  | 52.4        | 21     | 1  | US-09-422-978-11421 Sequence 11421, A |
| 2          | 14.8  | 51.0        | 20     | 1  | US-09-422-978-9340 Sequence 9340, Ap  |
| 3          | 14.2  | 49.0        | 20     | 1  | US-09-023-082A-97 Sequence 97, Appl   |
| 4          | 14.2  | 49.0        | 20     | 1  | US-09-218-444-18 Sequence 18, Appl    |
| 5          | 14.2  | 49.0        | 20     | 1  | US-09-248-998-97 Sequence 97, Appl    |
| 6          | 14.2  | 49.0        | 20     | 1  | US-09-853-666-18 Sequence 18, Appl    |
| 7          | 14.2  | 49.0        | 20     | 1  | US-09-610-651-97 Sequence 97, Appl    |
| 8          | 14.2  | 49.0        | 20     | 1  | US-09-345-373-97 Sequence 97, Appl    |
| 9          | 14.2  | 49.0        | 20     | 1  | US-10-075-446-97 Sequence 97, Appl    |
| C 10       | 13.4  | 46.2        | 19     | 1  | US-09-422-978-6482 Sequence 6482, Ap  |
| C 11       | 13.2  | 45.5        | 18     | 1  | US-09-357-072-27 Sequence 27, Appl    |
| C 12       | 12.8  | 44.1        | 18     | 1  | US-08-832-883-39 Sequence 39, Appl    |
| C 13       | 12.8  | 44.1        | 18     | 1  | US-08-832-877-39 Sequence 39, Appl    |
| 14         | 12.8  | 44.1        | 18     | 1  | US-08-679-645-1205 Sequence 1205, Ap  |
| C 15       | 12.8  | 44.1        | 18     | 1  | US-09-809-920-34 Sequence 34, Appl    |
| 16         | 12.4  | 42.8        | 17     | 1  | US-09-866-108A-2171 Sequence 2171, Ap |
| 17         | 12.4  | 42.8        | 17     | 1  | US-09-866-108A-2172 Sequence 2172, Ap |
| 18         | 12.4  | 42.8        | 17     | 1  | US-09-866-108A-2173 Sequence 2173, Ap |
| 19         | 12.4  | 42.8        | 17     | 1  | US-09-866-108A-2174 Sequence 2174, Ap |
| 20         | 12    | 41.4        | 17     | 1  | US-09-866-108A-2169 Sequence 2169, Ap |
| 21         | 12    | 41.4        | 17     | 1  | US-09-866-108A-2170 Sequence 2170, Ap |
| C 22       | 11.2  | 38.6        | 16     | 1  | US-09-112-096-13 Sequence 13, Appl    |
| C 23       | 11.2  | 38.6        | 16     | 1  | US-09-371-772B-5660 Sequence 5660, Ap |
| C 24       | 10.8  | 37.2        | 15     | 1  | US-08-182-968A-85 Sequence 85, Appl   |
| C 25       | 10.8  | 37.2        | 15     | 1  | US-08-774-306A-85 Sequence 85, Appl   |
| C 26       | 10.8  | 37.2        | 15     | 1  | US-09-064-156A-85 Sequence 85, Appl   |
| C 27       | 10.4  | 35.9        | 14     | 1  | US-08-535-249-1 Sequence 1, Appli     |
| C 28       | 10.4  | 35.9        | 14     | 1  | US-09-230-652-17 Sequence 17, Appl    |
| 29         | 9.8   | 33.8        | 13     | 1  | US-08-544-381B-25 Sequence 25, Appl   |
| 30         | 9.8   | 33.8        | 13     | 1  | US-08-778-794A-83 Sequence 83, Appl   |
| 31         | 9.8   | 33.8        | 14     | 1  | US-08-535-249-15 Sequence 15, Appl    |
| C 32       | 9.4   | 32.4        | 11     | 1  | US-09-249-155A-54 Sequence 54, Appl   |
| 33         | 9.4   | 32.4        | 11     | 1  | US-09-249-155A-269 Sequence 269, App  |

|      |     |      |    |   |                                      |
|------|-----|------|----|---|--------------------------------------|
| 34   | 9.4 | 32.4 | 13 | 1 | US-08-367-175A-27 Sequence 27, Appl  |
| 35   | 9.4 | 32.4 | 13 | 1 | 5225537-13 Patent No. 5225537        |
| C 36 | 9   | 31.0 | 11 | 1 | US-08-481-658B-73 Sequence 73, Appl  |
| C 37 | 9   | 31.0 | 11 | 1 | US-08-477-504A-73 Sequence 73, Appl  |
| C 38 | 9   | 31.0 | 11 | 1 | US-08-486-756A-73 Sequence 73, Appl  |
| C 39 | 9   | 31.0 | 11 | 1 | US-08-485-862B-73 Sequence 73, Appl  |
| C 40 | 9   | 31.0 | 11 | 1 | US-08-787-739-73 Sequence 73, Appl   |
| C 41 | 9   | 31.0 | 11 | 1 | US-08-487-077A-73 Sequence 73, Appl  |
| C 42 | 9   | 31.0 | 11 | 1 | US-08-485-863A-73 Sequence 73, Appl  |
| C 43 | 9   | 31.0 | 11 | 1 | US-08-485-049D-73 Sequence 73, Appl  |
| C 44 | 9   | 31.0 | 11 | 1 | US-09-178-115-73 Sequence 73, Appl   |
| C 45 | 9   | 31.0 | 11 | 1 | US-09-177-776-73 Sequence 73, Appl   |
| C 46 | 9   | 31.0 | 11 | 1 | US-09-115-407-3 Sequence 3, Appli    |
| C 47 | 9   | 31.0 | 11 | 1 | US-09-772-719B-73 Sequence 73, Appl  |
| 48   | 9   | 31.0 | 12 | 1 | US-10-286-387-30 Sequence 30, Appl   |
| C 49 | 8.8 | 30.3 | 12 | 1 | US-08-035-928-15 Sequence 15, Appl   |
| 50   | 8.8 | 30.3 | 12 | 1 | US-08-250-740-29 Sequence 29, Appl   |
| 51   | 8.8 | 30.3 | 12 | 1 | US-07-695-472B-9 Sequence 9, Appli   |
| C 52 | 8.8 | 30.3 | 12 | 1 | US-08-410-540-30 Sequence 30, Appl   |
| 53   | 8.8 | 30.3 | 12 | 1 | US-08-441-887A-69 Sequence 69, Appl  |
| 54   | 8.8 | 30.3 | 12 | 1 | US-09-106-375-9 Sequence 9, Appli    |
| 55   | 8.8 | 30.3 | 12 | 1 | US-09-374-174B-3 Sequence 3, Appli   |
| 56   | 8.6 | 29.7 | 12 | 1 | US-09-163-485-18 Sequence 18, Appl   |
| 57   | 8.4 | 29.0 | 10 | 1 | US-08-367-175A-23 Sequence 23, Appl  |
| C 58 | 8.4 | 29.0 | 10 | 1 | US-08-388-353-78 Sequence 78, Appl   |
| C 59 | 8.4 | 29.0 | 10 | 1 | US-08-388-353-381 Sequence 381, App  |
| 60   | 8.4 | 29.0 | 10 | 1 | US-08-388-353-782 Sequence 782, App  |
| 61   | 8.4 | 29.0 | 10 | 1 | US-08-388-353-783 Sequence 783, App  |
| 62   | 8.4 | 29.0 | 10 | 1 | US-08-388-353-784 Sequence 784, App  |
| C 63 | 8.4 | 29.0 | 10 | 1 | US-08-488-551B-78 Sequence 78, Appl  |
| C 64 | 8.4 | 29.0 | 10 | 1 | US-08-488-551B-381 Sequence 381, App |
| 65   | 8.4 | 29.0 | 10 | 1 | US-08-488-551B-782 Sequence 782, App |
| 66   | 8.4 | 29.0 | 10 | 1 | US-08-488-551B-783 Sequence 783, App |
| 67   | 8.4 | 29.0 | 10 | 1 | US-08-488-551B-784 Sequence 784, App |
| C 68 | 8.4 | 29.0 | 10 | 1 | US-09-245-041-129 Sequence 129, App  |
| 69   | 8.4 | 29.0 | 10 | 1 | US-08-870-511-13 Sequence 13, Appl   |
| C 70 | 8.4 | 29.0 | 10 | 1 | US-09-508-753B-118 Sequence 118, App |
| 71   | 8.4 | 29.0 | 10 | 1 | US-10-042-111-8 Sequence 8, Appli    |
| C 72 | 8.4 | 29.0 | 10 | 1 | US-09-358-055B-130 Sequence 130, App |
| C 73 | 8.4 | 29.0 | 10 | 1 | US-09-893-238-129 Sequence 129, App  |
| 74   | 8.4 | 29.0 | 11 | 1 | US-08-800-036-15 Sequence 15, Appl   |
| C 75 | 8.4 | 29.0 | 11 | 1 | US-08-481-658B-86 Sequence 86, Appl  |
| 76   | 8.4 | 29.0 | 11 | 1 | US-08-926-492-15 Sequence 15, Appl   |
| C 77 | 8.4 | 29.0 | 11 | 1 | US-08-477-504A-86 Sequence 86, Appl  |
| C 78 | 8.4 | 29.0 | 11 | 1 | US-08-486-756A-86 Sequence 86, Appl  |
| C 79 | 8.4 | 29.0 | 11 | 1 | US-08-485-862B-86 Sequence 86, Appl  |
| C 80 | 8.4 | 29.0 | 11 | 1 | US-08-787-739-86 Sequence 86, Appl   |
| 81   | 8.4 | 29.0 | 11 | 1 | US-09-048-505-15 Sequence 15, Appl   |
| C 82 | 8.4 | 29.0 | 11 | 1 | US-08-487-077A-86 Sequence 86, Appl  |
| C 83 | 8.4 | 29.0 | 11 | 1 | US-08-485-863A-86 Sequence 86, Appl  |
| C 84 | 8.4 | 29.0 | 11 | 1 | US-08-485-049D-86 Sequence 86, Appl  |
| C 85 | 8.4 | 29.0 | 11 | 1 | US-09-178-115-86 Sequence 86, Appl   |
| C 86 | 8.4 | 29.0 | 11 | 1 | US-09-177-776-86 Sequence 86, Appl   |
| C 87 | 8.4 | 29.0 | 11 | 1 | US-09-249-155A-113 Sequence 113, App |
| 88   | 8.4 | 29.0 | 11 | 1 | US-09-249-155A-285 Sequence 285, App |
| C 89 | 8.4 | 29.0 | 11 | 1 | US-09-772-719B-86 Sequence 86, Appl  |
| C 90 | 8.4 | 29.0 | 12 | 1 | US-08-435-350-76 Sequence 76, Appl   |
| 91   | 8.4 | 29.0 | 12 | 1 | US-09-281-418-141 Sequence 141, App  |
| C 92 | 8.4 | 29.0 | 12 | 1 | US-09-281-418-191 Sequence 191, App  |
| 93   | 8.4 | 29.0 | 12 | 1 | US-09-874-601-167 Sequence 167, App  |
| 94   | 8.4 | 29.0 | 12 | 1 | US-09-875-453B-77 Sequence 77, Appl  |
| 95   | 8   | 27.6 | 10 | 1 | US-08-634-350-11 Sequence 11, Appl   |
| 96   | 8   | 27.6 | 10 | 1 | US-08-388-353-39 Sequence 39, Appl   |
| 97   | 8   | 27.6 | 10 | 1 | US-08-388-353-40 Sequence 40, Appl   |
| 98   | 8   | 27.6 | 10 | 1 | US-08-388-353-41 Sequence 41, Appl   |
| 99   | 8   | 27.6 | 10 | 1 | US-08-388-353-785 Sequence 785, App  |
| 100  | 8   | 27.6 | 10 | 1 | US-08-388-353-786 Sequence 786, App  |
| 101  | 8   | 27.6 | 10 | 1 | US-08-388-353-788 Sequence 788, App  |
| 102  | 8   | 27.6 | 10 | 1 | US-08-488-551B-39 Sequence 39, Appl  |
| 103  | 8   | 27.6 | 10 | 1 | US-08-488-551B-40 Sequence 40, Appl  |
| 104  | 8   | 27.6 | 10 | 1 | US-08-488-551B-41 Sequence 41, Appl  |
| 105  | 8   | 27.6 | 10 | 1 | US-08-488-551B-785 Sequence 785, App |
| 106  | 8   | 27.6 | 10 | 1 | US-08-488-551B-786 Sequence 786, App |

Issued Patents NA

|       |     |      |    |   |                    |                    |
|-------|-----|------|----|---|--------------------|--------------------|
| 107   | 8   | 27.6 | 10 | 1 | US-08-488-551B-788 | Sequence 788, App  |
| c 108 | 8   | 27.6 | 10 | 1 | US-09-475-947A-279 | Sequence 279, App  |
| 109   | 8   | 27.6 | 10 | 1 | US-08-894-454-122  | Sequence 122, App  |
| c 110 | 8   | 27.6 | 10 | 1 | US-10-042-111-23   | Sequence 23, Appl  |
| 111   | 8   | 27.6 | 11 | 1 | US-09-249-155A-106 | Sequence 106, App  |
| c 112 | 8   | 27.6 | 11 | 1 | US-08-836-734E-90  | Sequence 90, Appl  |
| c 113 | 7.8 | 26.9 | 11 | 1 | US-09-793-146-36   | Sequence 36, Appl  |
| 114   | 7.8 | 26.9 | 11 | 1 | US-09-793-146-41   | Sequence 41, Appl  |
| 115   | 7.8 | 26.9 | 11 | 1 | US-09-793-146-59   | Sequence 59, Appl  |
| 116   | 7.8 | 26.9 | 11 | 1 | US-09-793-146-60   | Sequence 60, Appl  |
| c 117 | 7.8 | 26.9 | 11 | 1 | 5256558-12         | Patent No. 5256558 |
| c 118 | 7.4 | 25.5 | 10 | 1 | US-07-960-981-2    | Sequence 2, Appli  |
| 119   | 7.4 | 25.5 | 10 | 1 | US-07-651-710A-40  | Sequence 40, Appl  |
| c 120 | 7.4 | 25.5 | 10 | 1 | US-08-335-565A-21  | Sequence 21, Appl  |
| 121   | 7.4 | 25.5 | 10 | 1 | US-08-235-503B-24  | Sequence 24, Appl  |
| 122   | 7.4 | 25.5 | 10 | 1 | US-08-545-253A-7   | Sequence 7, Appli  |
| c 123 | 7.4 | 25.5 | 10 | 1 | US-08-265-484B-13  | Sequence 13, Appl  |
| c 124 | 7.4 | 25.5 | 10 | 1 | US-08-388-353-77   | Sequence 77, Appl  |
| c 125 | 7.4 | 25.5 | 10 | 1 | US-08-388-353-79   | Sequence 79, Appl  |
| c 126 | 7.4 | 25.5 | 10 | 1 | US-08-388-353-140  | Sequence 140, App  |
| c 127 | 7.4 | 25.5 | 10 | 1 | US-08-388-353-141  | Sequence 141, App  |
| c 128 | 7.4 | 25.5 | 10 | 1 | US-08-388-353-142  | Sequence 142, App  |
| c 129 | 7.4 | 25.5 | 10 | 1 | US-08-388-353-143  | Sequence 143, App  |
| c 130 | 7.4 | 25.5 | 10 | 1 | US-08-388-353-380  | Sequence 380, App  |
| c 131 | 7.4 | 25.5 | 10 | 1 | US-08-388-353-382  | Sequence 382, App  |
| 132   | 7.4 | 25.5 | 10 | 1 | US-08-388-353-770  | Sequence 770, App  |
| 133   | 7.4 | 25.5 | 10 | 1 | US-08-388-353-771  | Sequence 771, App  |
| 134   | 7.4 | 25.5 | 10 | 1 | US-08-388-353-781  | Sequence 781, App  |
| 135   | 7.4 | 25.5 | 10 | 1 | US-08-388-353-796  | Sequence 796, App  |
| 136   | 7.4 | 25.5 | 10 | 1 | US-08-388-353-797  | Sequence 797, App  |
| c 137 | 7.4 | 25.5 | 10 | 1 | US-08-488-551B-77  | Sequence 77, Appl  |
| c 138 | 7.4 | 25.5 | 10 | 1 | US-08-488-551B-79  | Sequence 79, Appl  |
| c 139 | 7.4 | 25.5 | 10 | 1 | US-08-488-551B-140 | Sequence 140, App  |
| c 140 | 7.4 | 25.5 | 10 | 1 | US-08-488-551B-141 | Sequence 141, App  |
| c 141 | 7.4 | 25.5 | 10 | 1 | US-08-488-551B-142 | Sequence 142, App  |
| c 142 | 7.4 | 25.5 | 10 | 1 | US-08-488-551B-143 | Sequence 143, App  |
| c 143 | 7.4 | 25.5 | 10 | 1 | US-08-488-551B-380 | Sequence 380, App  |
| c 144 | 7.4 | 25.5 | 10 | 1 | US-08-488-551B-382 | Sequence 382, App  |
| 145   | 7.4 | 25.5 | 10 | 1 | US-08-488-551B-770 | Sequence 770, App  |
| 146   | 7.4 | 25.5 | 10 | 1 | US-08-488-551B-771 | Sequence 771, App  |
| 147   | 7.4 | 25.5 | 10 | 1 | US-08-488-551B-781 | Sequence 781, App  |
| 148   | 7.4 | 25.5 | 10 | 1 | US-08-488-551B-796 | Sequence 796, App  |
| 149   | 7.4 | 25.5 | 10 | 1 | US-08-488-551B-797 | Sequence 797, App  |
| c 150 | 7.4 | 25.5 | 10 | 1 | US-08-719-337-7    | Sequence 7, Appli  |
| c 151 | 7.4 | 25.5 | 10 | 1 | US-08-765-257A-13  | Sequence 13, Appl  |
| c 152 | 7.4 | 25.5 | 10 | 1 | US-08-522-384-18   | Sequence 18, Appl  |
| 153   | 7.4 | 25.5 | 10 | 1 | US-08-522-384-120  | Sequence 120, App  |
| c 154 | 7.4 | 25.5 | 10 | 1 | US-09-034-205-51   | Sequence 51, Appl  |
| c 155 | 7.4 | 25.5 | 10 | 1 | US-08-934-097A-51  | Sequence 51, Appl  |
| c 156 | 7.4 | 25.5 | 10 | 1 | US-09-677-218B-51  | Sequence 51, Appl  |
| c 157 | 7.4 | 25.5 | 10 | 1 | US-09-677-192-51   | Sequence 51, Appl  |
| c 158 | 7.4 | 25.5 | 10 | 1 | US-09-154-750A-14  | Sequence 14, Appl  |
| c 159 | 7.4 | 25.5 | 10 | 1 | US-09-229-007A-81  | Sequence 81, Appl  |
| c 160 | 7.4 | 25.5 | 10 | 1 | US-09-261-115-57   | Sequence 57, Appl  |
| c 161 | 7.4 | 25.5 | 10 | 1 | US-09-914-259-119  | Sequence 119, App  |
| c 162 | 7.4 | 25.5 | 10 | 1 | US-09-914-259-120  | Sequence 120, App  |
| c 163 | 7.4 | 25.5 | 10 | 1 | US-09-508-753B-67  | Sequence 67, Appl  |
| c 164 | 7.4 | 25.5 | 10 | 1 | US-09-508-753B-78  | Sequence 78, Appl  |
| c 165 | 7.4 | 25.5 | 10 | 1 | US-09-508-753B-89  | Sequence 89, Appl  |
| c 166 | 7.4 | 25.5 | 10 | 1 | US-09-508-753B-164 | Sequence 164, App  |
| c 167 | 7.4 | 25.5 | 10 | 1 | US-09-508-753B-188 | Sequence 188, App  |
| c 168 | 7.4 | 25.5 | 10 | 1 | US-09-811-286-16   | Sequence 16, Appl  |
| c 169 | 7.4 | 25.5 | 10 | 1 | US-09-402-618B-51  | Sequence 51, Appl  |
| c 170 | 7.4 | 25.5 | 10 | 1 | US-09-825-574-51   | Sequence 51, Appl  |
| c 171 | 7.4 | 25.5 | 10 | 1 | US-10-113-424-81   | Sequence 81, Appl  |
| c 172 | 7.4 | 25.5 | 10 | 1 | US-09-821-694A-26  | Sequence 26, Appl  |
| c 173 | 7.4 | 25.5 | 10 | 1 | US-09-821-694A-30  | Sequence 30, Appl  |
| c 174 | 7.4 | 25.5 | 10 | 1 | US-10-053-883-70   | Sequence 70, Appl  |
| c 175 | 7.4 | 25.5 | 10 | 1 | PCT-US93-09634-2   | Sequence 2, Appli  |
| 176   | 7.4 | 25.5 | 10 | 1 | PCT-US94-08023-14  | Sequence 14, Appl  |
| 177   | 7.4 | 25.5 | 10 | 1 | PCT-US95-05265-24  | Sequence 24, Appl  |

ALIGNMENTS

RESULT 1

US-09-422-978-11421/c  
; Sequence 11421, Application US/094222978  
; Patent No. 6537751  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya  
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
; FILE REFERENCE: GENSET.020CP1  
; CURRENT APPLICATION NUMBER: US/09/422,978  
; CURRENT FILING DATE: 1999-10-20  
; EARLIER APPLICATION NUMBER: US 09/298,850  
; EARLIER FILING DATE: 1999-04-21  
; EARLIER APPLICATION NUMBER: US 60/109,732  
; EARLIER FILING DATE: 1998-11-23  
; EARLIER APPLICATION NUMBER: US 60/082,614  
; EARLIER FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 11421  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: primer\_bind  
; LOCATION: 1..21  
; OTHER INFORMATION: downstream amplification primer 99-5747 for SEQ 3556, in complemer  
US-09-422-978-11421

Query Match

Best Local Similarity 52.4%; Score 15.2; DB 1; Length 21;  
Pred. No. 6.5;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGTGACC 21

||| || ||||| |||||

Db 21 CATGACTGTGTGTGACC 2

RESULT 2

US-09-422-978-9340  
; Sequence 9340, Application US/094222978  
; Patent No. 6537751  
; GENERAL INFORMATION:

; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya

; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
; FILE REFERENCE: GENSET.020CP1  
; CURRENT APPLICATION NUMBER: US/09/422,978  
; CURRENT FILING DATE: 1999-10-20  
; EARLIER APPLICATION NUMBER: US 09/298,850  
; EARLIER FILING DATE: 1999-04-21  
; EARLIER APPLICATION NUMBER: US 60/109,732  
; EARLIER FILING DATE: 1998-11-23  
; EARLIER APPLICATION NUMBER: US 60/082,614  
; EARLIER FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 9340  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: primer\_bind  
; LOCATION: 1..20  
; OTHER INFORMATION: downstream amplification primer 99-25387 for SEQ 1475, in compleme  
US-09-422-978-9340

Query Match

Best Local Similarity 51.0%; Score 14.8; DB 1; Length 20;  
Pred. No. 7.3;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY      4  TCCACCTGCTGTGTGACC 21
      |  |||||  |||||
Db      3  TGCACCTGCTGTGTGACC 20

RESULT 3
US-09-023-082A-97
; Sequence 97, Application US/09023082A
; Patent No. 6077692
; GENERAL INFORMATION:
; APPLICANT: RUBEN, STEVEN M.
; APPLICANT: JIMENEZ, PABLO
; APPLICANT: DUAN, D. ROXANNE
; APPLICANT: RAMPY, MARK A.
; APPLICANT: MENDRICK, DONNA
; APPLICANT: ZHANG, JUN
; APPLICANT: NI, JIAN
; APPLICANT: MOORE, PAUL A.
; APPLICANT: COLEMAN, TIMOTHY A.
; APPLICANT: GRUBER, JOACHIM R.
; APPLICANT: DILLON, PATRICK J.
; APPLICANT: GENTZ, REINER L.
; TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,082A
; FILING DATE: 13-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01790
; FILING DATE: 14-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/461,195
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,852
; FILING DATE: 13-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/039,045
; FILING DATE: 28-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/862,432
; FILING DATE: 23-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/910,875
; FILING DATE: 13-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/055,561
; FILING DATE: 13-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0360008/EKS
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
```

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-023-082A-97

Query Match      49.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 9.8;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2  CATCCACCTGCTGTGTGAC 20
      |||||  |||||
Db      1  CAACCACCTGCAGGGTGAC 19

RESULT 4
US-09-218-444-18
; Sequence 18, Application US/09218444
; Patent No. 623888
; GENERAL INFORMATION:
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Chopra, Arvind
; APPLICANT: Kaushal, Parveen
; APPLICANT: Spitznagel, Thomas
; APPLICANT: Unsworth, Edward
; APPLICANT: Khan, Fazal
; TITLE OF INVENTION: Keratinocyte Growth Factor-2 Formulations
; FILE REFERENCE: 1488.1030001
; CURRENT APPLICATION NUMBER: US/09/218,444
; CURRENT FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: US 60/068,493
; EARLIER FILING DATE: 1997-12-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-218-444-18

Query Match      49.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 9.8;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2  CATCCACCTGCTGTGTGAC 20
      |||||  |||||
Db      1  CAACCACCTGCAGGGTGAC 19

RESULT 5
US-09-248-998-97
; Sequence 97, Application US/09248998
; Patent No. 6599879
; GENERAL INFORMATION:
; APPLICANT: Jimenez, Pablo
; APPLICANT: Rampy, Mark A.
; APPLICANT: Mendrick, Donna
; APPLICANT: Russell, Deborah
; APPLICANT: Louie, Arthur
; TITLE OF INVENTION: Therapeutic Uses of Keratinocyte Growth Factor-2
; FILE REFERENCE: 1488.1060002
; CURRENT APPLICATION NUMBER: US/09/248,998
; CURRENT FILING DATE: 1999-02-12
; EARLIER APPLICATION NUMBER: US 60/114,387
; EARLIER FILING DATE: 30-DEC-1998
; EARLIER APPLICATION NUMBER: US 60/074,585
; EARLIER FILING DATE: 13-FEB-1998
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 97
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-248-998-97
```

Query Match 49.0%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 9.8;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

**QY**            2 CATCCACCTGCTGTGTGAC 20  
               ||| ||||| ||||| | |||||  
**pB**            1 CAACCACCTGCAGGGTGAC 19

```

RESULT 6
US-09-853-666-18
; Sequence 18, Application US/09853666
; Patent No. 6653284
; GENERAL INFORMATION:
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Chopra, Arvind
; APPLICANT: Kaushal, Parveen
; APPLICANT: Spitznagel, Thomas
; APPLICANT: Unsworth, Edward
; APPLICANT: Khan, Fazal
; TITLE OF INVENTION: Keratinocyte Growth Factor-2 Formulations
; FILE REFERENCE: 1488.1030001
; CURRENT APPLICATION NUMBER: US/09/853,666
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/218,444
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
;
US-09-853-666-18

```

Query Match 49.0%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 9.8;  
Matches 16: Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCTGTGTGAC 20  
|||  
Db 1 CAACCCACCTGCAGGGTGTGAC 19

RESULT 7  
US-09-610-651-97  
; Sequence 97, Application US/09610651  
; Patent No. 6693077  
; GENERAL INFORMATION:  
; APPLICANT: Ruben, Steven M.  
; APPLICANT: Jimenez, Pablo  
; APPLICANT: Duan, D. Roxanne  
; APPLICANT: Rampy, Mark A.  
; APPLICANT: Mendrick, Donna  
; APPLICANT: Zhang, Jun  
; APPLICANT: Ni, Jian  
; APPLICANT: Moore, Paul A.  
; APPLICANT: Coleman, Timothy A.  
; APPLICANT: Gruber, Joachim R.  
; APPLICANT: Dillon, Patrick J.  
; APPLICANT: Gentz, Reiner L.  
; TITLE OF INVENTION: Keratinocyte Growth Factor-2  
; FILE REFERENCE: 1488.036000J  
; CURRENT APPLICATION NUMBER: US/09/610,651  
; CURRENT FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: PCT/US95/01790  
; PRIOR FILING DATE: 1995-02-14  
; PRIOR APPLICATION NUMBER: 08/461,195  
; PRIOR FILING DATE: 1995-06-05  
; PRIOR APPLICATION NUMBER: 08/696,135  
; PRIOR FILING DATE: 1996-08-13  
; PRIOR APPLICATION NUMBER: 08/862,432  
; PRIOR FILING DATE: 1997-05-23

```

; PRIOR APPLICATION NUMBER: 60/023,852
; PRIOR FILING DATE: 1996-08-13
; PRIOR APPLICATION NUMBER: 60/039,045
; PRIOR FILING DATE: 1997-02-28
; PRIOR APPLICATION NUMBER: 60/055,561
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 08/910,875
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 09/023,082
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 09/345,373
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: 60/142,343
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/143,648
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: 60/144,024
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: 60/148,628
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/149,935
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/163,375
; PRIOR FILING DATE: 1999-11-03
; PRIOR APPLICATION NUMBER: 60/171,677
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: 60/205,417
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 60/198,322
; PRIOR FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-610-651-97

```

Query Match 49.0%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 9.8;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGTGAC 20  
|||  
Db 1 CAACCACCTGCAGGGTGAC 19

RESULT 8  
US-09-345-373-97  
; Sequence 97, Application US/09345373  
; Patent No. 6903072  
; GENERAL INFORMATION:  
; APPLICANT: RUBEN, STEVEN M.  
; APPLICANT: JIMENEZ, PABLO  
; APPLICANT: DUAN, D. ROXANNE  
; APPLICANT: RAMPY, MARK A.  
; APPLICANT: MENDRICK, DONNA  
; APPLICANT: ZHANG, JUN  
; APPLICANT: NI, JIAN  
; APPLICANT: MOORE, PAUL A.  
; APPLICANT: COLEMAN, TIMOTHY A.  
; APPLICANT: GRUBER, JOACHIM R.  
; APPLICANT: DILLON, PATRICK J.  
; APPLICANT: GENTZ, REINER L.  
; TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2  
; NUMBER OF SEQUENCES: 148  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 NEW YORK AVE, NW, SUITE 600  
; CITY: WASHINGTON



STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/345,373  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/023,082  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/461,195  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/023,852  
FILING DATE: 13-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/039,045  
FILING DATE: 28-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/862,432  
FILING DATE: 23-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/910,875  
FILING DATE: 13-AUG-1997  
APPLICATION NUMBER: US 60/055,561  
FILING DATE: 13-AUG-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: STEFFEE, ERIC K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.0360008/EKS  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 97:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-345-373-97

Query Match 49.0%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 9.8;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCTGTGTGAC 20  
|| ||||| | |||||  
Db 1 CAACCCACCTGCAGGGTGAC 19

RESULT 9  
US-10-075-446-97  
; Sequence 97, Application US/10075446  
; Patent No. 6916786  
; GENERAL INFORMATION:  
; APPLICANT: RUBEN, STEVEN M.  
; JIMENEZ, PABLO  
; DUAN, D. ROXANNE  
; RAMPY, MARK A.  
; MENDRICK, DONNA  
; ZHANG, JUN  
; NI, JIAN  
; MOORE, PAUL A.  
; COLEMAN, TIMOTHY A.  
; GRUBER, JOACHIM R.

TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 NEW YORK AVE, NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/075,446  
FILING DATE: 15-Feb-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/023,082  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/US95/01790  
FILING DATE: 14-FEB-1995  
APPLICATION NUMBER: US 08/461,195  
FILING DATE: 05-JUN-1995  
APPLICATION NUMBER: US 60/023,852  
FILING DATE: 13-AUG-1996  
APPLICATION NUMBER: US 60/039,045  
FILING DATE: 28-FEB-1997  
APPLICATION NUMBER: US 08/862,432  
FILING DATE: 23-MAY-1997  
APPLICATION NUMBER: US 08/910,875  
FILING DATE: 13-AUG-1997  
APPLICATION NUMBER: US 60/055,561  
FILING DATE: 13-AUG-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: STEFFEE, ERIC K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.0360008/EKS  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 97:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 97:  
US-10-075-446-97

Query Match 49.0%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 9.8;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCTGTGTGAC 20  
|| ||||| | |||||  
Db 1 CAACCCACCTGCAGGGTGAC 19

RESULT 10  
US-09-422-978-6482/c  
; Sequence 6482, Application US/09422978  
; Patent No. 6537751  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya  
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
; FILE REFERENCE: GENSET.020CP1  
; CURRENT APPLICATION NUMBER: US/09/422,978  
; CURRENT FILING DATE: 1999-10-20

```
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6482
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-11745 for SEQ 2548,
US-09-422-978-6482

Query Match          46.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 13;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 CCACCTGCTGTGTGA 19
Db      19 CCGCCTGCTGTGTGA 5
      ||| ||||| ||||| |||

RESULT 11
US-09-357-072-27/c
; Sequence 27, Application US/09357072
; Patent No. 6015712
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Brenda F. Baker
; APPLICANT: Hong Zhang
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF FADD EXPRESSION
; FILE REFERENCE: RTS-0027
; CURRENT APPLICATION NUMBER: US/09/357,072
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 27
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-072-27

Query Match          45.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      9 CTGCTGTGTGACCTGGTA 26
Db      18 CTGGTGGCTGACCTGGTA 1
      ||| ||| ||||| |||||

RESULT 12
US-08-832-883-39/c
; Sequence 39, Application US/08832883
; Patent No. 5807681
; GENERAL INFORMATION:
; APPLICANT: Giordano, Antonio
; APPLICANT: Baldi, Alphonso
; TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS
; TITLE OF INVENTION: OF CANCER
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEIDEL, GONDA, LAVORGNA & MONACO, P.C.
; STREET: Suite 1800 Two Penn Center Plaza
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
,
```

```
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/832,883
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 8321-13 US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-832-883-39

Query Match          44.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      13 TGTGTGACCTGGTAAA 28
Db      17 TTTGTGACCTGGCAA 2
      | ||||| ||||| |||

RESULT 13
US-08-832-877-39/c
; Sequence 39, Application US/08832877
; Patent No. 5840506
; GENERAL INFORMATION:
; APPLICANT: Giordano, Antonio
; TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS OF
; TITLE OF INVENTION: CANCER
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEIDEL, GONDA, LAVORGNA & MONACO, P.C.
; STREET: Suite 1800 Two Penn Center Plaza
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/832,877
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 8321-13 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
```

```
; MOLECULE TYPE: DNA (genomic)
US-08-832-877-39

Query Match      44.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 13 TGTGTGACCTGGTAAA 28
Db 17 TTTGTGACCTGGCAAA 2

RESULT 14
US-08-679-645-1205
; Sequence 1205, Application US/08679645
; Patent No. 6350934
; GENERAL INFORMATION:
; APPLICANT: Zwick, Michael G.
; APPLICANT: Edington, Brent E.
; APPLICANT: McSwiggen, James A.
; APPLICANT: Merlo, Patricia Ann Owens
; APPLICANT: Guo, Lining
; APPLICANT: Skokut, Thomas A.
; APPLICANT: Young, Scott A.
; APPLICANT: Folkerts, Otto
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
; TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
; TITLE OF INVENTION: IN PLANTS
; NUMBER OF SEQUENCES: 1263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/679,645
; FILING DATE: July 12, 1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/001,135
; FILING DATE: July 13, 1995
; APPLICATION NUMBER: 08/300,726
; FILING DATE: September 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 219/247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1205:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-679-645-1205

Query Match      44.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 62.5%; Pred. No. 16;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 5 CCACCTGCTGTGTGAC 20
   |||||:|:|:|
Db 2 CCACCUGAUGUUUGAC 17

RESULT 15
US-09-809-920-34/c
; Sequence 34, Application US/09809920
; Patent No. 6812326
; GENERAL INFORMATION:
; APPLICANT: Sato, Takaaki
; TITLE OF INVENTION: TREX, A NOVEL GENE OF TRAF-INTERACTING
; EXT GENE FAMILY AND DIAGNOSTIC AND THERAPEUTIC USES
; THEREOF
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/809,920
; FILING DATE: 16-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/156,191
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51902
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-809-920-34

Query Match      44.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGTGTGAC 20
   |||||:|:|:|
Db 18 CCACATGCTGTGTAC 3

RESULT 16
US-09-866-108A-2171
; Sequence 2171, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
```

```

; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2171
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2171

Query Match      42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 18;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 CCACCTGCTGTGTG 18
Db      4 CCACCTGCTGTGAG 17

RESULT 17
US-09-866-108A-2172
; Sequence 2172, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2171
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2173

Query Match      42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 18;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 CCACCTGCTGTGTG 18
Db      4 CCACCTGCTGTGAG 17

RESULT 17
US-09-866-108A-2172
; Sequence 2172, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2171
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2173
```

```

; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2172
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2172

Query Match      42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 18;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 CCACCTGCTGTGTG 18
Db      3 CCACCTGCTGTGAG 16

RESULT 18
US-09-866-108A-2173
; Sequence 2173, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2173
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2173

Query Match      42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 18;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```





```

; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2170
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2170

Query Match      41.4%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 CCACCTGCTGTG 16
      |||||
Db      5 CCACCTGCTGTG 16

RESULT 22
US-09-112-096-13/c
; Sequence 13, Application US/09112096
; Patent No. 6194152
; GENERAL INFORMATION:
; APPLICANT: Reiner Laus
; APPLICANT: Michael H. Shapero
; APPLICANT: Larisa Tsavaler
; TITLE OF INVENTION: Prostate Tumor Polynucleotide and
; TITLE OF INVENTION: Antigen Compositions
; FILE REFERENCE: 7636-0015.30
; CURRENT APPLICATION NUMBER: US/09/112,096
; CURRENT FILING DATE: 1998-07-09
; EARLIER APPLICATION NUMBER: 60/056,110
; EARLIER FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: (1)...(16)
; OTHER INFORMATION: oligonucleotide primer
US-09-112-096-13

Query Match      38.6%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 28;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      10 TGCTGTGTGACCTGCT 25
      |||||
Db      16 TGCTGTGTGAAATTGT 1

RESULT 23
US-09-371-772B-5660
; Sequence 5660, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: MCSwiggan, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
,

```

```

; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5660
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-5660

Query Match      38.6%; Score 11.2; DB 1; Length 16;
Best Local Similarity 56.2%; Pred. No. 28;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      8 CCTGTGTGTGACCTG 23
      ||:|:|:|:|:|:|
Db      1 CCUGCUGUGCGGCUG 16

RESULT 24
US-08-182-968A-85/c
; Sequence 85, Application US/08182968A
; Patent No. 5610054
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,968A
; FILING DATE: 13-JANUARY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/882,888
; FILING DATE: 14-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-182-968A-85

Query Match      37.2%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 31;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 16 GTGACCTGGTAAAT 29  
          |||||  
Db 15 GTGACCTGATACAT 2

RESULT 25

US-08-774-306A-85/c  
; Sequence 85, Application US/08774306A  
; Patent No. 586253

; GENERAL INFORMATION:  
; APPLICANT: Draper, Kenneth G.  
; TITLE OF INVENTION: METHOD AND REAGENT FOR  
; TITLE OF INVENTION: INHIBITING HEPATITIS C  
; TITLE OF INVENTION: VIRUS REPLICATION  
; NUMBER OF SEQUENCES: 497

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066

COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/774,306A  
; FILING DATE: December 26, 1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/182,968  
; FILING DATE: January 13, 1994  
; APPLICATION NUMBER: 07/882,888  
; FILING DATE: May 14, 1992

ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 223/227  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 85:

SEQUENCE CHARACTERISTICS:

; LENGTH: 15  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-08-774-306A-85

Query Match 37.2%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 31;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 GTGACCTGGTAAAT 29  
          |||||  
Db 15 GTGACCTGATACAT 2

RESULT 26

US-09-064-156A-85/c  
; Sequence 85, Application US/09064156A  
; Patent No. 6132966

; GENERAL INFORMATION:  
; APPLICANT: Draper, Kenneth G.  
; TITLE OF INVENTION: METHOD AND REAGENT FOR  
; TITLE OF INVENTION: INHIBITING HEPATITIS C  
; TITLE OF INVENTION: VIRUS REPLICATION  
; NUMBER OF SEQUENCES: 498

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066

COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/064,156A  
; FILING DATE: April 21, 1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/774,306  
; FILING DATE: December 26, 1996  
; APPLICATION NUMBER: 08/182,968  
; FILING DATE: January 13, 1994  
; APPLICATION NUMBER: 07/882,888  
; FILING DATE: May 14, 1992

ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 234/083  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 85:

SEQUENCE CHARACTERISTICS:

; LENGTH: 15  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-09-064-156A-85

Query Match 37.2%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 31;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 GTGACCTGGTAAAT 29  
          |||||  
Db 15 GTGACCTGATACAT 2

RESULT 27

US-08-535-249-1/c  
; Sequence 1, Application US/08535249  
; Patent No. 6455689

GENERAL INFORMATION:

; APPLICANT: Schlingensiepen, Georg-Ferdinand  
; APPLICANT: Brysch, Wolfgang  
; APPLICANT: Schlingensiepen, Karl-Hermann  
; APPLICANT: Schlingensiepen, Reimar  
; APPLICANT: Bogdahn, Ulrich  
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta (7  
; NUMBER OF SEQUENCES: 137

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Jacobson, Price, Holman & Stern  
; STREET: 400 Seventh St. N.W.  
; CITY: Washington D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20004

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/535,249  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93 107 089.0  
; FILING DATE: 30-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93 107 849.7  
; FILING DATE: 13-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Player, William E.  
; REGISTRATION NUMBER: 31,409  
; REFERENCE/DOCKET NUMBER: 10577/P58418  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)638-6666  
; TELEFAX: (202) 393-5350  
; TELEX: RCA 248593 IDEA UR  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
; ANTI-SENSE: YES  
US-08-535-249-1

Query Match 35.9%; Score 10.4; DB 1; Length 14;  
Best Local Similarity 91.7%; Pred. No. 33;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCCACCTGC 12  
| |||||  
Db 13 CTATCCACCTGC 2

RESULT 28  
US-09-230-652-17/c  
; Sequence 17, Application US/09230652A  
; Patent No. 653775  
; GENERAL INFORMATION:  
; APPLICANT: Tournier-Lasserre, Elisabeth  
; APPLICANT: Joutel, Anne  
; APPLICANT: Bousser, Marie-Germaine  
; APPLICANT: Bach, Jean-Francois  
; TITLE OF INVENTION: GENE INVOLVED IN CADASIL, METHOD OF DIAGNOSIS AND  
; TITLE OF INVENTION: THERAPEUTIC APPLICATION  
; FILE REFERENCE: 03715.0048-00000  
; CURRENT APPLICATION NUMBER: US/09/230,652A  
; CURRENT FILING DATE: 1999-05-17  
; EARLIER APPLICATION NUMBER: FR 96 09733  
; EARLIER FILING DATE: 1996-08-01  
; EARLIER APPLICATION NUMBER: FR 97 04680  
; EARLIER FILING DATE: 1997-04-16  
; EARLIER APPLICATION NUMBER: PCT/FR97/01433  
; EARLIER FILING DATE: 1997-07-31  
; NUMBER OF SEQ ID NOS: 163  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 14  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-09-230-652-17

Query Match 35.9%; Score 10.4; DB 1; Length 14;  
Best Local Similarity 91.7%; Pred. No. 33;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCCACCTGC 12  
| |||||

Db 14 CCACCCACCTGC 3  
  
RESULT 29  
US-08-544-381B-25  
; Sequence 25, Application US/08544381B  
; Patent No. 6027880  
; GENERAL INFORMATION:  
; APPLICANT: Cronin, Maureen T.  
; APPLICANT: Miyada, Charles Garrett  
; APPLICANT: Hubbell, Earl A.  
; APPLICANT: Chee, Mark  
; APPLICANT: Fodor, Stephen P.A.  
; APPLICANT: Huang, Xiaohua C.  
; APPLICANT: Lipshutz, Robert J.  
; APPLICANT: Lobban, Peter E.  
; APPLICANT: Morris, Macdonald S.  
; APPLICANT: Sheldon, Edward L.  
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes for  
; TITLE OF INVENTION: Detecting Cystic Fibrosis  
; NUMBER OF SEQUENCES: 250  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/544,381B  
; FILING DATE: 10-OCT-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/510,521  
; FILING DATE: 02-AUG-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/12305  
; FILING DATE: 26-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/284,064  
; FILING DATE: 02-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/143,312  
; FILING DATE: 26-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Liebeschuetz, Joe  
; REGISTRATION NUMBER: 37,505  
; REFERENCE/DOCKET NUMBER: 018547-004130US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (oligonucleotide)  
US-08-544-381B-25

Query Match 33.8%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 39;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 TGCTGTGTGACCT 22  
| |||||  
Db 1 TGGTGTGTGCCCT 13

RESULT 30  
US-08-778-794A-83  
; Sequence 83, Application US/08778794A  
; Patent No. 6309823  
; GENERAL INFORMATION:  
; APPLICANT: Cronin, Maureen T.  
; APPLICANT: Miyada, Charles Garrett  
; APPLICANT: Hubbell, Earl A.  
; APPLICANT: Chee, Mark  
; APPLICANT: Fodor, Stephen P.A.  
; APPLICANT: Huang, Xiaohua C.  
; APPLICANT: Lipshutz, Robert J.  
; APPLICANT: Lobban, Peter E.  
; APPLICANT: Morris, MacDonald S.  
; APPLICANT: Sheldon, Edward L.  
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes  
; TITLE OF INVENTION: for Analyzing Biotransformation Genes  
; NUMBER OF SEQUENCES: 156  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/778,794A  
; FILING DATE: 03-JAN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/143,312  
; FILING DATE: 26-OCT-1993  
; APPLICATION NUMBER: US 08/284,064  
; FILING DATE: 02-AUG-1994  
; APPLICATION NUMBER: WO PCT/US94/12305  
; FILING DATE: 26-OCT-1994  
; APPLICATION NUMBER: US 08/510,521  
; FILING DATE: 02-AUG-1995  
; APPLICATION NUMBER: US 08/544,381  
; FILING DATE: 10-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Liebeschuetz, Joe  
; REGISTRATION NUMBER: 37,505  
; REFERENCE/DOCKET NUMBER: 018547-015700US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0200  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 83:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-778-794A-83

Query Match 33.8%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 39;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 10 TGCTGTGTGACCT 22  
||| ||||| |||  
Db 1 TGGTGTGTGCCCT 13

RESULT 31

US-08-535-249-15  
; Sequence 15, Application US/08535249  
; Patent No. 6455689  
; GENERAL INFORMATION:  
; APPLICANT: Schlingensiepen, Georg-Ferdinand  
; APPLICANT: Brysch, Wolfgang  
; APPLICANT: Schlingensiepen, Karl-Hermann  
; APPLICANT: Schlingensiepen, Reimar  
; APPLICANT: Bogdahn, Ulrich  
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta (1  
; NUMBER OF SEQUENCES: 137  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jacobson, Price, Holman & Stern  
; STREET: 400 Seventh St. N.W.  
; CITY: Washington D.C  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/535,249  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93 107 089.0  
; FILING DATE: 30-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93 107 849.7  
; FILING DATE: 13-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Player, William E.  
; REGISTRATION NUMBER: 31,409  
; REFERENCE/DOCKET NUMBER: 10577/P58418  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 638-6666  
; TELEFAX: (202) 393-5350  
; TELEX: RCA 248593 IDEA UR  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
; ANTI-SENSE: YES  
US-08-535-249-15  
  
Query Match 33.8%; Score 9.8; DB 1; Length 14;  
Best Local Similarity 84.6%; Pred. No. 44;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 10 TGCTGTGTGACCT 22  
||| ||||| |||  
Db 1 TGCTGTGTGTACT 13  
  
RESULT 32  
US-09-249-155A-54/c  
; Sequence 54, Application US/09249155A  
; Patent No. 6538173  
; GENERAL INFORMATION:  
; APPLICANT: Heber-Katz, Ellen  
; TITLE OF INVENTION: Compositions and Methods for Wound  
; TITLE OF INVENTION: Healing  
; FILE REFERENCE: 00486.78503  
; CURRENT APPLICATION NUMBER: US/09/249,155A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,737  
; PRIOR FILING DATE: 1998-02-13



```

; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-54

Query Match 32.4%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 36;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 TGTGTGACCTG 23
Db 11 TGTGTGGCCTG 1

RESULT 33
US-09-249-155A-269
; Sequence 269, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 269
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-269

Query Match 32.4%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 36;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTGT 15
Db 1 CCACCTCCTGT 11

RESULT 34
US-08-367-175A-27
; Sequence 27, Application US/08367175A
; Patent No. 5631115
; GENERAL INFORMATION:
; APPLICANT: OHTSUKA, Eiko
; APPLICANT: KOIZUMI, Makoto
; TITLE OF INVENTION: Looped, hairpin ribozyme
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FRISHAUF,HOLTZ,GOODMAN,
; ADDRESSEE: LANGER & CHICK, P.C.
; STREET: 767 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10017-2023
; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/367,175A
; FILING DATE: 29 Dec. 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: GOODMAN, Herbert
; REGISTRATION NUMBER: 17081
; REFERENCE/DOCKET NUMBER: 920081
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)319-4900
; TELEFAX: (212)319-5101
; TELEX: 236268
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: mRNA
; HYPOTHETICAL: N
; ANTI-SENSE: N
US-08-367-175A-27

Query Match 32.4%; Score 9.4; DB 1; Length 13;
Best Local Similarity 54.5%; Pred. No. 47;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTGCTGTGTGA 19
Db 3 CUGUUGUGUGA 13

RESULT 35
5225537-13
; Patent No. 5225537
; APPLICANT: FOSTER, DONALD
; TITLE OF INVENTION: METHODS FOR PRODUCING HYBRID
; PHOSPHOLIPID-BINDING PROTEINS
; NUMBER OF SEQUENCES: 14
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/459,082
; FILING DATE: 29-DEC-1989
; SEQ ID NO:13:
; LENGTH: 13
5225537-13

Query Match 32.4%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 47;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 17 TGACCTGGTAA 27
Db 3 TGACTTGGTAA 13

RESULT 36
US-08-481-658B-73/c
; Sequence 73, Application US/08481658B
; Patent No. 5955075
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon

```

```
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,658B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: 5' donor consensus splice sequence
US-08-481-658B-73

Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCTGCT 13
Db 9 CCACCTGCT 1

RESULT 37
US-08-477-504A-73/c
; Sequence 73, Application US/08477504A
; Patent No. 5972353
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,504A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
```

```
; REFERENCE/DOCKET NUMBER: D-0021.3D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: 5' donor consensus splice sequence
US-08-477-504A-73

Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCTGCT 13
Db 9 CCACCTGCT 1

RESULT 38
US-08-486-756A-73/c
; Sequence 73, Application US/08486756A
; Patent No. 5981711
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,756A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: 5' donor consensus splice sequence
US-08-486-756A-73

Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 5 CCACCTGCT 13  
| | | | |  
Db 9 CCACCTGCT 1

RESULT 39

US-08-485-862B-73/c  
; Sequence 73, Application US/08485862B  
; Patent No. 5989838  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 6 Mariposa Court  
; CITY: Tiburon  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94920  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,862B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/477,504  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/260,190  
; FILING DATE: 15-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lauder, Leona L.  
; REGISTRATION NUMBER: 30,863  
; REFERENCE/DOCKET NUMBER: D-0021.3D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-435-2034  
; TELEFAX: 415-435-0727  
; INFORMATION FOR SEQ ID NO: 73:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; DESCRIPTION: 5' donor consensus splice sequence  
US-08-485-862B-73

Query Match 31.0%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCTGCT 13  
| | | | |  
Db 9 CCACCTGCT 1

RESULT 40

US-08-787-739-73/c  
; Sequence 73, Application US/08787739  
; Patent No. 6027887  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 96  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Leona L. Lauder  
; STREET: 369 Pine Street, Suite 610  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/787,739  
; FILING DATE: 24-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,049  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/486,756  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/477,504  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/481,658  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,862  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,863  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/487,077  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lauder, Leona L.  
; REGISTRATION NUMBER: 30,863  
; REFERENCE/DOCKET NUMBER: D-0021.4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-981-2034  
; TELEFAX: 415-981-0332  
; INFORMATION FOR SEQ ID NO: 73:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; DESCRIPTION: 5' donor consensus splice sequence  
US-08-787-739-73

Query Match 31.0%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCTGCT 13  
| | | | |  
Db 9 CCACCTGCT 1

RESULT 41

US-08-487-077A-73/c  
; Sequence 73, Application US/08487077A  
; Patent No. 6069242  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder



STREET: 6 Mariposa Court  
CITY: Tiburon  
STATE: California  
COUNTRY: USA  
ZIP: 94920  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,077A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/260,190  
FILING DATE: 15-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L.  
REGISTRATION NUMBER: 30,863  
REFERENCE/DOCKET NUMBER: D-0021.3H  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-435-2034  
TELEFAX: 415-435-0727  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
DESCRIPTION: 5' donor consensus splice sequence  
US-08-487-077A-73

Query Match 31.0%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred.No. 44;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCACCTGCT 13  
|||||  
Db 9 CCACCTGCT 1

RESULT 42  
US-08-485-863A-73/c  
Sequence 73, Application US/08485863A  
Patent No. 6093548  
GENERAL INFORMATION:  
APPLICANT: Zavada, Jan  
APPLICANT: Pastorekova, Silvia  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leona L. Lauder  
STREET: 6 Mariposa Court  
CITY: Tiburon  
STATE: California  
COUNTRY: USA  
ZIP: 94920  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,863A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/260,190  
FILING DATE: 15-JUN-1994  
ATTORNEY/AGENT INFORMATION:

NAME: Lauder, Leona L.  
REGISTRATION NUMBER: 30,863  
REFERENCE/DOCKET NUMBER: D-0021.3G  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-435-2034  
TELEFAX: 415-435-0727  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
DESCRIPTION: 5' donor consensus splice sequence  
US-08-485-863A-73

Query Match 31.0%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred.No. 44;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCACCTGCT 13  
|||||  
Db 9 CCACCTGCT 1

RESULT 43  
US-08-485-049D-73/c  
Sequence 73, Application US/08485049D  
Patent No. 6204370  
GENERAL INFORMATION:  
APPLICANT: Zavada, Jan  
APPLICANT: Pastorekova, Silvia  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leona L. Lauder  
STREET: 369 Pine Street  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,049D  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/260,190  
FILING DATE: 15-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L.  
REGISTRATION NUMBER: 30,863  
REFERENCE/DOCKET NUMBER: D-0021.3E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-981-2034  
TELEFAX: 415-981-0332  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
DESCRIPTION: 5' donor consensus splice sequence  
US-08-485-049D-73

Query Match 31.0%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred.No. 44;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 CCACCTGCT 13  
| | | | | | | |  
Db 9 CCACCTGCT 1

RESULT 44  
US-09-178-115-73/c  
; Sequence 73, Application US/09178115  
; Patent No. 6297041  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; FILE REFERENCE: D-0021.5A  
; CURRENT APPLICATION NUMBER: US/09/178,115  
; CURRENT FILING DATE: 1998-10-23  
; EARLIER APPLICATION NUMBER: 09/177,776  
; EARLIER FILING DATE: 1998-10-23  
; EARLIER APPLICATION NUMBER: 08/787,739  
; EARLIER FILING DATE: 1997-01-24  
; EARLIER APPLICATION NUMBER: 08/485,049  
; EARLIER FILING DATE: 1995-06-07  
; EARLIER APPLICATION NUMBER: 08/486,756  
; EARLIER FILING DATE: 1995-06-07  
; EARLIER APPLICATION NUMBER: 08/477,504  
; EARLIER FILING DATE: 1995-06-07  
; EARLIER APPLICATION NUMBER: 08/481,658  
; EARLIER FILING DATE: 1995-06-07  
; EARLIER APPLICATION NUMBER: 08/485,862  
; EARLIER FILING DATE: 1995-06-07  
; EARLIER APPLICATION NUMBER: 08/485,863  
; EARLIER FILING DATE: 1995-06-07  
; EARLIER APPLICATION NUMBER: 08/487,077  
; EARLIER FILING DATE: 1995-06-07  
; EARLIER APPLICATION NUMBER: 08/260,190  
; EARLIER FILING DATE: 1994-06-15  
; EARLIER APPLICATION NUMBER: 08/177,093  
; EARLIER FILING DATE: 1993-12-30  
; EARLIER APPLICATION NUMBER: 07/964,589  
; EARLIER FILING DATE: 1992-10-21  
; EARLIER APPLICATION NUMBER: PV-709-92  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 73  
; LENGTH: 11  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-09-178-115-73

Query Match 31.0%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 CCACCTGCT 13  
| | | | | | | |  
Db 9 CCACCTGCT 1

RESULT 45  
US-09-177-776-73/c  
; Sequence 73, Application US/09177776A  
; Patent No. 6297051  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; FILE REFERENCE: D-0021.5A  
; CURRENT APPLICATION NUMBER: US/09/177,776A

; CURRENT FILING DATE: 1998-10-23  
; EARLIER APPLICATION NUMBER: 08/787,739  
; EARLIER FILING DATE: 1997-01-24  
; EARLIER APPLICATION NUMBER: 08/485,049  
; EARLIER FILING DATE: 1995-06-07  
; EARLIER APPLICATION NUMBER: 08/486,756  
; EARLIER FILING DATE: 1995-06-07  
; EARLIER APPLICATION NUMBER: 08/477,504  
; EARLIER FILING DATE: 1995-06-07  
; EARLIER APPLICATION NUMBER: 08/481,658  
; EARLIER FILING DATE: 1995-06-07  
; EARLIER APPLICATION NUMBER: 08/485,862  
; EARLIER FILING DATE: 1995-06-07  
; EARLIER APPLICATION NUMBER: 08/485,863  
; EARLIER FILING DATE: 1995-06-07  
; EARLIER APPLICATION NUMBER: 08/487,077  
; EARLIER FILING DATE: 1995-06-07  
; EARLIER APPLICATION NUMBER: 08/260,190  
; EARLIER FILING DATE: 1994-06-15  
; EARLIER APPLICATION NUMBER: 08/177,093  
; EARLIER FILING DATE: 1993-12-30  
; EARLIER APPLICATION NUMBER: 07/964,589  
; EARLIER FILING DATE: 1992-10-21  
; EARLIER APPLICATION NUMBER: PV-709-92  
; EARLIER FILING DATE: 1992-03-11  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 73  
; LENGTH: 11  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-09-177-776-73

Query Match 31.0%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 CCACCTGCT 13  
| | | | | | | |  
Db 9 CCACCTGCT 1

RESULT 46  
US-09-115-407-3  
; Sequence 3, Application US/09115407A  
; Patent No. 6410228  
; GENERAL INFORMATION:  
; APPLICANT: SCHWARTZ, ROBERT J.  
; APPLICANT: EASTMAN, ERIC M.  
; APPLICANT: LI, XUYANG  
; APPLICANT: NORDSTROM, JEFF  
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SYNTHETIC  
; TITLE OF INVENTION: CELL-OR-TISSUE-SPECIFIC TRANSCRIPTIONAL  
; TITLE OF INVENTION: REGULATORY REGIONS  
; FILE REFERENCE: 235/238  
; CURRENT APPLICATION NUMBER: US/09/115,407A  
; CURRENT FILING DATE: 1998-07-14  
; EARLIER APPLICATION NUMBER: US 60/052,403  
; EARLIER FILING DATE: 1997-07-14  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 11  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: E-box binding site recognized by basic-helix-loop-helix  
; OTHER INFORMATION: (bHLH) transcription factors.  
US-09-115-407-3

Query Match 31.0%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CACCTGCTG 14  
| | | | |  
Db 3 CACCTGCTG 11

RESULT 47

US-09-772-719B-73/c  
; Sequence 73, Application US/09772719B  
; Patent No. 6770438  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; Pastorekova, Silvia  
; Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 465 California Street, Suite 450  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/772,719B  
; FILING DATE: 30-Jan-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,049  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lauder, Leona L.  
; REGISTRATION NUMBER: 30,863  
; REFERENCE/DOCKET NUMBER: D-0021.3A-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-981-2034  
; TELEFAX: 415-981-0332  
; INFORMATION FOR SEQ ID NO: 73:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; DESCRIPTION: 5' donor consensus splice sequence  
; SEQUENCE DESCRIPTION: SEQ ID NO: 73:  
US-09-772-719B-73

Query Match 31.0%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCTGCT 13  
| | | | |  
Db 9 CCACCTGCT 1

RESULT 48

US-10-286-387-30  
; Sequence 30, Application US/10286387  
; Patent No. 6936443  
; GENERAL INFORMATION:  
; APPLICANT: Cytoc Corporation  
; TITLE OF INVENTION: Detection and Typing of Human Papillomavirus Using PNA Probes  
; FILE REFERENCE: cym-035Cp  
; CURRENT APPLICATION NUMBER: US/10/286,387  
; CURRENT FILING DATE: 2003-02-28  
; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 30  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: PNA probe  
US-10-286-387-30

Query Match 31.0%; Score 9; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GCTGTGTGA 19  
| | | | |  
Db 1 GCTGTGTGA 9

RESULT 49

US-08-035-928-15/c  
; Sequence 15, Application US/08035928  
; Patent No. 5538844  
; GENERAL INFORMATION:  
; APPLICANT: Duyao, Mabel P.  
; APPLICANT: MacDonald, Marcy E.  
; APPLICANT: Gusella, James F.  
; TITLE OF INVENTION: A No. 5538844el Transport Protein Gene from  
; TITLE OF INVENTION: the Huntington's Disease Region  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1225 Connecticut Avenue N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/035,928  
; FILING DATE: 19930323  
; CLASSIFICATION: 435  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 466-0800  
; TELEFAX: (202) 833-8716  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
US-08-035-928-15

Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 55;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATCCACCTGCTG 14  
| | | | |  
Db 12 ACCACCTACTG 1

RESULT 50

US-08-250-740-29  
; Sequence 29, Application US/08250740  
; Patent No. 5686240  
; GENERAL INFORMATION:  
; APPLICANT: Schuchman, Edward H.  
; APPLICANT: Desnick, Robert J.

```
;
; TITLE OF INVENTION: Acid Sphingomyelinase Gene and Diagnosis
; TITLE OF INVENTION: of Niemann-Pick Disease
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,740
; FILING DATE: 27-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30742
; REFERENCE/DOCKET NUMBER: 6923-038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-250-740-29

Query Match 30.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 CTGTGTGACCTG 23
Db 1 CTGTGCCACCTG 12

RESULT 51
US-07-695-472B-9
; Sequence 9, Application US/07695472B
; Patent No. 5773278
; GENERAL INFORMATION:
; APPLICANT: Schuchman, Edward H.
; APPLICANT: Desnick, Robert J.
; TITLE OF INVENTION: The Acid Sphingomyelinase Gene and
; TITLE OF INVENTION: Diagnosis of Niemann-Pick Disease
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/695,472B
; FILING DATE: 19910503
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
```

```
;
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6923-014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 7908864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..12
; US-07-695-472B-9

Query Match 30.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 CTGTGTGACCTG 23
Db 1 CTGTGCCACCTG 12

RESULT 52
US-08-410-540-30/c
; Sequence 30, Application US/08410540
; Patent No. 5807678
; GENERAL INFORMATION:
; APPLICANT: Miller, Walter L.
; APPLICANT: Lin, Dong
; APPLICANT: Strauss III, Jerome F.
; TITLE OF INVENTION: IDENTIFICATION OF GENE MUTATIONS
; TITLE OF INVENTION: ASSOCIATED WITH CONGENITAL LIPOID ADRENAL HYPERPLASIA
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,540
; FILING DATE: 23-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard L.
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-238/00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415 853 5070
; TELEFAX: 415 857 0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-410-540-30
```

Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 55;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 18 GACCTGGTAAAT 29  
Db 12 GACCTGGTTGAT 1

RESULT 53

US-08-441-887A-69  
; Sequence 69, Application US/08441887A  
; Patent No. 5837832  
; GENERAL INFORMATION:  
; APPLICANT: Chee, Mark  
; APPLICANT: Cronin, Maureen T.  
; APPLICANT: Fodor, Stephen P.A.  
; APPLICANT: Huang, Xiaohua X.  
; APPLICANT: Hubbell, Earl A.  
; APPLICANT: Lipshutz, Robert J.  
; APPLICANT: Lobban, Peter E.  
; APPLICANT: Morris, Macdonald S.  
; APPLICANT: Sheldon, Edward L.  
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on  
; TITLE OF INVENTION: Biological Chips  
; NUMBER OF SEQUENCES: 360  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,887A  
; FILING DATE: 16-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/143,312  
; FILING DATE: 26-OCT-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/082,937  
; FILING DATE: 25-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Liebeschuetz, Joseph O.  
; REGISTRATION NUMBER: 37,505  
; REFERENCE/DOCKET NUMBER: 018547-004160US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-326-2400  
; TELEFAX: 650-326-2422  
; INFORMATION FOR SEQ ID NO: 69:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (probe)  
US-08-441-887A-69

Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 55;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 13 TGTGTGACCTGG 24  
Db 1 TGTGTGTGCTGG 12

RESULT 54

US-09-106-375-9  
; Sequence 9, Application US/09106375  
; Patent No. 6541218  
; GENERAL INFORMATION:  
; APPLICANT: Schuchman, Edward H.  
; APPLICANT: Desnick, Robert J.  
; TITLE OF INVENTION: The Acid Sphingomyelinase Gene and  
; TITLE OF INVENTION: Diagnosis of Niemann-Pick Disease  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/106,375  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/695,472  
; FILING DATE: 03-MAY-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 6923-014  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 790864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..12  
US-09-106-375-9

Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 55;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 12 CTGTGTGACCTG 23  
Db 1 CTGTGCCACCTG 12

RESULT 55

US-09-374-174B-3  
; Sequence 3, Application US/09374174B  
; Patent No. 6554985  
; GENERAL INFORMATION:  
; APPLICANT: Ruiz-Martinez, Maria C.  
; APPLICANT: Berka, Jan  
; APPLICANT: Simpson, John W.  
; TITLE OF INVENTION: Methods and Formulations for the Separation of  
; TITLE OF INVENTION: Biological Macromolecules  
; FILE REFERENCE: Cura-31: MegabACE (15966-531)  
; CURRENT APPLICATION NUMBER: US/09/374,174B  
; CURRENT FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: USSN 60/107,798



```

; PRIOR FILING DATE: 1998-11-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Bacteriophage M13mpl8
US-09-374-174B-3

Query Match      30.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 TCCACCTGCTGT 15
      |||||||
Db      1 TCCACCTGGTTT 12

RESULT 56
US-09-163-485-18
; Sequence 18, Application US/09163485
; Patent No. 6277571
; GENERAL INFORMATION:
; APPLICANT: FILLMORE, HELEN
; APPLICANT: BROADDUS, WILLIAM
; APPLICANT: GILLIES, GEORGE
; TITLE OF INVENTION: SEQUENTIAL CONSENSUS REGION-DIRECTED AMPLIFICATION OF
; TITLE OF INVENTION: KNOWN AND NOVEL MEMBERS OF GENE FAMILIES
; FILE REFERENCE: VCUIP4B
; CURRENT APPLICATION NUMBER: US/09/163,485
; CURRENT FILING DATE: 1998-08-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide, consensus sequence from human
; OTHER INFORMATION: matrix metalloproteinases
US-09-163-485-18

Query Match      29.7%; Score 8.6; DB 1; Length 12;
Best Local Similarity 88.9%; Pred. No. 60;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      9 CTGCTGTGT 17
      |||||||
Db      4 CTGCTGTGY 12

RESULT 57
US-08-367-175A-23
; Sequence 23, Application US/08367175A
; Patent No. 5631115
; GENERAL INFORMATION:
; APPLICANT: OHTSUKA, Eiko
; APPLICANT: KOIZUMI, Makoto
; TITLE OF INVENTION: Looped, hairpin ribozyme
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FRISHAUF,HOLTZ,GOODMAN,
; ADDRESSEE: LANGER & CHICK, P.C.
; STREET: 767 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10017-2023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/367,175A
; FILING DATE: 29 Dec. 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: GOODMAN, Herbert
; REGISTRATION NUMBER: 17081
; REFERENCE/DOCKET NUMBER: 920081
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)319-4900
; TELEFAX: (212)319-5101
; TELEX: 236268
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: mRNA
; HYPOTHETICAL: N
; ANTI-SENSE: N
US-08-367-175A-23

Query Match      29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 49;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      10 TGCTGTGTGA 19
      :|:|:|:|
Db      1 UGUUGUGUGA 10

RESULT 58
US-08-388-353-78/c
; Sequence 78, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid

```

; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-388-353-78

Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 49;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTG 14  
||| |||||  
Db 10 CCATCTGCTG 1

RESULT 59

US-08-388-353-381/c  
; Sequence 381, Application US/08388353  
; Patent No. 6010895  
; GENERAL INFORMATION:  
; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.  
; APPLICANT: Crowe, Suzanne  
; APPLICANT: Cooper, David  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,353  
; FILING DATE: 14-FEB-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DiGiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 9606  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 381:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-388-353-381

Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 49;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGT 17  
||| |||||  
Db 10 CCTGGTGTGT 1

RESULT 60

US-08-388-353-782  
; Sequence 782, Application US/08388353  
; Patent No. 6010895  
; GENERAL INFORMATION:

; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.  
; APPLICANT: Crowe, Suzanne  
; APPLICANT: Cooper, David  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,353  
; FILING DATE: 14-FEB-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DiGiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 9606  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 782:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-388-353-782

Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 49;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTGCTGTGTG 18  
||| |||||  
Db 1 CTGTTGTGTG 10

RESULT 61

US-08-388-353-783  
; Sequence 783, Application US/08388353  
; Patent No. 6010895  
; GENERAL INFORMATION:  
; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.  
; APPLICANT: Crowe, Suzanne  
; APPLICANT: Cooper, David  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25





```
; Sequence 381, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 381:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-381

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGT 17
Db 10 CCTGCTGTGT 1

RESULT 65
US-08-488-551B-782
; Sequence 782, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
```

```
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 782:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-782

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTGCTGTGTG 18
Db 1 CTGTTGTGTG 10

RESULT 66
US-08-488-551B-783
; Sequence 783, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 782:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-782
```

```
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 783:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-783

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 TGCTGTGTGA 19
Db 1 TGTGTGTGA 10

RESULT 67
US-08-488-551B-784
; Sequence 784, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
;
```

```
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 784:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-784

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCTGTGTGAC 20
Db 1 GTTGTGTGAC 10

RESULT 68
US-09-245-041-129/c
; Sequence 129, Application US/09245041
; Patent No. 6274339
; GENERAL INFORMATION:
; APPLICANT: Moore, K.
; APPLICANT: Nagle, D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT
; OF BODY WEIGHT DISORDERS INCLUDING OBESITY
; FILE REFERENCE: 7853-136
; CURRENT APPLICATION NUMBER: US/09/245,041
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/093,630
; EARLIER FILING DATE: 1998-07-21
; EARLIER APPLICATION NUMBER: 60/104,978
; EARLIER FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 129
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-245-041-129

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CTGTGTGACC 21
Db 10 CTGTGTGTCC 1

RESULT 69
US-08-870-511-13
; Sequence 13, Application US/08870511
; Patent No. 6287763
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank
; APPLICANT: Huszar, Dennis
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE
; REGULATION OF BODY WEIGHT
; FILE REFERENCE: 7853-083
; CURRENT APPLICATION NUMBER: US/08/870,511
; CURRENT FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
;
```

```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-08-870-511-13

Query Match      29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 ATCCACCTGC 12
Db      1 ATCCACTTGC 10
      ||||| |||

RESULT 70
US-09-508-753B-118/c
; Sequence 118, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 118
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-118

Query Match      29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 GTGACCTGGT 25
Db      10 GTGACCTTGT 1
      ||||| |||

RESULT 71
US-10-042-111-8
; Sequence 8, Application US/10042111
; Patent No. 6551476
; GENERAL INFORMATION:
; APPLICANT: ZHEJIANG ACADEMY OF AGRICULTURAL SCIENCES
; APPLICANT: CHEN, Jingjing
; TITLE OF INVENTION: A METHOD FOR CONTROLLING RATIO OF PROTEINS/LIPIDS IN CROP SEEDS
; FILE REFERENCE: ref.
; CURRENT APPLICATION NUMBER: US/10/042,111
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: CN 99124511.3
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: primer
US-10-042-111-8
```

```

Query Match      29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CATCCACCTG 11
Db      1 CATCCCCCTG 10
      ||||| |||

RESULT 72
US-09-358-055B-130/c
; Sequence 130, Application US/09358055B
; Patent No. 6713277
; GENERAL INFORMATION:
; APPLICANT: Moore, K.
; APPLICANT: Nagle, D.L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS INCLUDING
; TITLE OF INVENTION: OBESITY
; FILE REFERENCE: 7853-151
; CURRENT APPLICATION NUMBER: US/09/358,055B
; CURRENT FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 09/245,041
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 130
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-358-055B-130

Query Match      29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CTGTGTGACC 21
Db      10 CTGTGTGTCC 1
      ||||| |||

RESULT 73
US-09-893-238-129/c
; Sequence 129, Application US/09893238
; Patent No. 6727348
; GENERAL INFORMATION:
; APPLICANT: Moore, K.
; APPLICANT: Nagle, D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; FILE REFERENCE: 7853-237
; CURRENT APPLICATION NUMBER: US/09/893,238
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/245,041
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/093,630
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: 60/104,978
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 129
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-893-238-129

Query Match      29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 49;
```

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CTGTGTGACC 21  
|||||

Db 10 CTGTGTGTCC 1

RESULT 74  
US-08-800-036-15  
; Sequence 15, Application US/08800036  
; Patent No. 5830661  
; GENERAL INFORMATION:  
; APPLICANT: Sarfarazi, Mansoor  
; TITLE OF INVENTION: Diagnosis and Treatment of Glaucoma  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David E. Brook, Esq.  
; STREET: Hamilton, Brook, Smith & Reynolds, Two  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02173

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/800,036  
FILING DATE: 13-FEB-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: UCT97-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540

INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-800-036-15

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 58;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 ACCTGGTAAA 28  
|||||

Db 1 ACCAGGTAAA 10

RESULT 75  
US-08-481-658B-86/c  
; Sequence 86, Application US/08481658B  
; Patent No. 5955075  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 6 Mariposa Court  
; CITY: Tiburon  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94920

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/481,658B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/260,190  
FILING DATE: 15-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L.  
REGISTRATION NUMBER: 30,863  
REFERENCE/DOCKET NUMBER: D-0021.3E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-435-2034  
TELEFAX: 415-435-0727

INFORMATION FOR SEQ ID NO: 86:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
DESCRIPTION: 3' acceptor consensus splice sequence  
US-08-481-658B-86

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 58;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGT 17  
|||||

Db 10 CCTTCTGTGT 1

RESULT 76  
US-08-926-492-15  
; Sequence 15, Application US/08926492  
; Patent No. 5962230  
; GENERAL INFORMATION:  
; APPLICANT: Sarfarazi, Mansoor  
; TITLE OF INVENTION: Diagnosis and Treatment of Glaucoma  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David E. Brook, Esq.  
; STREET: Hamilton, Brook, Smith & Reynolds, Two  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02173

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/926,492  
FILING DATE: 10-SEP-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/800,036  
FILING DATE: 13-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: UCT97-01A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540





;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/485,862B  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/477,504  
;; FILING DATE: 07-JUN-1995  
;; APPLICATION NUMBER: US 08/260,190  
;; FILING DATE: 15-JUN-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: lauder, Leona L.  
;; REGISTRATION NUMBER: 30,863  
;; REFERENCE/DOCKET NUMBER: D-0021.3D  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-435-2034  
;; TELEFAX: 415-435-0727  
;; INFORMATION FOR SEQ ID NO: 86:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 11 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; DESCRIPTION: 3' acceptor consensus splice sequence  
US-08-485-862B-86

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 58;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGT 17  
||| |||||  
Db 10 CCTTCTGTGT 1

RESULT 80  
US-08-787-739-86/c  
; Sequence 86, Application US/08787739  
; Patent No. 6027887  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 96  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 369 Pine Street, Suite 610  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/787,739  
; FILING DATE: 24-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,049  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/486,756  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/477,504  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/481,658  
;; FILING DATE: 07-JUN-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/485,862  
;; FILING DATE: 07-JUN-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/485,863  
;; FILING DATE: 07-JUN-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/487,077  
;; FILING DATE: 07-JUN-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Lauder, Leona L.  
;; REGISTRATION NUMBER: 30,863  
;; REFERENCE/DOCKET NUMBER: D-0021.4  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-981-2034  
;; TELEFAX: 415-981-0332  
;; INFORMATION FOR SEQ ID NO: 86:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 11 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: double  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; DESCRIPTION: 3' acceptor consensus splice sequence  
US-08-787-739-86

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 58;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGT 17  
||| |||||  
Db 10 CCTTCTGTGT 1

RESULT 81  
US-09-048-505-15  
; Sequence 15, Application US/09048505  
; Patent No. 6046009  
; GENERAL INFORMATION:  
; APPLICANT: Sarfarazi, Mansoor  
; TITLE OF INVENTION: Diagnosis and Treatment of Glaucoma  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David E. Brook, Esq.  
; STREET: Hamilton, Brook, Smith & Reynolds, Two  
; STREET: Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02421-4799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/048,505  
; FILING DATE: 26-MAR-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/926,492  
; FILING DATE: 10-SEP-97  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/800,036  
; FILING DATE: 13-FEB-97  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brook, David E.  
; REGISTRATION NUMBER: 22,592  
; REFERENCE/DOCKET NUMBER: UCT97-01A2  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (781) 861-6240  
; TELEFAX: (781) 861-9540  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-048-505-15

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 58;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 ACCTGGTAAA 28  
||| |||||  
Db 1 ACCAGGTAAA 10

RESULT 82  
US-08-487-077A-86/c  
; Sequence 86, Application US/08487077A  
; Patent No. 6069242  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 6 Mariposa Court  
; CITY: Tiburon  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94920

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487,077A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/260,190  
; FILING DATE: 15-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lauder, Leona L.  
; REGISTRATION NUMBER: 30,863  
; REFERENCE/DOCKET NUMBER: D-0021.3H  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-435-2034  
; TELEFAX: 415-435-0727  
; INFORMATION FOR SEQ ID NO: 86:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; DESCRIPTION: 3' acceptor consensus splice sequence  
US-08-487-077A-86

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 58;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGT 17  
||| |||||  
Db 10 CCTTCTGTGT 1

RESULT 83  
US-08-485-863A-86/c  
; Sequence 86, Application US/08485863A  
; Patent No. 6093548  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 6 Mariposa Court  
; CITY: Tiburon  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94920  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,863A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/260,190  
; FILING DATE: 15-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lauder, Leona L.  
; REGISTRATION NUMBER: 30,863  
; REFERENCE/DOCKET NUMBER: D-0021.3G  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-435-2034  
; TELEFAX: 415-435-0727  
; INFORMATION FOR SEQ ID NO: 86:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; DESCRIPTION: 3' acceptor consensus splice sequence  
US-08-485-863A-86

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 58;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGT 17  
||| |||||  
Db 10 CCTTCTGTGT 1

RESULT 84  
US-08-485-049D-86/c  
; Sequence 86, Application US/08485049D  
; Patent No. 6204370  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 369 Pine Street  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,049D  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/260,190  
FILING DATE: 15-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L.  
REGISTRATION NUMBER: 30,863  
REFERENCE/DOCKET NUMBER: D-0021.3E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-981-2034  
TELEFAX: 415-981-0332  
INFORMATION FOR SEQ ID NO: 86:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
DESCRIPTION: 3' acceptor consensus splice sequence  
US-08-485-049D-86

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 58;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGT 17  
||| |||||  
Db 10 CCTTCTGTGT 1

RESULT 85  
US-09-178-115-86/c  
Sequence 86, Application US/09178115  
Patent No. 6297041  
GENERAL INFORMATION:  
APPLICANT: Zavada, Jan  
APPLICANT: Pastorekova, Silvia  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
FILE REFERENCE: D-0021.5A  
CURRENT APPLICATION NUMBER: US/09/178,115  
CURRENT FILING DATE: 1998-10-23  
EARLIER APPLICATION NUMBER: 09/177,776  
EARLIER FILING DATE: 1998-10-23  
EARLIER APPLICATION NUMBER: 08/787,739  
EARLIER FILING DATE: 1997-01-24  
EARLIER APPLICATION NUMBER: 08/485,049  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/486,756  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/477,504  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/481,658  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/485,862  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/485,863  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/487,077  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/260,190  
EARLIER FILING DATE: 1994-06-15  
EARLIER APPLICATION NUMBER: 08/177,093  
EARLIER FILING DATE: 1993-12-30  
EARLIER APPLICATION NUMBER: 07/964,589  
EARLIER FILING DATE: 1992-10-21  
EARLIER APPLICATION NUMBER: PV-709-92  
EARLIER FILING DATE: 1992-03-11  
NUMBER OF SEQ ID NOS: 116  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 86  
LENGTH: 11  
TYPE: DNA  
ORGANISM: HUMAN  
US-09-177-776-86

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 58;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGT 17  
||| |||||  
Db 10 CCTTCTGTGT 1

EARLIER FILING DATE: 1992-10-21  
EARLIER APPLICATION NUMBER: PV-709-92  
EARLIER FILING DATE: 1992-03-11  
NUMBER OF SEQ ID NOS: 116  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 86  
LENGTH: 11  
TYPE: DNA  
ORGANISM: HUMAN  
US-09-178-115-86

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 58;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGT 17  
||| |||||  
Db 10 CCTTCTGTGT 1

RESULT 86  
US-09-177-776-86/c  
Sequence 86, Application US/09177776A  
Patent No. 6297051  
GENERAL INFORMATION:  
APPLICANT: Zavada, Jan  
APPLICANT: Pastorekova, Silvia  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
FILE REFERENCE: D-0021.5A  
CURRENT APPLICATION NUMBER: US/09/177,776A  
CURRENT FILING DATE: 1998-10-23  
EARLIER APPLICATION NUMBER: 08/787,739  
EARLIER FILING DATE: 1997-01-24  
EARLIER APPLICATION NUMBER: 08/485,049  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/486,756  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/477,504  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/481,658  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/485,862  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/485,863  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/487,077  
EARLIER FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: 08/260,190  
EARLIER FILING DATE: 1994-06-15  
EARLIER APPLICATION NUMBER: 08/177,093  
EARLIER FILING DATE: 1993-12-30  
EARLIER APPLICATION NUMBER: 07/964,589  
EARLIER FILING DATE: 1992-10-21  
EARLIER APPLICATION NUMBER: PV-709-92  
EARLIER FILING DATE: 1992-03-11  
NUMBER OF SEQ ID NOS: 116  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 86  
LENGTH: 11  
TYPE: DNA  
ORGANISM: HUMAN  
US-09-177-776-86



```

RESULT 87
US-09-249-155A-113
; Sequence 113, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 113
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-113

Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9 CTGCTGTGTG 18
      ||||| |||||
Db      1 CTGCTTTGTG 10

RESULT 88
US-09-249-155A-285
; Sequence 285, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 285
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-285

Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9 CTGCTGTGTG 18
      ||||| |||||
Db      1 CTGCTTTGTG 10

RESULT 89
US-09-772-719B-86/c
; Sequence 86, Application US/09772719B
; Patent No. 6770438
; GENERAL INFORMATION:
```

```

; APPLICANT: Zavada, Jan
; Pastorekova, Silvia
; Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 465 California Street, Suite 450
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/772,719B
; FILING DATE: 30-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,049
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3A-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-981-2034
; TELEFAX: 415-981-0332
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: 3' acceptor consensus splice sequence
; SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-09-772-719B-86

Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 CCTGCTGTGT 17
      ||| |||||
Db      10 CCTTCTGTGT 1

RESULT 90
US-08-435-350-76/c
; Sequence 76, Application US/08435350
; Patent No. 5599704
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: TREATMENT OF BREAST CANCER
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,350
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936,531
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 197/245
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-350-76

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCCACCT 10
Db 10 CCATCCACTT 1

RESULT 91
US-09-281-418-141
; Sequence 141, Application US/09281418
; Patent No. 6287769
; GENERAL INFORMATION:
; APPLICANT: Inoue, Takakazu
; TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA F
; TITLE OF INVENTION: agment, Method of Assaying Microorganisms, Method of Analyzing Mi
; TITLE OF INVENTION: nisms and Method of Assaying Contaminant
; FILE REFERENCE: 9982-7
; CURRENT APPLICATION NUMBER: US/09/281,418
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: JP/1998/87651
; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: JP/1999/69694
; EARLIER FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 216
; SEQ ID NO 141
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-281-418-141

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CACCTGCTGT 15
Db 1 CTCCTGCTGT 10

RESULT 92
US-09-281-418-191/c
; Sequence 191, Application US/09281418
; Patent No. 6287769
; GENERAL INFORMATION:
; APPLICANT: Inoue, Takakazu
; TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA F
```

```

; TITLE OF INVENTION: agment, Method of Assaying Microorganisms, Method of Analyzing Mic
; TITLE OF INVENTION: nisms and Method of Assaying Contaminant
; FILE REFERENCE: 9982-7
; CURRENT APPLICATION NUMBER: US/09/281,418
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: JP/1998/87651
; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: JP/1999/69694
; EARLIER FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 216
; SEQ ID NO 191
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-281-418-191

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTG 14
Db 11 CCACCTCCTG 2

RESULT 93
US-09-874-601-167
; Sequence 167, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD
; TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/874,601
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 167
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: ().{ }
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-167

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 70.0%; Pred. No. 66;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCCACCTGCT 13
Db 1 UCCACCAGCU 10

RESULT 94
US-09-875-453B-77
; Sequence 77, Application US/09875453B
; Patent No. 683856
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsuh P.
```

```
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135.US00
; CURRENT APPLICATION NUMBER: US/09/875,453B
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 77
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-875-453B-77
```

```
Query Match          29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 20 CCTGGTAAAT 29
      |||||
Db 3 CCTGATAAAT 12
```

```
RESULT 95
US-08-634-350-11
; Sequence 11, Application US/08634350
; Patent No. 5911982
; GENERAL INFORMATION:
; APPLICANT: Chao, Yu-Chan
; TITLE OF INVENTION: H2-1 VIRUS PERSISTENCE-ASSOCIATED
; TITLE OF INVENTION: GENE 1(pag1) PROMOTER, USES
; TITLE OF INVENTION: THEREFOR, AND COMPOSITIONS
; TITLE OF INVENTION: CONTAINING SAME OR PRODUCTS
; TITLE OF INVENTION: THEREFROM
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/634,350
; FILING DATE: 18-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, William F.
; REGISTRATION NUMBER: 28,029
; REFERENCE/DOCKET NUMBER: 516450-2008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
```

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-634-350-11
```

```
Query Match          27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 21 CTGGTAAA 28
      |||||
Db 3 CTGGTAAA 10
```

```
RESULT 96
US-08-388-353-39
; Sequence 39, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-39
```

```
Query Match          27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 8 CCTGCTGT 15
      |||||
Db 3 CCTGCTGT 10
```

```
RESULT 97
US-08-388-353-40
; Sequence 40, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
```

APPLICANT: Deacon, Nicholas J.  
APPLICANT: Learmont, Jennifer C.  
APPLICANT: McPhee, Dale A.  
APPLICANT: Crowe, Suzanne  
APPLICANT: Cooper, David  
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
NUMBER OF SEQUENCES: 800  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: United States  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,353  
FILING DATE: 14-FEB-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: DiGiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9606  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-388-353-40

Query Match 27.6%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCTGCTGT 15  
|||||  
Db 2 CCTGCTGT 9

RESULT 98  
US-08-388-353-41  
Sequence 41, Application US/08388353  
Patent No. 6010895  
GENERAL INFORMATION:  
APPLICANT: Deacon, Nicholas J.  
APPLICANT: Learmont, Jennifer C.  
APPLICANT: McPhee, Dale A.  
APPLICANT: Crowe, Suzanne  
APPLICANT: Cooper, David  
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
NUMBER OF SEQUENCES: 800  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: United States  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,353  
FILING DATE: 14-FEB-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: DiGiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9606  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-388-353-41

Query Match 27.6%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCTGCTGT 15  
|||||  
Db 1 CCTGCTGT 8

RESULT 99  
US-08-388-353-785  
Sequence 785, Application US/08388353  
Patent No. 6010895  
GENERAL INFORMATION:  
APPLICANT: Deacon, Nicholas J.  
APPLICANT: Learmont, Jennifer C.  
APPLICANT: McPhee, Dale A.  
APPLICANT: Crowe, Suzanne  
APPLICANT: Cooper, David  
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
NUMBER OF SEQUENCES: 800  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: United States  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,353  
FILING DATE: 14-FEB-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: DiGiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9606  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 785:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

```
US-08-388-353-785
Query Match      27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13 TGTGTGAC 20
Db      2 TGTGTGAC 9

RESULT 100
US-08-388-353-786
; Sequence 786, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 786:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-786

Query Match      27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13 TGTGTGAC 20
Db      1 TGTGTGAC 8

RESULT 101
US-08-388-353-788
; Sequence 788, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
```

```
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 788:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-788

Query Match      27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13 TGTGTGAC 20
Db      1 TGTGTGAC 8

RESULT 102
US-08-488-551B-39
; Sequence 39, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
```



```

; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-39

Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCTGCTGT 15
Db 3 CCTGCTGT 10

RESULT 103
US-08-488-551B-40
; Sequence 40, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-41

Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCTGCTGT 15
Db 2 CCTGCTGT 9

RESULT 104
US-08-488-551B-41
; Sequence 41, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-41

Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-39

Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCTGCTGT 15
Db 3 CCTGCTGT 10

RESULT 103
US-08-488-551B-40
; Sequence 40, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
```

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCTGCTGT 15  
|||||

Db 1 CCTGCTGT 8

RESULT 105  
US-08-488-551B-785  
; Sequence 785, Application US/08488551B  
; Patent No. 6015661  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas J. Deacon  
; APPLICANT: Dale A. McPhee  
; APPLICANT: David Cooper  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 841  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
; STREET: 400 GARDEN CITY PLAZA  
; CITY: GARDEN CITY  
; STATE: NEW YORK  
; COUNTRY: U.S.A.  
; ZIP: 11530-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,551B  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PM3864 (AU)  
; FILING DATE: 14-FEB-1994  
; APPLICATION NUMBER: PM4002 (AU)  
; FILING DATE: 21-FEB-1994  
; APPLICATION NUMBER: PN0284 (AU)  
; FILING DATE: 23-DEC-1994  
; APPLICATION NUMBER: US 08/388,353  
; FILING DATE: 14-FEB-1995  
; APPLICATION NUMBER: PN3021/95  
; FILING DATE: 17-MAY-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FRANK S. DIGIGLIO  
; REFERENCE/DOCKET NUMBER: 9606Z  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; INFORMATION FOR SEQ ID NO: 785:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-488-551B-785

Query Match 27.6%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TGTGTGAC 20  
|||||

Db 2 TGTGTGAC 9

RESULT 106  
US-08-488-551B-786  
; Sequence 786, Application US/08488551B  
; Patent No. 6015661  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas J. Deacon

; APPLICANT: Dale A. McPhee  
; APPLICANT: David Cooper  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 841  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
; STREET: 400 GARDEN CITY PLAZA  
; CITY: GARDEN CITY  
; STATE: NEW YORK  
; COUNTRY: U.S.A.  
; ZIP: 11530-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,551B  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PM3864 (AU)  
; FILING DATE: 14-FEB-1994  
; APPLICATION NUMBER: PM4002 (AU)  
; FILING DATE: 21-FEB-1994  
; APPLICATION NUMBER: PN0284 (AU)  
; FILING DATE: 23-DEC-1994  
; APPLICATION NUMBER: US 08/388,353  
; FILING DATE: 14-FEB-1995  
; APPLICATION NUMBER: PN3021/95  
; FILING DATE: 17-MAY-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FRANK S. DIGIGLIO  
; REFERENCE/DOCKET NUMBER: 9606Z  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; INFORMATION FOR SEQ ID NO: 786:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-488-551B-786

Query Match 27.6%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TGTGTGAC 20  
|||||

Db 1 TGTGTGAC 8

RESULT 107  
US-08-488-551B-788  
; Sequence 788, Application US/08488551B  
; Patent No. 6015661  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas J. Deacon  
; APPLICANT: Dale A. McPhee  
; APPLICANT: David Cooper  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 841  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
; STREET: 400 GARDEN CITY PLAZA  
; CITY: GARDEN CITY  
; STATE: NEW YORK  
; COUNTRY: U.S.A.  
; ZIP: 11530-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,551B  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PM3864 (AU)  
; FILING DATE: 14-FEB-1994  
; APPLICATION NUMBER: PM4002 (AU)  
; FILING DATE: 21-FEB-1994  
; APPLICATION NUMBER: PN0284 (AU)  
; FILING DATE: 23-DEC-1994  
; APPLICATION NUMBER: US 08/388,353  
; FILING DATE: 14-FEB-1995  
; APPLICATION NUMBER: PN3021/95  
; FILING DATE: 17-MAY-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FRANK S. DIGIGLIO  
; REFERENCE/DOCKET NUMBER: 9606Z  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; INFORMATION FOR SEQ ID NO: 788:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-488-551B-788

Query Match 27.6%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TGTGTGAC 20  
|||||  
Db 1 TGTGTGAC 8

RESULT 108  
US-09-475-947A-279/c  
; Sequence 279, Application US/09475947A  
; Patent No. 6472154  
; GENERAL INFORMATION:  
; APPLICANT: Garner, Harold R.  
; APPLICANT: Wren, Jonathan D.  
; APPLICANT: Minna, John D.  
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes  
; FILE REFERENCE: UTSD0667  
; CURRENT APPLICATION NUMBER: US/09/475,947A  
; CURRENT FILING DATE: 1999-12-31  
; NUMBER OF SEQ ID NOS: 346  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 279  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: human  
US-09-475-947A-279

Query Match 27.6%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCCAC 8  
|||||  
Db 8 CCATCCAC 1

RESULT 109  
US-08-894-454-122  
; Sequence 122, Application US/08894454

; Patent No. 6544784  
; GENERAL INFORMATION:  
; APPLICANT: VAN DEN VEN, W.J.M.  
; APPLICANT: SCHOENMAKERS, H.F.P.M.  
; TITLE OF INVENTION: MULTIPLE-TUMOR ABERRENT GROWTH  
; TITLE OF INVENTION: GENES  
; NUMBER OF SEQUENCES: 164  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Webb Law Firm  
; STREET: 700 Koppers Building, 436 Seventh Avenue  
; CITY: Pittsburgh  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 15219-1818  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/894,454  
; FILING DATE: 15-AUG-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP/00716  
; FILING DATE: 19-FEB-1996  
; APPLICATION NUMBER: 95200390.3  
; FILING DATE: 17-FEB-1995  
; APPLICATION NUMBER: 95201951.1  
; FILING DATE: 14-JUL-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Johnson, Barbara E  
; REGISTRATION NUMBER: 31,198  
; REFERENCE/DOCKET NUMBER: 702-971100  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 412-471-8815  
; TELEFAX: 412-471-4094  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 122:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-894-454-122

Query Match 27.6%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCTGCTG 14  
|||||  
Db 3 ACCTGCTG 10

RESULT 110  
US-10-042-111-23/c  
; Sequence 23, Application US/10042111  
; Patent No. 6551476  
; GENERAL INFORMATION:  
; APPLICANT: ZHEJIANG ACADEMY OF AGRICULTURAL SCIENCES  
; APPLICANT: CHEN, Jinqing  
; TITLE OF INVENTION: A METHOD FOR CONTROLLING RATIO OF PROTEINS/LIPIDS IN CROP SEEDS  
; FILE REFERENCE: ref.  
; CURRENT APPLICATION NUMBER: US/10/042,111  
; CURRENT FILING DATE: 2002-05-08  
; PRIOR APPLICATION NUMBER: CN 99124511.3  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 23  
; LENGTH: 10  
; TYPE: DNA

```
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: primer
US-10-042-111-23

Query Match      27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 60;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 CTGCTGTG 16
Db      9 CTGCTGTG 2

RESULT 111
US-09-249-155A-106
; Sequence 106, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-106

Query Match      27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 69;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      12 CTGTGTGA 19
Db      2 CTGTGTGA 9

RESULT 112
US-08-836-734E-90/c
; Sequence 90, Application US/08836734E
; Patent No. 6846623
; GENERAL INFORMATION:
; APPLICANT: BECKMANN, JACQUES
; APPLICANT: RICHARD, ISABELLE
; TITLE OF INVENTION: LGMD GENE CODING FOR A CALCIUM DEPENDENT PROTEASE
; FILE REFERENCE: 960-29 AFMB2628AD/FL/SDU
; CURRENT APPLICATION NUMBER: US/08/836,734E
; CURRENT FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: PCT/EP95/04575
; PRIOR FILING DATE: 1995-11-21
; PRIOR APPLICATION NUMBER: EP 94402668.1
; PRIOR FILING DATE: 1994-11-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: MS Word
; SEQ ID NO 90
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(11)

; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: primer
US-10-042-111-23

Query Match      27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 69;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 CCACCTGC 12
Db      9 CCACCTGC 2

RESULT 113
US-09-793-146-36/c
; Sequence 36, Application US/09793146
; Patent No. 6919441
; GENERAL INFORMATION:
; APPLICANT: UHLMANN, EUGEN
; APPLICANT: BREIPOHL, GERHARD
; TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; FILE REFERENCE: 02481.1437-02
; CURRENT APPLICATION NUMBER: US/09/793,146
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: P 44 08 528.1
; PRIOR FILING DATE: 1994-03-14
; PRIOR APPLICATION NUMBER: 08/402,838
; PRIOR FILING DATE: 1995-03-13
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA
US-09-793-146-36

Query Match      26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 76;
Matches      9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      5 CCACCTGCTGT 15
Db      11 CGACCTGATGT 1

RESULT 114
US-09-793-146-41
; Sequence 41, Application US/09793146
; Patent No. 6919441
; GENERAL INFORMATION:
; APPLICANT: UHLMANN, EUGEN
; APPLICANT: BREIPOHL, GERHARD
; TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; FILE REFERENCE: 02481.1437-02
; CURRENT APPLICATION NUMBER: US/09/793,146
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: P 44 08 528.1
; PRIOR FILING DATE: 1994-03-14
; PRIOR APPLICATION NUMBER: 08/402,838
; PRIOR FILING DATE: 1995-03-13
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA
US-09-793-146-41
```

Query Match 26.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 76;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TCCACCTGCTG 14  
| | | | | | | |  
Db 1 TCCTCCTGCGG 11

RESULT 115  
US-09-793-146-59  
; Sequence 59, Application US/09793146  
; Patent No. 6919441  
; GENERAL INFORMATION:  
; APPLICANT: UHLMANN, EUGEN  
; APPLICANT: BREIPOHL, GERHARD  
; TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR  
; TITLE OF INVENTION: PREPARATION AND USE  
; FILE REFERENCE: 02481.1437-02  
; CURRENT APPLICATION NUMBER: US/09/793,146  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: P 44 08 528.1  
; PRIOR FILING DATE: 1994-03-14  
; PRIOR APPLICATION NUMBER: 08/402,838  
; PRIOR FILING DATE: 1995-03-13  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 59  
; LENGTH: 11  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA  
US-09-793-146-59

Query Match 26.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 76;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TCCACCTGCTG 14  
| | | | | | | |  
Db 1 TCCTCCTGCGG 11

RESULT 116  
US-09-793-146-60  
; Sequence 60, Application US/09793146  
; Patent No. 6919441  
; GENERAL INFORMATION:  
; APPLICANT: UHLMANN, EUGEN  
; APPLICANT: BREIPOHL, GERHARD  
; TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR  
; TITLE OF INVENTION: PREPARATION AND USE  
; FILE REFERENCE: 02481.1437-02  
; CURRENT APPLICATION NUMBER: US/09/793,146  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: P 44 08 528.1  
; PRIOR FILING DATE: 1994-03-14  
; PRIOR APPLICATION NUMBER: 08/402,838  
; PRIOR FILING DATE: 1995-03-13  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 60  
; LENGTH: 11  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA  
US-09-793-146-60

Query Match 26.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 76;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TCCACCTGCTG 14  
| | | | | | | |  
Db 1 TCCTCCTGCGG 11

RESULT 117  
5256558-12/c  
; Patent No. 5256558  
; APPLICANT: CORUZZUI, GLORIA M.; TSAI, FONG-YING  
; TITLE OF INVENTION: GENE ENCODING PLANT ASPARAGINE SYNTHETASE  
; NUMBER OF SEQUENCES: 17  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/514,816  
; FILING DATE: 26-APR-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 347,302  
; FILING DATE: 03-MAY-1989  
; SEQ ID NO:12:  
; LENGTH: 11  
5256558-12

Query Match 26.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 76;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCACCTGCTGT 15  
| | | | | | | |  
Db 11 CTACGTGCTGT 1

RESULT 118  
US-07-960-981-2/c  
; Sequence 2, Application US/07960981  
; Patent No. 5322801  
; GENERAL INFORMATION:  
; APPLICANT: Kingston, Robert E.  
; APPLICANT: Bunker, Christopher  
; TITLE OF INVENTION: Protein Partner Screening Assays and  
; TITLE OF INVENTION: Uses Thereof  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox  
; STREET: 1225 Connecticut Avenue  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/960,981  
; FILING DATE: 19921014  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cimbala, Michelle A.  
; REGISTRATION NUMBER: 33,851  
; REFERENCE/DOCKET NUMBER: 0609.3630004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 833-7533  
; TELEFAX: (202) 833-8716  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-07-960-981-2



Query Match 25.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 78;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCT 13  
    | | | | |  
Db 9 CCAGCTGCT 1

RESULT 119  
US-07-651-710A-40  
; Sequence 40, Application US/07651710A  
; Patent No. 5362864  
; GENERAL INFORMATION:  
; APPLICANT: Chua, Nam-Hai  
; TITLE OF INVENTION: Trans-Activating Factor-1  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/651,710A  
; FILING DATE: 19910206  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 3288-014  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 790-9090  
; TELEFAX: 212 8698864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 40:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: double  
; TOPOLOGY: unknown  
; MOLECULE TYPE: TAF-1 binding motif  
US-07-651-710A-40

Query Match 25.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 78;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 GTGACCTGG 24  
    | | | | |  
Db 1 GTGACGTGG 9

RESULT 120  
US-08-335-565A-21/c  
; Sequence 21, Application US/08335565A  
; Patent No. 5527671  
; GENERAL INFORMATION:  
; APPLICANT: Li, Kening  
; APPLICANT: Rouse, Douglas I.  
; APPLICANT: German, Thomas L.  
; TITLE OF INVENTION: ASSAY FOR VERTICILLIUM DAHLIAE  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Quarles and Brady  
; STREET: 1 South Pinckney St., PO BOX 2113  
; CITY: Madison

; STATE: WI  
; COUNTRY: USA  
; ZIP: 53701-2113  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/335,565A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seay, Nicholas J  
; REGISTRATION NUMBER: 27,386  
; REFERENCE/DOCKET NUMBER: 960296.93065  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 608-251-5000  
; TELEFAX: 608-251-9166  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-335-565A-21

Query Match 25.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 78;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 17 TGACCTGGT 25  
    | | | | |  
Db 10 TCACCTGGT 2

RESULT 121  
US-08-235-503B-24  
; Sequence 24, Application US/082355503B  
; Patent No. 5563036  
; GENERAL INFORMATION:  
; APPLICANT: Peterson, Michael G  
; APPLICANT: Baichwal, Vijay R  
; APPLICANT: Strulovici, Berta  
; TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA ASSAY  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/235,503B  
; FILING DATE: 29-APR-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Osman, Richard A  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: A-59332/RAO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:

;  
;  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; US-08-235-503B-24

Query Match 25.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 78;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCT 13  
||| |||||  
Db 2 CCATCTGCT 10

RESULT 122  
US-08-545-253A-7  
; Sequence 7, Application US/08545253A  
; Patent No. 5908978  
; GENERAL INFORMATION:  
; APPLICANT: O'Malley, David M.  
; APPLICANT: Sederoff, Ronald R.  
; APPLICANT: Grattapaglia, Dario  
; APPLICANT: Henry V. Amerson  
; APPLICANT: Phillip Wilcox  
; APPLICANT: E. George Kuhlman  
; TITLE OF INVENTION: METHODS FOR WITHIN FAMILY  
; TITLE OF INVENTION: SELECTION IN  
; TITLE OF INVENTION: WOODY PERENNIALS USING GENETIC MARKERS  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Kenneth D. Sibley  
; STREET: Post Office Drawer 34009  
; CITY: Charlotte  
; STATE: No. 5908978th Carolina  
; COUNTRY: U.S.A.  
; ZIP: 28234  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/545,253A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sibley, Kenneth D.  
; REGISTRATION NUMBER: 31,665  
; REFERENCE/DOCKET NUMBER: 5051-281  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919) 881-3140  
; TELEFAX: (919) 881-3175  
; TELEX: 575102  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; US-08-545-253A-7

Query Match 25.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 78;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTG 16  
||| |||||  
Db 2 CCAGCTGTG 10

RESULT 123  
US-08-265-484B-13/c  
; Sequence 13, Application US/08265484B  
; Patent No. 5998193  
; GENERAL INFORMATION:  
; APPLICANT: Keese, Paul  
; APPLICANT: Stapper, Marianne  
; APPLICANT: Perriman, Rhonda  
; TITLE OF INVENTION: Ribozymes With Optimized Hybridizing  
; TITLE OF INVENTION: Arms, Stems And Loops, tRNA Embedded  
; TITLE OF INVENTION: Ribozymes and Compositions Thereof  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/265,484B  
; FILING DATE: 24-JUN-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 45284  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other Nucleic Acid  
; US-08-265-484B-13

Query Match 25.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 78;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATCCACCT 10  
||| |||||  
Db 10 CATCCACTT 2

RESULT 124  
US-08-388-353-77/c  
; Sequence 77, Application US/08388353  
; Patent No. 6010895  
; GENERAL INFORMATION:  
; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.  
; APPLICANT: Crowe, Suzanne  
; APPLICANT: Cooper, David  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:

```
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-77

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

Qy      6 CACCTGCTG 14
Db      10 CATCTGCTG 2

RESULT 125
US-08-388-353-79/c
; Sequence 79, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
```

```
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-79

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

Qy      5 CCACCTGCT 13
Db      9 CCATCTGCT 1

RESULT 126
US-08-388-353-140/c
; Sequence 140, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-140

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

Qy      9 CTGCTGTGT 17
Db      10 CTGCTGTAT 2

RESULT 127
US-08-388-353-141/c
; Sequence 141, Application US/08388353
; Patent No. 6010895
```

;  
; GENERAL INFORMATION:  
; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.  
; APPLICANT: Crowe, Suzanne  
; APPLICANT: Cooper, David  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,353  
; FILING DATE: 14-FEB-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DiGiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 9606  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 141:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-388-353-141

Query Match 25.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 78;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTGCTGTGT 17  
| | | | | | | |  
Db 9 CTGCTGTAT 1

RESULT 128  
US-08-388-353-142/c  
; Sequence 142, Application US/08388353  
; Patent No. 6010895  
; GENERAL INFORMATION:  
; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.  
; APPLICANT: Crowe, Suzanne  
; APPLICANT: Cooper, David  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

;  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,353  
; FILING DATE: 14-FEB-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DiGiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 9606  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 142:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-388-353-142

Query Match 25.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 78;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ACCTGCTGT 15  
| | | | | | | |  
Db 10 AGCTGCTGT 2

RESULT 129  
US-08-388-353-143/c  
; Sequence 143, Application US/08388353  
; Patent No. 6010895  
; GENERAL INFORMATION:  
; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.  
; APPLICANT: Crowe, Suzanne  
; APPLICANT: Cooper, David  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,353  
; FILING DATE: 14-FEB-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DiGiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 9606  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 143:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

```

; MOLECULE TYPE: DNA (genomic)
US-08-388-353-143

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 ACCTGCTGT 15
Db      9 AGCTGCTGT 1

RESULT 130
US-08-388-353-380/c
; Sequence 380, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 380:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-380

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9 CTGCTGTGT 17
Db      10 CTGGTGTGT 2

RESULT 131
US-08-388-353-382/c
; Sequence 382, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
```

```

; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 382:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-382

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 CCTGCTGTG 16
Db      9 CCTGGTGTG 1

RESULT 132
US-08-388-353-770
; Sequence 770, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
```



```

; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 770:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-770

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 TGTGTGACC 21
Db 2 TGTGTGCCC 10

RESULT 133
US-08-388-353-771
; Sequence 771, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 771:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-771
```

```

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 TGTGTGACC 21
Db 1 TGTGTGCCC 9

RESULT 134
US-08-388-353-781
; Sequence 781, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 781:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-781

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTGCTGTGT 17
Db 2 CTGTTGTGT 10

RESULT 135
US-08-388-353-796
; Sequence 796, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
```

```

; TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES:  800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Scully, Scott, Murphy & Presser
; STREET:  400 Garden City Plaza
; CITY:  Garden City
; STATE:  New York
; COUNTRY:  United States
; ZIP:  11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Floppy disk
; COMPUTER:  IBM PC compatible
; OPERATING SYSTEM:  PC-DOS/MS-DOS
; SOFTWARE:  PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/08/388,353
; FILING DATE:  14-FEB-1995
; CLASSIFICATION:  424
; ATTORNEY/AGENT INFORMATION:
; NAME:  DiGiglio, Frank S.
; REGISTRATION NUMBER:  31,346
; REFERENCE/DOCKET NUMBER:  9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:  (516) 742-4343
; TELEFAX:  (516) 742-4366
; TELEX:  230 901 SANS UR
; INFORMATION FOR SEQ ID NO:  796:
; SEQUENCE CHARACTERISTICS:
; LENGTH:  10 base pairs
; TYPE:  nucleic acid
; STRANDEDNESS:  single
; TOPOLOGY:  linear
; MOLECULE TYPE:  DNA (genomic)
; US-08-388-353-796

Query Match      25.5%;  Score 7.4;  DB 1;  Length 10;
Best Local Similarity  88.9%;  Pred. No. 78;
Matches  8;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

QY      21 CTGGTAAAT 29
      |||||
Db      2 CTGGTAACT 10

RESULT 136
US-08-388-353-797
; Sequence 797, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT:  Deacon, Nicholas J.
; APPLICANT:  Learmont, Jennifer C.
; APPLICANT:  McPhee, Dale A.
; APPLICANT:  Crowe, Suzanne
; APPLICANT:  Cooper, David
; TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES:  800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Scully, Scott, Murphy & Presser
; STREET:  400 Garden City Plaza
; CITY:  Garden City
; STATE:  New York
; COUNTRY:  United States
; ZIP:  11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Floppy disk
; COMPUTER:  IBM PC compatible
; OPERATING SYSTEM:  PC-DOS/MS-DOS
; SOFTWARE:  PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/08/388,353
; FILING DATE:  14-FEB-1995
; CLASSIFICATION:  424
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME:  DiGiglio, Frank S.
; REGISTRATION NUMBER:  31,346
; REFERENCE/DOCKET NUMBER:  9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:  (516) 742-4343
; TELEFAX:  (516) 742-4366
; TELEX:  230 901 SANS UR
; INFORMATION FOR SEQ ID NO:  797:
; SEQUENCE CHARACTERISTICS:
; LENGTH:  10 base pairs
; TYPE:  nucleic acid
; STRANDEDNESS:  single
; TOPOLOGY:  linear
; MOLECULE TYPE:  DNA (genomic)
; US-08-388-353-797

Query Match      25.5%;  Score 7.4;  DB 1;  Length 10;
Best Local Similarity  88.9%;  Pred. No. 78;
Matches  8;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

QY      21 CTGGTAAAT 29
      |||||
Db      1 CTGGTAACT 9

RESULT 137
US-08-488-551B-77/c
; Sequence 77, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT:  Nicholas J. Deacon
; APPLICANT:  Dale A. McPhee
; APPLICANT:  David Cooper
; TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES:  841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
; STREET:  400 GARDEN CITY PLAZA
; CITY:  GARDEN CITY
; STATE:  NEW YORK
; COUNTRY:  U.S.A.
; ZIP:  11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Floppy disk
; COMPUTER:  IBM PC compatible
; OPERATING SYSTEM:  PC-DOS/MS-DOS
; SOFTWARE:  PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/08/488,551B
; FILING DATE:  07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:  PM3864 (AU)
; FILING DATE:  14-FEB-1994
; APPLICATION NUMBER:  PM4002 (AU)
; FILING DATE:  21-FEB-1994
; APPLICATION NUMBER:  PN0284 (AU)
; FILING DATE:  23-DEC-1994
; APPLICATION NUMBER:  US 08/388,353
; FILING DATE:  14-FEB-1995
; APPLICATION NUMBER:  PN3021/95
; FILING DATE:  17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME:  FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER:  9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:  (516) 742-4343
; TELEFAX:  (516) 742-4366
; INFORMATION FOR SEQ ID NO:  77:
; SEQUENCE CHARACTERISTICS:
; LENGTH:  10 base pairs
; TYPE:  nucleic acid
; STRANDEDNESS:  single
; TOPOLOGY:  linear

```

```
; MOLECULE TYPE: DNA
US-08-488-551B-77

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 CACCTGCTG 14
      ||| |||||
Db     10 CATCTGCTG 2

RESULT 138
US-08-488-551B-79/c
; Sequence 79, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-79

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 CCACCTGCT 13
      ||| |||||
Db      9 CCATCTGCT 1

RESULT 139
```

```
US-08-488-551B-140/c
; Sequence 140, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-140

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9 CTGCTGTGT 17
      ||||| |||
Db     10 CTGCTGTAT 2

RESULT 140
US-08-488-551B-141/c
; Sequence 141, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
```

```
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 141:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-141

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTGCTGTGT 17
Db 9 CTGCTGTAT 1

RESULT 141
US-08-488-551B-142/c
; Sequence 142, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
```

```
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 142:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-142

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ACCTGCTGT 15
Db 10 AGCTGCTGT 2

RESULT 142
US-08-488-551B-143/c
; Sequence 143, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
```

```

; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 143:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-143

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      7 ACCTGCTGT 15
      | | | | |
Db      9 AGCTGCTGT 1

RESULT 143
US-08-488-551B-380/c
; Sequence 380, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 380:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-380

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      8 CCTGCTGTG 16
      | | | | |
Db      9 CCTGGTGTG 1

RESULT 145
US-08-488-551B-770
; Sequence 770, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
```

```

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9 CTGCTGTGT 17
      | | | | |
Db      10 CTGGTGTGT 2

RESULT 144
US-08-488-551B-382/c
; Sequence 382, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 382:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-382

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 CCTGCTGTG 16
      | | | | |
Db      9 CCTGGTGTG 1

RESULT 145
US-08-488-551B-770
; Sequence 770, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
```



```
;
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 770:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-770

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 TGTGTGACC 21
Db 2 TGTGTGCC 10

RESULT 146
US-08-488-551B-771
; Sequence 771, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

```
;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 771:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-771

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 TGTGTGACC 21
Db 1 TGTGTGCC 9

RESULT 147
US-08-488-551B-781
; Sequence 781, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
```

```

; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 781:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-781

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTGCTGTGT 17
Db 2 CTGTTGTGT 10

RESULT 148
US-08-488-551B-796
; Sequence 796, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 796:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-796

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 21 CTGCTAAAT 29
Db 2 CTGCTAACT 10

RESULT 149
US-08-488-551B-797
; Sequence 797, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 797:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-797

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 21 CTGCTAAAT 29
Db 1 CTGCTAACT 9
```

```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-796

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 21 CTGCTAAAT 29
Db 2 CTGCTAACT 10

RESULT 149
US-08-488-551B-797
; Sequence 797, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 797:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-797

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 21 CTGCTAAAT 29
Db 1 CTGCTAACT 9
```

RESULT 150  
US-08-719-337-7  
; Sequence 7, Application US/08719337  
; Patent No. 6054634  
; GENERAL INFORMATION:  
; APPLICANT: O'Malley, David M.  
; APPLICANT: Sederoff, Ronald R.  
; APPLICANT: Grattapaglia, Dario  
; TITLE OF INVENTION: METHODS FOR WITHIN FAMILY SELECTION IN  
; TITLE OF INVENTION: WOODY PERENNIALS USING GENETIC MARKERS  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kenneth D. Sibley  
; STREET: Post Office Drawer 34009  
; CITY: Charlotte  
; STATE: No. 6054634th Carolina  
; COUNTRY: U.S.A.  
; ZIP: 28234  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/719,337  
; FILING DATE: 25-SEP-1996  
; CLASSIFICATION: 047  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/184,567  
; FILING DATE: 21-JAN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sibley, Kenneth D.  
; REGISTRATION NUMBER: 31,665  
; REFERENCE/DOCKET NUMBER: 5051-247  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919) 881-3140  
; TELEFAX: (919) 881-3175  
; TELEX: 575102  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-719-337-7  
  
Query Match 25.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 78;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 8 CCTGCTGTG 16  
|||  
Db 2 CCAGCTGTG 10  
  
RESULT 151  
US-08-765-257A-13/c  
; Sequence 13, Application US/08765257A  
; Patent No. 6107078  
; GENERAL INFORMATION:  
; APPLICANT: Keese, Paul  
; APPLICANT: Stapper, Marianne  
; APPLICANT: Perriman, Rhonda  
; TITLE OF INVENTION: Ribozymes With Optimized Hybridizing Arms,  
; TITLE OF INVENTION: Stems And Loops, tRNA Embedded Ribozymes  
; TITLE OF INVENTION: and Compositions Thereof  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham  
; STREET: 30 Rockefeller Plaza

; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH, 1.44Mb  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/765,257A  
; FILING DATE: June 24, 1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 45284  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 977 9550  
; TELEFAX: 212 977 9809  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other Nucleic Acid  
US-08-765-257A-13  
  
Query Match 25.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 78;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 CATCCACCT 10  
|||||||  
Db 10 CATCCACTT 2  
  
RESULT 152  
US-08-522-384-18  
; Sequence 18, Application US/08522384  
; Patent No. 6110667  
; GENERAL INFORMATION:  
; APPLICANT: LOPEZ-NIETO, CARLOS E  
; APPLICANT: NIGAM, SANJAY KUMAR  
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR  
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES  
; FILE REFERENCE: 2458-4029  
; CURRENT APPLICATION NUMBER: US/08/522,384  
; CURRENT FILING DATE: 1996-11-15  
; NUMBER OF SEQ ID NOS: 122  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Primer  
US-08-522-384-18  
  
Query Match 25.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 78;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 6 CACCTGCTG 14  
|||  
Db 1 CATCTGCTG 9  
  
RESULT 153  
US-08-522-384-120  
; Sequence 120, Application US/08522384  
; Patent No. 6110667

; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 120
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-120

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CACCTGCTG 14
||| |||||
DB 2 CATCTGCTG 10

RESULT 154
US-09-034-205-51/c
; Sequence 51, Application US/09034205
; Patent No. 6194149
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING
; TITLE OF INVENTION: STRUCTURE-BRIDGING OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/034,205
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: FORS-03268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-09-034-205-51

Query Match 25.5%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCTGTGTGA 19
||||| |||
DB 9 GCTGTCTGA 1

RESULT 155
US-08-934-097A-51/c
; Sequence 51, Application US/08934097A
; Patent No. 6210880
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce P.
; TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
; TITLE OF INVENTION: Structure Probing With Structure-Bridging
; TITLE OF INVENTION: Oligonucleotides.
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,097A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: FORS-02980
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-08-934-097A-51

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCTGTGTGA 19
||||| |||
DB 9 GCTGTCTGA 1

RESULT 156
US-09-677-218B-51/c
; Sequence 51, Application US/09677218B
; Patent No. 6355437
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING

STRUCTURE-BRIDGING OLIGONUCLEOTIDES

NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/677,218B  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/034,205  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 51:  
US-09-677-218B-51

Query Match 25.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 78;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCTGTGTGA 19  
|||  
Db 9 GCTGTCTGA 1

RESULT 157

US-09-677-192-51/c  
; Sequence 51, Application US/09677192  
; Patent No. 6358691  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor I.  
; APPLICANT: Brow, Mary Ann D.  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce P.  
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING  
; TITLE OF INVENTION: OLIGONUCLEOTIDES  
; FILE REFERENCE: FORS-04708  
; CURRENT APPLICATION NUMBER: US/09/677,192  
; CURRENT FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 09/034,205  
; PRIOR FILING DATE: 1998-03-03  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 51  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-677-192-51

Query Match 25.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 78;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCTGTGTGA 19  
|||  
Db 9 GCTGTCTGA 1

RESULT 158

US-09-154-750A-14  
; Sequence 14, Application US/09154750A  
; Patent No. 6432640  
; GENERAL INFORMATION:  
; APPLICANT: Vogelstein, Bert  
; APPLICANT: Kinzler, Kenneth  
; APPLICANT: Polyak, Kornelia  
; TITLE OF INVENTION: p53-Induced Apoptosis  
; FILE REFERENCE: 1107.75357  
; CURRENT APPLICATION NUMBER: US/09/154,750A  
; CURRENT FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/059,153  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/079817  
; PRIOR FILING DATE: 1998-03-30  
; NUMBER OF SEQ ID NOS: 93  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 14  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-154-750A-14

Query Match 25.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 78;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 17 TGACCTGGT 25  
|||  
Db 1 TGTCTGGT 9

RESULT 159

US-09-229-007A-81/c  
; Sequence 81, Application US/09229007A  
; Patent No. 6453242  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Case, Casey C.  
; APPLICANT: Cox III, George N.  
; APPLICANT: Jamieson, Andrew  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger  
; TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins  
; TITLE OF INVENTION: to Bind to Preslected Sites  
; FILE REFERENCE: 019496-001800US  
; CURRENT APPLICATION NUMBER: US/09/229,007A  
; CURRENT FILING DATE: 1999-01-12  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 81  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: soybean FAD2-1 cDNA target segment FAD 4  
US-09-229-007A-81

Query Match 25.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 78;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



QY 2 CATCCACCT 10  
Db 10 CTTCACCT 2

RESULT 160  
US-09-261-115-57  
; Sequence 57, Application US/09261115  
; Patent No. 6458584  
; GENERAL INFORMATION:  
; APPLICANT: MIRZABEKOV, ANDREI  
; APPLICANT: GUSCHIN, DMITRY Y.  
; APPLICANT: SHIK, VALENTINE  
; APPLICANT: DROBYSHEV, ALEKSEI  
; APPLICANT: FOTIN, ALEXANDER  
; APPLICANT: YERSHOV, GENNADIY  
; APPLICANT: LYSOV, YU  
; TITLE OF INVENTION: CUSTOMIZED OLIGONUCLEOTIDE MICROCHIPS THAT CONVERT  
; TITLE OF INVENTION: MULTIPLE GENETIC INFORMATION TO SIMPLE PATTERNS, ARE  
; TITLE OF INVENTION: PORTABLE AND REUSABLE  
; FILE REFERENCE: 21416/90184  
; CURRENT APPLICATION NUMBER: US/09/261,115  
; CURRENT FILING DATE: 1999-03-03  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 57  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Customized  
; OTHER INFORMATION: oligonucleotide  
US-09-261-115-57

Query Match 25.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 78;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 GTGACCTGG 24  
Db 2 GTGAACCTGG 10

RESULT 161  
US-09-914-259-119/c  
; Sequence 119, Application US/09914259  
; Patent No. 6495336  
; GENERAL INFORMATION:  
; APPLICANT: Makowski, Lee  
; APPLICANT: Hyman, Paul  
; APPLICANT: Williams, Mark  
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES  
; FILE REFERENCE: 8471-010-999  
; CURRENT APPLICATION NUMBER: US/09/914,259  
; CURRENT FILING DATE: 2000-11-21  
; NUMBER OF SEQ ID NOS: 180  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 119  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Theoretical sequence designed to show proper and improper joining  
; OTHER INFORMATION: elements  
US-09-914-259-119

Query Match 25.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 78;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 TGCTGTGTG 18  
Db 10 CTTCACCT 2

Db 9 TCCTGTGTG 1

RESULT 162  
US-09-914-259-120  
; Sequence 120, Application US/09914259  
; Patent No. 6495336  
; GENERAL INFORMATION:  
; APPLICANT: Makowski, Lee  
; APPLICANT: Hyman, Paul  
; APPLICANT: Williams, Mark  
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES  
; FILE REFERENCE: 8471-010-999  
; CURRENT APPLICATION NUMBER: US/09/914,259  
; CURRENT FILING DATE: 2000-11-21  
; NUMBER OF SEQ ID NOS: 180  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 120  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Theoretical sequence designed to show proper and improper joining  
; OTHER INFORMATION: elements  
US-09-914-259-120

Query Match 25.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 78;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 GTGTGACCT 22  
Db 1 GTGTGTCT 9

RESULT 163  
US-09-508-753B-67/c  
; Sequence 67, Application US/09508753B  
; Patent No. 6544736  
; GENERAL INFORMATION:  
; APPLICANT: Akira SHIMAMOTO  
; APPLICANT: Yasuhiro FURUICHI  
; APPLICANT: Yuko SHIBATA  
; APPLICANT: Hiroko FUNAKI  
; APPLICANT: Eiji OHARA  
; APPLICANT: Masanori WATAHIKI  
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample  
; FILE REFERENCE: 00162/HG  
; CURRENT APPLICATION NUMBER: US/09/508,753B  
; CURRENT FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: JP 9/270324  
; PRIOR FILING DATE: 1997-09-18  
; NUMBER OF SEQ ID NOS: 472  
; SEQ ID NO 67  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-508-753B-67

Query Match 25.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 78;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATCCACCT 10  
Db 10 CATTCACCT 2

RESULT 164  
US-09-508-753B-78  
; Sequence 78, Application US/09508753B

```
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 78
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-78
```

```
Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      10 TGCTGTGTG 18
      ||||| |||
Db      2 TGCTGAGTG 10
```

```
RESULT 165
US-09-508-753B-89/c
; Sequence 89, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 89
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-89
```

```
Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      11 GCTGTGTGA 19
      | |||||
Db      10 GGTGTGTGA 2
```

```
RESULT 166
US-09-508-753B-164
; Sequence 164, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
```

```
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 164
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-164
```

```
Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      17 TGACCTGGT 25
      ||| |||||
Db      1 TGAACCTGGT 9
```

```
RESULT 167
US-09-508-753B-188
; Sequence 188, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 188
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-188
```

```
Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      2 CATCCACCT 10
      ||| |||||
Db      1 CATCACCT 9
```

```
RESULT 168
US-09-811-286-16/c
; Sequence 16, Application US/09811286
; Patent No. 6586183
; GENERAL INFORMATION:
; APPLICANT: Drysdale, Connie M
; APPLICANT: Judson, Richard S
; APPLICANT: Liggett, Stephen B
; APPLICANT: Nandabalan, Krishnan
```

```
; APPLICANT: Stack, Catherine B.
; APPLICANT: Stephens, J. Claiborne
; TITLE OF INVENTION: Association of beta2-adrenergic receptor haplotypes
; TITLE OF INVENTION: with drug response
; FILE REFERENCE: MWH-0303US1
; CURRENT APPLICATION NUMBER: US/09/811,286
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-811-286-16

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 GTGACCTGG 24
      ||||| |||||
Db      9 GTGAGCTGG 1

RESULT 169
US-09-402-618B-51/c
; Sequence 51, Application US/09402618B
; Patent No. 6709815
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotides
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/09/402,618B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 51
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-402-618B-51

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      11 GCTGTGTGA 19
      ||||| |||||
Db      9 GCTGTCTGA 1

RESULT 170
US-09-825-574-51/c
; Sequence 51, Application US/09825574
; Patent No. 6709819
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
;           Brow, Mary Ann D.
;           Fors, Lance
;           Neri, Bruce P.
; TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
;           Structure Probing With Structure-Bridging
```

```
; Oligonucleotides.
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/825,574
; FILING DATE: 03-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/934,097
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: FORS-02980
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-825-574-51

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      11 GCTGTGTGA 19
      ||||| |||||
Db      9 GCTGTCTGA 1

RESULT 171
US-10-113-424-81/c
; Sequence 81, Application US/10113424
; Patent No. 6785613
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Case, Casey C.
; APPLICANT: Cox III, George N.
; APPLICANT: Jamieson, Andrew
; APPLICANT: Rebar, Edward J.
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger
; TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins
; TITLE OF INVENTION: to Bind to Preselected Sites
; FILE REFERENCE: 019496-001800US
; CURRENT APPLICATION NUMBER: US/10/113,424
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US/09/229,007A
; PRIOR FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Glycine max
```

```
; FEATURE:
; OTHER INFORMATION: soybean FAD2-1 cDNA target segment FAD 4
US-10-113-424-81

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CATCCACCT 10
Db      10 CTTCACCT 2

RESULT 172
US-09-821-694A-26
; Sequence 26, Application US/09821694A
; Patent No. 6949340
; GENERAL INFORMATION:
; APPLICANT: HILLS, WILLIAM D.
; TITLE OF INVENTION: METHOD AND SEQUENCES FOR DETERMINATE NUCLEIC ACID
; FILE REFERENCE: HYBRIDIZATION
; CURRENT APPLICATION NUMBER: 0450-0001
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Decoder
; OTHER INFORMATION: binding sequence
US-09-821-694A-26

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CATCCACCT 10
Db      2 CATCCATCT 10

RESULT 173
US-09-821-694A-30/c
; Sequence 30, Application US/09821694A
; Patent No. 6949340
; GENERAL INFORMATION:
; APPLICANT: HILLS, WILLIAM D.
; TITLE OF INVENTION: METHOD AND SEQUENCES FOR DETERMINATE NUCLEIC ACID
; FILE REFERENCE: HYBRIDIZATION
; CURRENT APPLICATION NUMBER: 0450-0001
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Decoder probe
; OTHER INFORMATION: sequence
US-09-821-694A-30

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CATCCACCT 10
Db      9 CATCCATCT 1
```

```
RESULT 174
US-10-053-883-70/c
; Sequence 70, Application US/10053883
; Patent No. 6958217
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Morten Lorentz
; TITLE OF INVENTION: ASSAY AND KIT FOR ANALYZING GENE EXPRESSION
; FILE REFERENCE: PEDERSEN=1A
; CURRENT APPLICATION NUMBER: US/10/053,883
; CURRENT FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: PA 2001 00126
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 60/267,704
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-053-883-70

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 CCTGCTGTG 16
Db      9 CATGCTGTG 1

RESULT 175
PCT-US93-09634-2/c
; Sequence 2, Application PC/TUS9309634
; GENERAL INFORMATION:
; APPLICANT: Kingston, Robert E.
; APPLICANT: Bunker, Christopher Alden
; TITLE OF INVENTION: Protein Partner Screening Assays and
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox
; STREET: 1100 New York Avenue, N.W.; Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/09634
; FILING DATE: (herewith)
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0609.274PC03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
```

```
; MOLECULE TYPE: DNA
PCT-US93-09634-2

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 CCACCTGCT 13
      ||| |||||
Db      9 CCAGCTGCT 1

RESULT 176
PCT-US94-08023-14
; Sequence 14, Application PC/TUS9408023
; GENERAL INFORMATION:
; APPLICANT: de Kloet, Siwo R.
; TITLE OF INVENTION: Sex-Specific DNA Probe For Parrots,
; TITLE OF INVENTION: Methods And Kits
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell, P.A.
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/08023
; FILING DATE: 15-JUL-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093,198
; FILING DATE: 15-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: FL20979-34
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US94-08023-14

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      21 CTGTTAAAT 29
      ||| |||||
Db      1 CTTGTTAAAT 9

RESULT 177
PCT-US95-05265-24
; Sequence 24, Application PC/TUS9505265
; GENERAL INFORMATION:
; APPLICANT: TULARIK, INC.
; TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA BINDING ASSAY
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05265
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,503
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: FP-59232-PC/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
PCT-US95-05265-24

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 CCACCTGCT 13
      ||| |||||
Db      2 CCATCTGCT 10

Search completed: May 15, 2006, 14:59:59
Job time : 1 secs
```



GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 15, 2006, 15:06:04 ; Search time 0.001 Seconds  
(without alignments)  
96.860 Million cell updates/sec

Title: US-09-904-968A-3-COPY  
Perfect score: 29  
Sequence: 1 ccattccacctgtgtgtgacctggttaaat 29

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 0.5

Searched: 106 seqs, 1670 residues

Total number of hits satisfying chosen parameters: 212

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 106 summaries

Database : pubmaindb:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result |       | Query |        | ID | Description          |
|--------|-------|-------|--------|----|----------------------|
| No.    | Score | Match | Length |    |                      |
| 1      | 29    | 100.0 | 29     | 1  | US-09-904-968A-3     |
| 2      | 17.8  | 61.4  | 25     | 1  | US-10-719-956-622076 |
| 3      | 15.6  | 53.8  | 22     | 1  | US-10-021-425-62     |
| 4      | 15.6  | 53.8  | 22     | 1  | US-10-900-856-65     |
| 5      | 15.2  | 52.4  | 21     | 1  | US-10-349-143-11421  |
| 6      | 14.8  | 51.0  | 20     | 1  | US-10-349-143-9340   |
| 7      | 14.8  | 51.0  | 20     | 1  | US-10-831-901A-19537 |
| 8      | 14.8  | 51.0  | 20     | 1  | US-10-831-901A-19538 |
| 9      | 14.8  | 51.0  | 20     | 1  | US-10-831-901A-19539 |
| 10     | 14.2  | 49.0  | 20     | 1  | US-09-853-666-18     |
| 11     | 14.2  | 49.0  | 20     | 1  | US-09-345-373-97     |
| 12     | 14.2  | 49.0  | 20     | 1  | US-10-075-446-97     |
| 13     | 14.2  | 49.0  | 20     | 1  | US-10-035-212-97     |
| 14     | 14.2  | 49.0  | 20     | 1  | US-10-695-957-18     |
| 15     | 14.2  | 49.0  | 20     | 1  | US-10-733-311-97     |
| 16     | 14.2  | 49.0  | 20     | 1  | US-10-901-210-97     |
| 17     | 13.4  | 46.2  | 19     | 1  | US-10-349-143-6482   |
| 18     | 13.2  | 45.5  | 18     | 1  | US-10-084-839-3261   |
| 19     | 12.8  | 44.1  | 17     | 1  | US-10-061-201-1638   |
| 20     | 12.8  | 44.1  | 17     | 1  | US-10-061-201-1639   |
| 21     | 12.8  | 44.1  | 18     | 1  | US-09-961-077-1205   |
| 22     | 12.8  | 44.1  | 18     | 1  | US-09-809-920-34     |
| 23     | 12.4  | 42.8  | 15     | 1  | US-10-672-866-142    |
| 24     | 12.4  | 42.8  | 17     | 1  | US-09-866-108-2171   |
| 25     | 12.4  | 42.8  | 17     | 1  | US-09-866-108-2172   |
| 26     | 12.4  | 42.8  | 17     | 1  | US-09-866-108-2173   |
| 27     | 12.4  | 42.8  | 17     | 1  | US-09-866-108-2174   |
| 28     | 12.4  | 42.8  | 17     | 1  | US-10-723-361-2171   |
| 29     | 12.4  | 42.8  | 17     | 1  | US-10-723-361-2172   |
| 30     | 12.4  | 42.8  | 17     | 1  | US-10-723-361-2173   |
| 31     | 12.4  | 42.8  | 17     | 1  | US-10-723-361-2174   |
| 32     | 12.2  | 42.1  | 17     | 1  | US-09-864-785-1502   |
| 33     | 12.2  | 42.1  | 17     | 1  | US-09-864-785-2052   |

|    |      |   |                       |                    |
|----|------|---|-----------------------|--------------------|
| 17 | 42.1 | 1 | US-10-060-830-780     | Sequence 780, Appl |
| 17 | 42.1 | 1 | US-10-061-201-1640    | Sequence 1640, Ap  |
| 17 | 42.1 | 1 | US-10-061-201-1641    | Sequence 1641, Ap  |
| 17 | 42.1 | 1 | US-10-061-201-1642    | Sequence 1642, Ap  |
| 17 | 42.1 | 1 | US-10-084-839-3258    | Sequence 3258, Ap  |
| 17 | 41.4 | 1 | US-09-866-108-2169    | Sequence 2169, Ap  |
| 17 | 41.4 | 1 | US-09-866-108-2170    | Sequence 2170, Ap  |
| 17 | 41.4 | 1 | US-10-723-361-2170    | Sequence 2170, Ap  |
| 13 | 39.3 | 1 | US-10-257-017B-145361 | Sequence 145361,   |
| 13 | 39.3 | 1 | US-10-257-017B-145362 | Sequence 145362,   |
| 15 | 39.3 | 1 | US-10-160-358-48      | Sequence 48, Appl  |
| 15 | 39.3 | 1 | US-10-433-542A-31     | Sequence 31, Appl  |
| 15 | 39.3 | 1 | US-10-257-480A-17     | Sequence 17, Appl  |
| 16 | 38.6 | 1 | US-10-084-839-3252    | Sequence 3252, Ap  |
| 16 | 38.6 | 1 | US-10-276-775-32      | Sequence 32, Appl  |
| 16 | 38.6 | 1 | US-10-138-674-5660    | Sequence 5660, Ap  |
| 16 | 38.6 | 1 | US-10-287-949A-5660   | Sequence 5660, Ap  |
| 16 | 38.6 | 1 | US-10-776-934-93      | Sequence 93, Appl  |
| 16 | 38.6 | 1 | US-10-776-934-512     | Sequence 512, App  |
| 16 | 38.6 | 1 | US-10-776-934-513     | Sequence 513, App  |
| 16 | 38.6 | 1 | US-10-776-934-514     | Sequence 514, App  |
| 16 | 38.6 | 1 | US-10-776-934-515     | Sequence 515, App  |
| 15 | 37.9 | 1 | US-10-010-802-40      | Sequence 40, Appl  |
| 15 | 37.2 | 1 | US-09-504-231A-107    | Sequence 107, App  |
| 15 | 37.2 | 1 | US-09-274-553D-107    | Sequence 107, App  |
| 15 | 37.2 | 1 | US-10-339-674-1871    | Sequence 1871, Ap  |
| 15 | 37.2 | 1 | US-10-984-919-371     | Sequence 371, App  |
| 13 | 35.9 | 1 | US-10-271-429A-17     | Sequence 17, Appl  |
| 14 | 35.9 | 1 | US-10-146-098-1       | Sequence 1, Appl   |
| 14 | 35.9 | 1 | US-10-356-625-17      | Sequence 17, Appl  |
| 14 | 35.9 | 1 | US-10-468-753-30      | Sequence 30, Appl  |
| 14 | 35.9 | 1 | US-10-984-919-1139    | Sequence 1139, Ap  |
| 11 | 34.5 | 1 | US-09-942-310-56      | Sequence 56, Appl  |
| 11 | 34.5 | 1 | US-09-942-310-63      | Sequence 63, Appl  |
| 11 | 34.5 | 1 | US-10-450-797-855     | Sequence 855, App  |
| 12 | 34.5 | 1 | US-10-219-446-50      | Sequence 50, Appl  |
| 12 | 34.5 | 1 | US-10-257-017B-305438 | Sequence 305438,   |
| 12 | 34.5 | 1 | US-10-257-017B-343129 | Sequence 343129,   |
| 13 | 34.5 | 1 | US-10-091-281-243     | Sequence 243, App  |
| 13 | 34.5 | 1 | US-10-257-017B-14111  | Sequence 14111, A  |
| 13 | 34.5 | 1 | US-10-257-017B-14112  | Sequence 14112, A  |
| 13 | 34.5 | 1 | US-10-257-017B-14113  | Sequence 14113, A  |
| 13 | 34.5 | 1 | US-10-257-017B-14114  | Sequence 14114, A  |
| 13 | 34.5 | 1 | US-10-257-017B-35449  | Sequence 35449, A  |
| 13 | 34.5 | 1 | US-10-257-017B-35450  | Sequence 35450, A  |
| 13 | 34.5 | 1 | US-10-257-017B-112883 | Sequence 112883,   |
| 13 | 34.5 | 1 | US-10-257-017B-112884 | Sequence 112884,   |
| 13 | 34.5 | 1 | US-10-257-017B-201617 | Sequence 201617,   |
| 13 | 34.5 | 1 | US-10-257-017B-201618 | Sequence 201618,   |
| 14 | 34.5 | 1 | US-09-504-231A-1393   | Sequence 1393, Ap  |
| 14 | 34.5 | 1 | US-09-274-553D-1393   | Sequence 1393, Ap  |
| 14 | 34.5 | 1 | US-10-024-944-6       | Sequence 6, Appl   |
| 14 | 34.5 | 1 | US-10-721-157-6       | Sequence 6, Appl   |
| 14 | 34.5 | 1 | US-10-984-919-1309    | Sequence 1309, Ap  |
| 13 | 33.8 | 1 | US-09-510-378-25      | Sequence 25, Appl  |
| 13 | 33.8 | 1 | US-09-798-260-83      | Sequence 83, Appl  |
| 13 | 33.8 | 1 | US-10-043-875-397     | Sequence 397, App  |
| 13 | 33.8 | 1 | US-10-043-875-422     | Sequence 422, App  |
| 13 | 33.8 | 1 | US-10-311-645A-118    | Sequence 118, App  |
| 13 | 33.8 | 1 | US-10-257-017B-145363 | Sequence 145363,   |
| 13 | 33.8 | 1 | US-10-257-017B-145364 | Sequence 145364,   |
| 14 | 33.8 | 1 | US-09-771-933-166     | Sequence 166, App  |
| 14 | 33.8 | 1 | US-10-146-058-15      | Sequence 15, Appl  |
| 14 | 33.8 | 1 | US-10-043-875-394     | Sequence 394, App  |
| 14 | 33.8 | 1 | US-10-043-875-398     | Sequence 398, App  |
| 14 | 33.8 | 1 | US-10-043-875-412     | Sequence 412, App  |
| 14 | 33.8 | 1 | US-10-043-875-414     | Sequence 414, App  |
| 14 | 33.8 | 1 | US-10-043-875-417     | Sequence 417, App  |
| 14 | 33.8 | 1 | US-10-043-875-421     | Sequence 421, App  |
| 14 | 33.8 | 1 | US-10-984-919-367     | Sequence 367, App  |
| 14 | 33.8 | 1 | US-10-984-919-1153    | Sequence 1153, Ap  |
| 14 | 33.8 | 1 | US-10-984-919-1469    | Sequence 1469, Ap  |

ALIGNMENTS

RESULT 1  
US-09-904-968A-3  
; Sequence 3, Application US/09904968A  
; Publication No. US20030008288A1  
; GENERAL INFORMATION:  
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
; APPLICANT: GERMINO, Gregory  
; APPLICANT: WATNICK, Terry  
; APPLICANT: PHAKOEEKITCHAROEN, Bunyong  
; TITLE OF INVENTION: DETECTION AND TREATMENT OF POLYCYSTIC KIDNEY DISEASE  
; FILE REFERENCE: JHU1680-2  
; CURRENT APPLICATION NUMBER: US/09/904,968A  
; CURRENT FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/283,691  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/218,261  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 29  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: PCR primer BPF14  
US-09-904-968A-3

Query Match 100.0%; Score 29; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 0.21;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGTGACCTGGTAAAT 29  
|||||  
Db 1 CCATCCACCTGCTGTGTGACCTGGTAAAT 29

RESULT 2  
US-10-719-956-622076  
; Sequence 622076, Application US/10719956  
; Publication No. US20040146910A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
; FILE REFERENCE: 3527.1  
; CURRENT APPLICATION NUMBER: US/10/719,956  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,836  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 699466  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 622076  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-10-719-956-622076

Query Match 61.4%; Score 17.8; DB 1; Length 25;  
Best Local Similarity 90.5%; Pred. No. 8;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CCTGCTGTGTGACCTGGTAAA 28  
|||||  
Db 3 CCTGCTGGGTGACCTTGTAAA 23

RESULT 3  
US-10-021-425-62  
; Sequence 62, Application US/10021425

; Publication No. US20030148420A1  
; GENERAL INFORMATION:  
; APPLICANT: Suzanne L. Bolten  
; APPLICANT: Alan M. Easton  
; APPLICANT: Leslie C. Engel  
; APPLICANT: Dean M. Messing  
; APPLICANT: John S. Ng  
; APPLICANT: Beverly A. Reitz  
; APPLICANT: Scott A. Vaccaro  
; APPLICANT: Mark C. Walker  
; APPLICANT: Ping T. Wang  
; APPLICANT: Robin A. Weinberg  
; TITLE OF INVENTION: Aspergillus ochraceus 11 alpha  
; FILE REFERENCE: S03196-00-US  
; CURRENT APPLICATION NUMBER: US/10/021,425  
; CURRENT FILING DATE: 2001-10-30  
; PRIOR APPLICATION NUMBER: USSN 60/244,300  
; PRIOR FILING DATE: 2000-10-30  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 62  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: human oxidoreductase primer 2C  
US-10-021-425-62

Query Match 53.8%; Score 15.6; DB 1; Length 22;  
Best Local Similarity 81.8%; Pred. No. 14;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGTGACCTG 23  
|||||  
Db 1 CATCGACCACCTGTGTGAGCTG 22

RESULT 4  
US-10-900-856-65  
; Sequence 65, Application US/109000856  
; Publication No. US20050003473A1  
; GENERAL INFORMATION:  
; APPLICANT: Bolten, Suzanne L  
; APPLICANT: Leslie, Engel C  
; APPLICANT: Dean, Messing M  
; APPLICANT: John, Ng S  
; APPLICANT: Beverly, Reitz A  
; APPLICANT: Scott, Vaccaro A  
; APPLICANT: Mark, Walker C  
; APPLICANT: Ping, Wang T  
; APPLICANT: Robin, Weinberg A  
; TITLE OF INVENTION: Aspergillus ochraceus 11 alpha hydroxylase and oxidoreductase  
; FILE REFERENCE: 3196  
; CURRENT APPLICATION NUMBER: US/10/900,856  
; CURRENT FILING DATE: 2004-07-28  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 65  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: homo sapiens oxidoreductase primer 2C  
US-10-900-856-65

Query Match 53.8%; Score 15.6; DB 1; Length 22;  
Best Local Similarity 81.8%; Pred. No. 14;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGTGACCTG 23  
|||||  
Db 1 CATCGACCACCTGTGTGAGCTG 22

RESULT 5  
US-10-349-143-11421/c

```
; Sequence 11421, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11421
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..21
; OTHER INFORMATION: downstream amplification primer 99-5747 for SEQ 3556, in complete
US-10-349-143-11421

Query Match
Best Local Similarity 52.4%; Score 15.2; DB 1; Length 21;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCTGTGTGACC 21
Db 21 CATTGACTTGCTGTGTGACC 2

RESULT 6
US-10-349-143-9340
; Sequence 9340, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9340
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: downstream amplification primer 99-25387 for SEQ 1475, in complete
US-10-349-143-9340

Query Match
Best Local Similarity 51.0%; Score 14.8; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 4 TCCACCTGCTGTGTGACC 21
Db 3 TGCACCTGCTCTGTGACC 20

RESULT 7
US-10-831-901A-19537
; Sequence 19537, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL00008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19537
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-19537

Query Match
Best Local Similarity 51.0%; Score 14.8; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 12 CTGTGTGACCTGGTAAAT 29
Db 1 CTCTGTAACCTGGTAAAT 18

RESULT 8
US-10-831-901A-19538
; Sequence 19538, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; OTHER INFORMATION: Acute Respiratory Syndrome (SARS)
```



;  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/345,373  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/023,082  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/461,195  
; FILING DATE: 05-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,852  
; FILING DATE: 13-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/039,045  
; FILING DATE: 28-FEB-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/862,432  
; FILING DATE: 23-MAY-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/910,875  
; FILING DATE: 13-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/055,561  
; FILING DATE: 13-AUG-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFEE, ERIC K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0360008/EKS  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 97:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; US-09-345-373-97

Query Match 49.0%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 19;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGTGAC 20  
||| ||||| |||||  
Db 1 CAACCACCTGCAGGTGAC 19

RESULT 12  
US-10-075-446-97  
; Sequence 97, Application US/10075446  
; Publication No. US20030129687A1  
; GENERAL INFORMATION:  
; APPLICANT: RUBEN, STEVEN M.  
; JIMENEZ, PABLO  
; DUAN, D. ROXANNE  
; RAMPY, MARK A.  
; MENDRICK, DONNA  
; ZHANG, JUN  
; NI, JIAN  
; MOORE, PAUL A.  
; COLEMAN, TIMOTHY A.  
; GRUBER, JOACHIM R.  
; TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2  
; NUMBER OF SEQUENCES: 148  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.

;  
; STREET: 1100 NEW YORK AVE, NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/075,446  
; FILING DATE: 15-Feb-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/023,082  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: PCT/US95/01790  
; FILING DATE: 14-FEB-1995  
; APPLICATION NUMBER: US 08/461,195  
; FILING DATE: 05-JUN-1995  
; APPLICATION NUMBER: US 60/023,852  
; FILING DATE: 13-AUG-1996  
; APPLICATION NUMBER: US 60/039,045  
; FILING DATE: 28-FEB-1997  
; APPLICATION NUMBER: US 08/862,432  
; FILING DATE: 23-MAY-1997  
; APPLICATION NUMBER: US 08/910,875  
; FILING DATE: 13-AUG-1997  
; APPLICATION NUMBER: US 60/055,561  
; FILING DATE: 13-AUG-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFEE, ERIC K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0360008/EKS  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 97:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 97:  
US-10-075-446-97  
  
Query Match 49.0%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 19;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 CATCCACCTGCTGTGTGAC 20  
||| ||||| |||||  
Db 1 CAACCACCTGCAGGTGAC 19  
  
RESULT 13  
US-10-035-212-97  
; Sequence 97, Application US/10035212  
; Publication No. US20030186904A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben, Steven M.  
; APPLICANT: Jimenez, Pablo  
; APPLICANT: Duan, D. Roxanne  
; APPLICANT: Rampy, Mark A.  
; APPLICANT: Mendrick, Donna  
; APPLICANT: Zhang, Jun  
; APPLICANT: Ni, Jian  
; APPLICANT: Moore, Paul A.  
; APPLICANT: Coleman, Timothy A.  
; APPLICANT: Gruber, Joachim R.  
; APPLICANT: Dillon, Patrick J.



```
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Keratinocyte Growth Factor-2
; FILE REFERENCE: 1488.0360000
; CURRENT APPLICATION NUMBER: US/10/035,212
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/286,368
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/331,168
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-10-035-212-97

Query Match          49.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 19;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATCCACCTGCTGTGTGAC 20
Db      1 CAACCACCTGCAGGGTGAC 19
      || ||||| || |||||

RESULT 14
US-10-695-957-18
; Sequence 18, Application US/10695957
; Publication No. US20040063639A1
; GENERAL INFORMATION:
; APPLICANT: Gentz et al.
; TITLE OF INVENTION: Keratinocyte Growth Factor-2 Formulations
; FILE REFERENCE: PF402C1D1
; CURRENT APPLICATION NUMBER: US/10/695,957
; CURRENT FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: 09/853,666
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/218,444
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/068,493
; PRIOR FILING DATE: 1997-12-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-695-957-18

Query Match          49.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 19;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATCCACCTGCTGTGTGAC 20
Db      1 CAACCACCTGCAGGGTGAC 19
      || ||||| || |||||

RESULT 15
US-10-733-311-97
; Sequence 97, Application US/10733311
; Publication No. US20040224387A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; APPLICANT: Jimenez, Pablo
; APPLICANT: Duan, D. Roxanne
; APPLICANT: Rampy, Mark A.
```

```
; APPLICANT: Mendrick, Donna
; APPLICANT: Zhang, Jun
; APPLICANT: Ni, Jian
; APPLICANT: Moore, Paul A.
; APPLICANT: Coleman, Timothy A.
; APPLICANT: Gruber, Joachim R.
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Keratinocyte Growth Factor-2
; FILE REFERENCE: 1488.036000J
; CURRENT APPLICATION NUMBER: US/10/733,311
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US/09/610,651
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: PCT/US95/01790
; PRIOR FILING DATE: 1995-02-14
; PRIOR APPLICATION NUMBER: 08/461,195
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 08/696,135
; PRIOR FILING DATE: 1996-08-13
; PRIOR APPLICATION NUMBER: 08/862,432
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/023,852
; PRIOR FILING DATE: 1996-08-13
; PRIOR APPLICATION NUMBER: 60/039,045
; PRIOR FILING DATE: 1997-02-28
; PRIOR APPLICATION NUMBER: 60/055,561
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 08/910,875
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 09/023,082
; PRIOR FILING DATE: 1998-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-10-733-311-97

Query Match          49.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 19;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATCCACCTGCTGTGTGAC 20
Db      1 CAACCACCTGCAGGGTGAC 19
      || ||||| || |||||

RESULT 16
US-10-901-210-97
; Sequence 97, Application US/10901210
; Publication No. US20050037966A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Keratinocyte Growth Factor-2
; FILE REFERENCE: PFI55P2D1
; CURRENT APPLICATION NUMBER: US/10/901,210
; CURRENT FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: 10/035,212
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,853
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/286,368
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/331,168
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 97
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer for construction of codon-optimized KGF-2?33
US-10-901-210-97

Query Match      49.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 19;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATCCACCTGCTGTGTGAC 20
Db      1 CAACCACCTGCAGGGTGAC 19

RESULT 17
US-10-349-143-6482/c
; Sequence 6482, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6482
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-11745 for SEQ 2548,
US-10-349-143-6482

Query Match      46.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 23;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 CCACCTGCTGTGTGA 19
Db      19 CCGCCTGCTGTGTGA 5

RESULT 18
US-10-084-839-3261/c
; Sequence 3261, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allawi, Hatim
; APPLICANT: Argue, Brad T.
; APPLICANT: Bartholomay, Christian T.
; APPLICANT: Chehak, LuAnne
; APPLICANT: Curtis, Michelle L.
; APPLICANT: Eis, Peggy S.
; APPLICANT: Hall, Jeff G.
; APPLICANT: Ip, Hon S.
; APPLICANT: Ji, Lin
; APPLICANT: Kaiser, Michael
```

```
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Lukowiak, Andrew A.
; APPLICANT: Lyamichev, Victor
; APPLICANT: Lymaicheva, Natalie E.
; APPLICANT: Ma, WuPo
; APPLICANT: Neri, Bruce P.
; APPLICANT: Olson, Sarah M.
; APPLICANT: Olson-Munoz, Marilyn C.
; APPLICANT: Schaefer, James J.
; APPLICANT: Skrzypczynski, Zbigniew
; APPLICANT: Takova, Tsetska Y.
; APPLICANT: Thompson, Lisa C.
; APPLICANT: Vedvik, Kevin L.
; TITLE OF INVENTION: RNA Detection Assays
; FILE REFERENCE: FORS-06666
; CURRENT APPLICATION NUMBER: US/10/084,839
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 4004
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3261
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-084-839-3261

Query Match      45.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 23;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CCATCCACCTGCTGTGTG 18
Db      18 CCATCCTTCTGCTGAGTG 1

RESULT 19
US-10-061-201-1638
; Sequence 1638, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1638
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1638
```

Query Match 44.1%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 24;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATCCACCTGCTGTGTG 18  
||| ||| ||| ||| |||  
Db 2 ATCCACCTCCTCTGTG 17

RESULT 20  
US-10-061-201-1639  
; Sequence 1639, Application US/10061201  
; Publication No. US20030166229A1  
; GENERAL INFORMATION:  
; APPLICANT: Shannon, Mark  
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1  
; FILE REFERENCE: PB0178  
; CURRENT APPLICATION NUMBER: US/10/061,201  
; CURRENT FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 09/864,761  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/328,205  
; PRIOR FILING DATE: 2001-10-10  
; NUMBER OF SEQ ID NOS: 4162  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 1639  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-061-201-1639

Query Match 44.1%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 24;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATCCACCTGCTGTGTG 18  
||| ||| ||| ||| |||  
Db 1 ATCCACCTCCTCTGTG 16

RESULT 21  
US-09-961-077-1205  
; Sequence 1205, Application US/09961077  
; Publication No. US20030014775A1  
; GENERAL INFORMATION:  
; APPLICANT: Zwick, Michael G.  
; Edington, Brent E.  
; McSwiggen, James A.  
; Merlo, Patricia Ann Owens  
; Guo, Lining  
; Skokut, Thomas A.  
; Young, Scott A.  
; Folkerts, Otto  
; Merlo, Donald J.  
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR  
; MODULATION OF GENE EXPRESSION  
;

IN PLANTS  
NUMBER OF SEQUENCES: 1263  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/961,077  
FILING DATE: 21-Sep-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/679,645  
FILING DATE: July 12, 1996  
APPLICATION NUMBER: 60/001,135  
FILING DATE: July 13, 1995  
APPLICATION NUMBER: 08/300,726  
FILING DATE: September 2, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 219/247  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1205:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1205:  
US-09-961-077-1205

Query Match 44.1%; Score 12.8; DB 1; Length 18;  
Best Local Similarity 62.5%; Pred. No. 26;  
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTGAC 20  
|||||:|:|:|  
Db 2 CCACCUGAUGUUUGAC 17

RESULT 22  
US-09-809-920-34/c  
; Sequence 34, Application US/09809920  
; Publication No. US20030139584A1  
; GENERAL INFORMATION:  
; APPLICANT: Sato, Takaaki  
; TITLE OF INVENTION: TREX, A NOVEL GENE OF TRAF-INTERACTING  
; EXT GENE FAMILY AND DIAGNOSTIC AND THERAPEUTIC USES  
; THEREOF  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
;

;  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/809,920  
; FILING DATE: 16-Mar-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/156,191  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51902  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 34:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:  
US-09-809-920-34

Query Match 44.1%; Score 12.8; DB 1; Length 18;  
Best Local Similarity 87.5%; Pred. No. 26;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGTGTGAC 20  
||| ||||| ||  
Db 18 CCACATGCTGTGTAC 3

RESULT 23  
US-10-672-866-142  
; Sequence 142, Application US/10672866  
; Publication No. US20050019915A1  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Kenneth Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF SUPEROXIDE DISMUTASE 1,  
; TITLE OF INVENTION: SOLUBLE  
; TITLE OF INVENTION: EXPRESSION  
; FILE REFERENCE: RTS-0242  
; CURRENT APPLICATION NUMBER: US/10/672,866  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 10/633,843  
; PRIOR FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: 09/888,360  
; PRIOR FILING DATE: 2001-06-21  
; NUMBER OF SEQ ID NOS: 339  
; SEQ ID NO 142  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-672-866-142

Query Match 42.8%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 23;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCTGT 15  
|| ||||| ||  
Db 1 CACCCACCTGCTGT 14

RESULT 24  
US-09-866-108-2171  
; Sequence 2171, Application US/09866108

; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aecomica Sequence Listing Engine  
; SEQ ID NO 2171  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-2171

Query Match 42.8%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 92.9%; Pred. No. 27;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGTGTG 18  
||| ||||| ||  
Db 4 CCACCTGCTGTGAG 17

RESULT 25  
US-09-866-108-2172  
; Sequence 2172, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE





```

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2174
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-2174

Query Match          42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 27;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 CCACCTGCTGTGTG 18
      |||||||
Db      1 CCACCTGCTGTGAG 14

RESULT 28
US-10-723-361-2171
; Sequence 2171, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2171
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-866-108-2174

Query Match          42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 27;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 CCACCTGCTGTGTG 18
      |||||||
Db      1 CCACCTGCTGTGAG 14

RESULT 28
US-10-723-361-2171
; Sequence 2171, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2171
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-866-108-2174
```

```

US-10-723-361-2171

Query Match          42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 27;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 CCACCTGCTGTGTG 18
      |||||||
Db      4 CCACCTGCTGTGAG 17

RESULT 29
US-10-723-361-2172
; Sequence 2172, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2172
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-2172

Query Match          42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 27;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 CCACCTGCTGTGTG 18
      |||||||
Db      3 CCACCTGCTGTGAG 16

RESULT 30
US-10-723-361-2173
; Sequence 2173, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
```



```
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2052
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-2052

Query Match          42.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 29;
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      3 ATCCACCTGCTGTGTGA 19
Db      1 AUCUCCUACUGUGUGA 17

RESULT 34
US-10-060-830-780/c
; Sequence 780, Application US/10060830
; Publication No. US20030032154A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: HUMAN LCCL DOMAIN CONTAINING PROTEIN
; FILE REFERENCE: PB0169
; CURRENT APPLICATION NUMBER: US/10/060,830
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006655
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/325,062
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 1123
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 780
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-830-780

Query Match          42.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      12 CTGTGTGACCTGGTAAA 28
Db      17 CTGTGGCACCTGGTACA 1

RESULT 35
US-10-061-201-1640
; Sequence 1640, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
```

```
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1640
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1640

Query Match          42.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      4 TCCACCTGCTGTGTGAC 20
Db      1 TCCACCTCCTCTGTGTC 17

RESULT 36
US-10-061-201-1641
; Sequence 1641, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1641
; LENGTH: 17
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
US-10-061-201-1641

Query Match          42.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5 CCACCTGCTGTGTGACC 21
        ||||| || ||||| ||
Db      1 CCACCTCCTCTGTGTCC 17

RESULT 37
US-10-061-201-1642
; Sequence 1642, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1642
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1642

Query Match          42.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      6 CACCTGCTGTGTGACCT 22
        ||||| || ||||| |||
Db      1 CACCTCCTCTGTGTCC 17

RESULT 38
US-10-084-839-3258/c
; Sequence 3258, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allawi, Hatim
; APPLICANT: Argue, Brad T.
; APPLICANT: Bartholomay, Christian T.
; APPLICANT: Chehak, LuAnne
; APPLICANT: Curtis, Michelle L.
; APPLICANT: Eis, Peggy S.
; APPLICANT: Hall, Jeff G.
; APPLICANT: Ip, Hon S.
```

```
; APPLICANT: Ji, Lin
; APPLICANT: Kaiser, Michael
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Lukowiak, Andrew A.
; APPLICANT: Lyamichev, Victor
; APPLICANT: Lymaicheva, Natalie E.
; APPLICANT: Ma, WuPo
; APPLICANT: Neri, Bruce P.
; APPLICANT: Olson, Sarah M.
; APPLICANT: Olson-Munoz, Marilyn C.
; APPLICANT: Schaefer, James J.
; APPLICANT: Skrzypczynski, Zbigniew
; APPLICANT: Takova, Tsetska Y.
; APPLICANT: Thompson, Lisa C.
; APPLICANT: Vedvik, Kevin L.
; TITLE OF INVENTION: RNA Detection Assays
; FILE REFERENCE: FORS-06666
; CURRENT APPLICATION NUMBER: US/10/084,839
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 4004
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3258
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-084-839-3258

Query Match          42.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CCATCCACCTGCTGTGT 17
        ||||| ||||| |||
Db      17 CCATCCTTCTGTGAGT 1

RESULT 39
US-09-866-108-2169
; Sequence 2169, Application US/098666108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: Ji, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
```

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2169
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-2169

Query Match 41.4%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTG 16
|||||
Db 6 CCACCTGCTGTG 17

RESULT 40
US-09-866-108-2170
; Sequence 2170, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860

; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2170
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-2170

Query Match 41.4%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTG 16
|||||
Db 5 CCACCTGCTGTG 16

RESULT 41
US-10-723-361-2169
; Sequence 2169, Application US/107233361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANI
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2169
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-2169

Query Match 41.4%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTG 16
|||||
Db 6 CCACCTGCTGTG 17

RESULT 42



```
US-10-723-361-2170
; Sequence 2170, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2170
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-2170

Query Match          41.4%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 CCACCTGCTGTG 16
      |||||
Db      5 CCACCTGCTGTG 16

RESULT 43
US-10-257-017B-145361/c
; Sequence 145361, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence

Query Match          41.4%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 CCACCTGCTGTG 16
      |||||
Db      5 CCACCTGCTGTG 16

US-10-723-361-2170
```

```
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0036590
US-10-257-017B-145361

Query Match          39.3%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 26;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCATCCACCTGCT 13
      |||||
Db      13 CCATCCACCTACT 1

RESULT 44
US-10-257-017B-145362
; Sequence 145362, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 145362
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0036590
US-10-257-017B-145362

Query Match          39.3%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 26;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCATCCACCTGCT 13
      |||||
Db      1 CCATCCACCTACT 13

RESULT 45
US-10-160-358-48
; Sequence 48, Application US/10160358
; Publication No. US20030198969A1
; GENERAL INFORMATION:
; APPLICANT: Genaissance Pharmaceuticals, Inc.
; APPLICANT: Bieglecki, Karyn
; APPLICANT: Cappola, Gina-Marie
; APPLICANT: Koshy, Beena
; APPLICANT: Monroe, Glen
; TITLE OF INVENTION: HAPLOTYPES OF THE TACR2 GENE
; FILE REFERENCE: TACR2 MWH-0225US
; CURRENT APPLICATION NUMBER: US/10/160,358
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/47394
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/247,649
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-160-358-48

Query Match          39.3%; Score 11.4; DB 1; Length 15;
```

```
Best Local Similarity 80.0%; Pred. No. 32;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 ACCTGCTGTGTGACC 21
Db 1 ACTTGCTGTGTAAYC 15

RESULT 46
US-10-433-542A-31/c
; Sequence 31, Application US/10433542A
; Publication No. US20040209263A1
; GENERAL INFORMATION:
; APPLICANT: Clawson, Gary A.
; APPLICANT: Pan, Wei-Hua
; TITLE OF INVENTION: SELECTION OF CATALYTIC NUCLEIC ACIDS
; TITLE OF INVENTION: TARGETED TO INFECTIOUS AGENTS
; FILE REFERENCE: 14017-007US1
; CURRENT APPLICATION NUMBER: US/10/433,542A
; CURRENT FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: PCT/US01/46178
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/251,810
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated oligonucleotide
US-10-433-542A-31

Query Match 39.3%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 32;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCCACCTGCTGTG 16
Db 13 TCCACCTGCTGCG 1

RESULT 47
US-10-257-480A-17/c
; Sequence 17, Application US/10257480A
; Publication No. US20040220123A1
; GENERAL INFORMATION:
; APPLICANT: Norris, James S.
; APPLICANT: Westwater, Caroline
; APPLICANT: Schofield, David A.
; APPLICANT: Schmidt, Michael G.
; APPLICANT: Hoel, Brian D.
; APPLICANT: Dolan, Joseph W.
; APPLICANT: Clawson, Gary A.
; APPLICANT: Pan, Wei-Hua
; TITLE OF INVENTION: TISSUE-SPECIFIC AND PATHOGEN-SPECIFIC TOXIC AGENTS, AND
; TITLE OF INVENTION: RIBOZYMES, DNAZYMES AND ANTISENSE OLIGONUCLEOTIDES, AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 14017-006US1 (PSU 99-2157)
; CURRENT APPLICATION NUMBER: US/10/257,480A
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: PCT/US01/12130
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/251,810
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/548,449
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 15
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV mlRz-247
US-10-257-480A-17

Query Match 39.3%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 32;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCCACCTGCTGTG 16
Db 13 TCCACCTGCTGCG 1

RESULT 48
US-10-084-839-3252/c
; Sequence 3252, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allawi, Hatim
; APPLICANT: Argue, Brad T.
; APPLICANT: Bartholomay, Christian T.
; APPLICANT: Chehak, LuAnne
; APPLICANT: Curtis, Michelle L.
; APPLICANT: Eis, Peggy S.
; APPLICANT: Hall, Jeff G.
; APPLICANT: Ip, Hon S.
; APPLICANT: Ji, Lin
; APPLICANT: Kaiser, Michael
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Lukowiak, Andrew A.
; APPLICANT: Lyamichev, Victor
; APPLICANT: Lymaicheva, Natalie E.
; APPLICANT: Ma, WuPo
; APPLICANT: Neri, Bruce P.
; APPLICANT: Olson, Sarah M.
; APPLICANT: Olson-Munoz, Marilyn C.
; APPLICANT: Schaefer, James J.
; APPLICANT: Skrzypczynski, Zbigniew
; APPLICANT: Takova, Tsetska Y.
; APPLICANT: Thompson, Lisa C.
; APPLICANT: Vedvik, Kevin L.
; TITLE OF INVENTION: RNA Detection Assays
; FILE REFERENCE: FORS-06666
; CURRENT APPLICATION NUMBER: US/10/084,839
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 4004
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3252
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-084-839-3252

Query Match 38.6%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 37;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTG 16
Db 16 CCATCCTTCTGCTGAG 1

RESULT 49
US-10-276-775-32/c
; Sequence 32, Application US/10276775
; Publication No. US20040072170A1
; GENERAL INFORMATION:
; APPLICANT: Bunk, Daniela
; APPLICANT: Reuner, Birgit
```

; APPLICANT: Beck, Joachim
; APPLICANT: Henkel, Thomas
; TITLE OF INVENTION: Novel Target Genes For Diseases of the
; TITLE OF INVENTION: Heart
; FILE REFERENCE: 50290/004002
; CURRENT APPLICATION NUMBER: US/10/276,775
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: PCT/EP01/06165
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: US 60/207,400
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-276-775-32

Query Match 38.6%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 37;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 TGCTGTGTGACCTGGT 25
||| ||||| |||
Db 16 TGCTGTGTGAAATTGT 1

RESULT 50
US-10-138-674-5660
; Sequence 5660, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5660
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-5660

Query Match 38.6%; Score 11.2; DB 1; Length 16;
Best Local Similarity 56.2%; Pred. No. 37;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 8 CCTGCTGTGTGACCTG 23
||:|:|:| | | |
Db 1 CCUGCUGUGCGCGCUG 16

RESULT 51
US-10-287-949A-5660
; Sequence 5660, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5660
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-5660

Query Match 38.6%; Score 11.2; DB 1; Length 16;
Best Local Similarity 56.2%; Pred. No. 37;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 8 CCTGCTGTGTGACCTG 23
||:|:|:| | | |
Db 1 CCUGCUGUGCGCGCUG 16

RESULT 52
US-10-776-934-93/c
; Sequence 93, Application US/10776934
; Publication No. US20050014712A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THRUE, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: WISSENBACH, MARGIT
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: 58610(71432)
; CURRENT APPLICATION NUMBER: US/10/776,934
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/446,372
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/523,591
; PRIOR FILING DATE: 2003-11-19
; NUMBER OF SEQ ID NOS: 741
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-776-934-93

Query Match 38.6%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 37;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TCCACCTGCTGTGTGA 19
| | | | | | | | |
Db 16 TGCCACTGCTGTGTGA 1

RESULT 53
US-10-776-934-512/c
; Sequence 512, Application US/10776934
; Publication No. US20050014712A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THRUE, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: WISSENBACH, MARGIT
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: 58610(71432)
; CURRENT APPLICATION NUMBER: US/10/776,934
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/446,372

```
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/523,591
; PRIOR FILING DATE: 2003-11-19
; NUMBER OF SEQ ID NOS: 741
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 512
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: modified_base
; LOCATION: (1)..(4)
; OTHER INFORMATION: beta-D-oxy-LNA modified base
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (13)..(16)
; OTHER INFORMATION: beta-D-oxy-LNA modified base
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(16)
; OTHER INFORMATION: phosphorthioate linkage
US-10-776-934-512
```

Query Match 38.6%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 37;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
QY 4 TCCACCTGCTGTGTGA 19
   ||| ||||| |||||
Db 16 TGCCACTGCTGTGTGA 1
```

```
RESULT 54
US-10-776-934-513/c
; Sequence 513, Application US/10776934
; Publication No. US20050014712A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THRUE, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: WISSENBACH, MARGIT
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: 58610(71432)
; CURRENT APPLICATION NUMBER: US/10/776,934
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/446,372
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/523,591
; PRIOR FILING DATE: 2003-11-19
; NUMBER OF SEQ ID NOS: 741
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 513
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(4)
; OTHER INFORMATION: beta-D-oxy-LNA modified base
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (13)..(15)
; OTHER INFORMATION: beta-D-oxy-LNA modified base
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(16)
; OTHER INFORMATION: phosphorthioate linkage
US-10-776-934-513
```

Query Match 38.6%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 37;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
QY 4 TCCACCTGCTGTGTGA 19
   ||| ||||| |||||
Db 16 TGCCACTGCTGTGTGA 1
```

```
RESULT 55
US-10-776-934-514/c
; Sequence 514, Application US/10776934
; Publication No. US20050014712A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THRUE, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: WISSENBACH, MARGIT
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: 58610(71432)
; CURRENT APPLICATION NUMBER: US/10/776,934
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/446,372
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/523,591
; PRIOR FILING DATE: 2003-11-19
; NUMBER OF SEQ ID NOS: 741
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 514
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(4)
; OTHER INFORMATION: beta-D-oxy-LNA modified base
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (13)..(16)
; OTHER INFORMATION: beta-D-oxy-LNA modified base
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(13)
; OTHER INFORMATION: phosphorthioate linkage
US-10-776-934-514
```

Query Match 38.6%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 37;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
QY 4 TCCACCTGCTGTGTGA 19
   ||| ||||| |||||
Db 16 TGCCACTGCTGTGTGA 1
```

```
RESULT 56
US-10-776-934-515/c
; Sequence 515, Application US/10776934
; Publication No. US20050014712A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THRUE, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: WISSENBACH, MARGIT
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: 58610(71432)
; CURRENT APPLICATION NUMBER: US/10/776,934
; CURRENT FILING DATE: 2004-02-10
```

```
; PRIOR APPLICATION NUMBER: 60/446,372
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/523,591
; PRIOR FILING DATE: 2003-11-19
; NUMBER OF SEQ ID NOS: 741
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 515
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (1)..(16)
; OTHER INFORMATION: phosphorthioate linkage
US-10-776-934-515

Query Match          38.6%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 37;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      4 TCCACCTGCTGTGTGA 19
Db      16 TGCCACTGCTGTGTGA 1

RESULT 57
US-10-010-802-40
; Sequence 40, Application US/10010802
; Publication No. US20030078220A1
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals
; APPLICANT: Chew, Anne
; APPLICANT: Denton, R. Rex
; APPLICANT: Duda, Amy
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Stephens, J. Claiborne
; APPLICANT: Windemuth, Andreas
; TITLE OF INVENTION: Drug Target Isogenes: Polymorphisms in the Interleukin
; FILE REFERENCE: MWH-0002US2 IL4R alpha
; CURRENT APPLICATION NUMBER: US/10/010,802
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/US00/19094
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-010-802-40

Query Match          37.9%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 CACCTGCTGTG 16
Db      1 CACCTGCTGTG 11

RESULT 58
US-09-504-231A-107/c
; Sequence 107, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; ;
```

```
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATEI
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: rpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 107
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-107

Query Match          37.2%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      16 GTGACCTGGTAAAT 29
Db      15 GTGACCTGATACAT 2

RESULT 59
US-09-274-553D-107/c
; Sequence 107, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATEI
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: rpi 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 107
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-107

Query Match          37.2%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      16 GTGACCTGGTAAAT 29
Db      15 GTGACCTGATACAT 2

RESULT 60
```



```
US-10-339-674-1871
; Sequence 1871, Application US/10339674
; Publication No. US20030204318A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/339,674
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 3537
; SOFTWARE: Proprietary
; SEQ ID NO 1871
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
; FEATURE:
; LOCATION: (2551260)...(2551274)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 2480
US-10-339-674-1871

Query Match      37.2%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 12 CTGTGTGACCTGGT 25
Db 1 CTGTTTAACCTGGT 14

RESULT 61
US-10-984-919-371
; Sequence 371, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 371
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-371

Query Match      37.2%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTG 14
Db 1 CCATCCACTTGATG 14

RESULT 62
US-10-271-429A-17/c
; Sequence 17, Application US/10271429A
; Publication No. US2004002323A1
; GENERAL INFORMATION:
; APPLICANT: Atherogenics, Inc.
; TITLE OF INVENTION: Protection Against Oxidative Stress and Inflammation by a Cytoprod
```

```
; TITLE OF INVENTION: Response Element
; FILE REFERENCE: ATH118
; CURRENT APPLICATION NUMBER: US/10/271,429A
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/329,870
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/329,870
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 13
; TYPE: DNA
; ORGANISM: human
US-10-271-429A-17

Query Match      35.9%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 36;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTGAC 20
Db 12 CTGCTGTGTGAC 1

RESULT 63
US-10-146-058-1/c
; Sequence 1, Application US/10146058
; Publication No. US20030040499A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta (
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,058
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/535,249
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
```



```

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 11
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-942-310-56

Query Match          34.5%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATCCACCT 10
Db      11 CCATCCACCT 2

RESULT 68
US-09-942-310-63
; Sequence 63, Application US/09942310
; Publication No. US20030044797A1
; GENERAL INFORMATION:
; APPLICANT: Risinger, Carl
; APPLICANT: Andersson, Maria K.
; APPLICANT: Lewander, Tommy
; APPLICANT: Olaisson, Erik
; TITLE OF INVENTION: Detection of CYP2D6 Polymorphisms
; FILE REFERENCE: GG119.1US
; CURRENT APPLICATION NUMBER: US/09/942,310
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: GB 0021286.0
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 11
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-942-310-63

Query Match          34.5%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATCCACCT 10
Db      1 CCATCCACCT 10

RESULT 69
US-10-450-797-855
; Sequence 855, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 855
; LENGTH: 11
; TYPE: DNA
```

```

; ORGANISM: Homo sapiens
US-10-450-797-855

Query Match          34.5%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 ATCCACCTGC 12
Db      1 ATCCACCTGC 10

RESULT 70
US-10-219-446-50/c
; Sequence 50, Application US/10219446
; Publication No. US20040033497A1
; GENERAL INFORMATION:
; APPLICANT: Alarcon-Riquelme, Marta E.
; APPLICANT: Prokunina, Ludmila
; TITLE OF INVENTION: Polymorphisms of PD-1
; FILE REFERENCE: sthp-004
; CURRENT APPLICATION NUMBER: US/10/219,446
; CURRENT FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-219-446-50

Query Match          34.5%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATCCACCT 10
Db      12 CCATCCACCT 3

RESULT 71
US-10-257-017B-305438
; Sequence 305438, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 305438
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0021446
US-10-257-017B-305438

Query Match          34.5%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATCCACCT 10
Db      2 CCATCCACCT 11
```

```
RESULT 72
US-10-257-017B-343129
; Sequence 343129, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 343129
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC00042904
US-10-257-017B-343129

Query Match          34.5%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATCCACCT 10
        |||||
Db       3 CCATCCACCT 12

RESULT 73
US-10-091-281-243
; Sequence 243, Application US/10091281
; Publication No. US20030190617A1
; GENERAL INFORMATION:
; APPLICANT: RAYMOND, VINCENT
; APPLICANT: SI, ERWIN
; APPLICANT: MORISSETTE, JEAN
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 13587.338
; CURRENT APPLICATION NUMBER: US/10/091,281
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 243
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Putative AREB/AREB6.01 motif
US-10-091-281-243

Query Match          34.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 ATCCACCTGC 12
        |||||
Db       2 ATCCACCTGC 11

RESULT 74
US-10-257-017B-14111/c
; Sequence 14111, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
```

```
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 14111
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0003223
US-10-257-017B-14111

Query Match          34.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATCCACCT 10
        |||||
Db       13 CCATCCACCT 4

RESULT 75
US-10-257-017B-14112
; Sequence 14112, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 14112
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0003223
US-10-257-017B-14112

Query Match          34.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATCCACCT 10
        |||||
Db       1 CCATCCACCT 10

RESULT 76
US-10-257-017B-14113/c
; Sequence 14113, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
```

```

; SEQ ID NO 14113
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0003223
US-10-257-017B-14113

Query Match      34.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATCCACCT 10
Db      13 CCATCCACCT 4

RESULT 77
US-10-257-017B-14114
; Sequence 14114, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 14114
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0003223
US-10-257-017B-14114

Query Match      34.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATCCACCT 10
Db      1 CCATCCACCT 10

RESULT 78
US-10-257-017B-35449/c
; Sequence 35449, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 35449
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0011230
US-10-257-017B-35449
```

```

Query Match      34.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATCCACCT 10
Db      12 CCATCCACCT 3

RESULT 79
US-10-257-017B-35450
; Sequence 35450, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 35450
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0011230
US-10-257-017B-35450

Query Match      34.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATCCACCT 10
Db      2 CCATCCACCT 11

RESULT 80
US-10-257-017B-112883/c
; Sequence 112883, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 112883
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0028229
US-10-257-017B-112883

Query Match      34.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATCCACCT 10
Db      1 CCATCCACCT 11
```



Db 10 CCATCCACCT 1

RESULT 81

US-10-257-017B-112884

; Sequence 112884, Application US/10257017B

; Publication No. US20040241651A1

; GENERAL INFORMATION:

; APPLICANT: Alexander Olek

; APPLICANT: Christian Piepenbrock

; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine

; TITLE OF INVENTION: methylations

; FILE REFERENCE: E01/1193/WO

; CURRENT APPLICATION NUMBER: US/10/257,017B

; CURRENT FILING DATE: 2002-10-07

; PRIOR APPLICATION NUMBER: DE 10019173.8

; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 382046

; SEQ ID NO 112884

; LENGTH: 13

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC00282229

US-10-257-017B-112884

Query Match 34.5%; Score 10; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 41;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCCACCT 10

Db 4 CCATCCACCT 13

RESULT 82

US-10-257-017B-201617/c

; Sequence 201617, Application US/10257017B

; Publication No. US20040241651A1

; GENERAL INFORMATION:

; APPLICANT: Alexander Olek

; APPLICANT: Christian Piepenbrock

; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine

; TITLE OF INVENTION: methylations

; FILE REFERENCE: E01/1193/WO

; CURRENT APPLICATION NUMBER: US/10/257,017B

; CURRENT FILING DATE: 2002-10-07

; PRIOR APPLICATION NUMBER: DE 10019173.8

; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 382046

; SEQ ID NO 201617

; LENGTH: 13

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0049588

US-10-257-017B-201617

Query Match 34.5%; Score 10; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 41;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCCACCT 10

Db 11 CCATCCACCT 2

RESULT 83

US-10-257-017B-201618

; Sequence 201618, Application US/10257017B

; Publication No. US20040241651A1

; GENERAL INFORMATION:

; APPLICANT: Alexander Olek

; APPLICANT: Christian Piepenbrock

; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine

; TITLE OF INVENTION: methylations

; FILE REFERENCE: E01/1193/WO

; CURRENT APPLICATION NUMBER: US/10/257,017B

; CURRENT FILING DATE: 2002-10-07

; PRIOR APPLICATION NUMBER: DE 10019173.8

; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 382046

; SEQ ID NO 201618

; LENGTH: 13

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0049588

US-10-257-017B-201618

Query Match 34.5%; Score 10; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 41;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCCACCT 10

Db 3 CCATCCACCT 12

RESULT 84

US-09-504-231A-1393

; Sequence 1393, Application US/09504231A

; Patent No. US20020013458A1

; GENERAL INFORMATION:

; APPLICANT: Blatt, Lawrence

; APPLICANT: McSwiggen, James

; APPLICANT: Roberts, Beth

; APPLICANT: Pavco, Pamela

; APPLICANT: Macejak, Dennis

; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE

; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION

; FILE REFERENCE: rpi 247/282

; CURRENT APPLICATION NUMBER: US/09/504,231A

; CURRENT FILING DATE: 2000-02-15

; PRIOR APPLICATION NUMBER: 09/274,553

; PRIOR FILING DATE: 1999-03-23

; PRIOR APPLICATION NUMBER: 09/257,608

; PRIOR FILING DATE: 1999-02-24

; PRIOR APPLICATION NUMBER: 60/100,842

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: 60/083,217

; PRIOR FILING DATE: 1998-04-27

; NUMBER OF SEQ ID NOS: 3242

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1393

; LENGTH: 14

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target

US-09-504-231A-1393

Query Match 34.5%; Score 10; DB 1; Length 14;

Best Local Similarity 60.0%; Pred. No. 45;

Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 9 CTGCTGTGTG 18

Db 4 CUGCUGUGUG 13

RESULT 85

US-09-274-553D-1393

```
; Sequence 1393, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: IPI 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1393
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-1393

Query Match          34.5%; Score 10; DB 1; Length 14;
Best Local Similarity 60.0%; Pred. No. 45;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 9 CTGCTGTGTG 18
    |:|:|:|:|
Db 4 CUGCUGUGUG 13

RESULT 86
US-10-024-944-6
; Sequence 6, Application US/10024944
; Publication No. US20020123060A1
; GENERAL INFORMATION:
; APPLICANT: EXACT Science Corporation
; APPLICANT: Boles, T. Christian
; APPLICANT: Weir, Lawrence
; APPLICANT: Stone, Benjamin
; TITLE OF INVENTION: Detection of No. US20020123060A1-Viral Organisms With SRP RNA
; FILE REFERENCE: EXT-073
; CURRENT APPLICATION NUMBER: US/10/024,944
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 60/090,063
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 08/971,845
; PRIOR FILING DATE: 1997-08-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: a short probe derived from th
; OTHER INFORMATION: complementary sequence of E. coli 4.5S RNA region 44-65
US-10-024-944-6

Query Match          34.5%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGACCTGGTA 26
    |||||
Db 5 TGACCTGGTA 14

RESULT 87
US-10-721-157-6
; Sequence 6, Application US/10721157
; Publication No. US20040086932A1
; GENERAL INFORMATION:
; APPLICANT: Boles, T. Christian
; APPLICANT: Weir, Lawrence
; APPLICANT: Stone, Benjamin B
; TITLE OF INVENTION: Detection of Non-Viral Organisms with SRP RNA
; FILE REFERENCE: EXT-072C2
; CURRENT APPLICATION NUMBER: US/10/721,157
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: US 60/090,063
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 10/024,944
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 09/336,609
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: a short probe derived from th
; OTHER INFORMATION: e complementary sequence of E. coli 4.5S RNA region 44-65
US-10-721-157-6

Query Match          34.5%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGACCTGGTA 26
    |||||
Db 5 TGACCTGGTA 14

RESULT 88
US-10-984-919-1309/c
; Sequence 1309, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlengersiepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1309
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-1309

Query Match          34.5%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ATCCACCTGC 12
```

Db 10 ATCCACCTGC 1

RESULT 89

US-09-510-378-25

; Sequence 25, Application US/09510378

; Publication No. US20030165823A1

; GENERAL INFORMATION:

; APPLICANT: Cronin, Maureen T.

; Miyada, Charles Garrett

; Hubbell, Earl A.

; Chee, Mark

; Fodor, Stephen P.A.

; Huang, Xiaohua C.

; Lipshutz, Robert J.

; Lobban, Peter E.

; Morris, Macdonald S.

; Sheldon, Edward L.

; TITLE OF INVENTION: Arrays of Nucleic Acid Probes for

; Detecting Cystic Fibrosis

; NUMBER OF SEQUENCES: 250

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/510,378

; FILING DATE: 22-Feb-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/544,381

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 08/510,521

; FILING DATE: 02-AUG-1995

; APPLICATION NUMBER: PCT/US94/12305

; FILING DATE: 26-OCT-1994

; APPLICATION NUMBER: US 08/284,064

; FILING DATE: 02-AUG-1994

; APPLICATION NUMBER: US 08/143,312

; FILING DATE: 26-OCT-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Liebeschuetz, Joe

; REGISTRATION NUMBER: 37,505

; REFERENCE/DOCKET NUMBER: 018547-004130US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-576-0200

; TELEFAX: 415-576-0300

; INFORMATION FOR SEQ ID NO: 25:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 13 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (oligonucleotide)

; SEQUENCE DESCRIPTION: SEQ ID NO: 25:

US-09-510-378-25

Query Match 33.8%; Score 9.8; DB 1; Length 13;

Best Local Similarity 84.6%; Pred. No. 44;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 TGCTGTGTGACCT 22

Db 1 TGGTGTGTGCCCT 13

RESULT 90

US-09-798-260-83

; Sequence 83, Application US/09798260

; Publication No. US20030165830A1

; GENERAL INFORMATION:

; APPLICANT: Cronin, Maureen T.

; APPLICANT: Miyada, Charles G.

; APPLICANT: Hubbell, Earl A.

; APPLICANT: Chee, Mark

; APPLICANT: Fodor, Stephen P. A.

; APPLICANT: Huang, Xiaohua C.

; APPLICANT: Lipshutz, Robert J.

; APPLICANT: Lobban, Peter E.

; APPLICANT: Morris, Macdonald S.

; APPLICANT: Sheldon, Edward L.

; TITLE OF INVENTION: ARRAYS OF NUCLEIC ACID PROBES FOR ANALYZING

; BIOTRANSFORMATION GENES

; FILE REFERENCE: 018547-015720US

; CURRENT APPLICATION NUMBER: US/09/798,260

; CURRENT FILING DATE: 2002-05-01

; PRIOR APPLICATION NUMBER: US 08/778,794

; PRIOR FILING DATE: 1997-01-03

; PRIOR APPLICATION NUMBER: US 08/544,381

; PRIOR FILING DATE: 1995-10-10

; PRIOR APPLICATION NUMBER: US 08/510,521

; PRIOR FILING DATE: 1995-08-02

; PRIOR APPLICATION NUMBER: WO PCT/US94/12305

; PRIOR FILING DATE: 1994-10-26

; PRIOR APPLICATION NUMBER: US 08/284,064

; PRIOR FILING DATE: 1994-08-02

; PRIOR APPLICATION NUMBER: US 08/143,312

; PRIOR FILING DATE: 1993-10-26

; NUMBER OF SEQ ID NOS: 156

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 83

; LENGTH: 13

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Probe

US-09-798-260-83

Query Match 33.8%; Score 9.8; DB 1; Length 13;

Best Local Similarity 84.6%; Pred. No. 44;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 TGCTGTGTGACCT 22

Db 1 TGGTGTGTGCCCT 13

RESULT 91

US-10-043-875-397/c

; Sequence 397, Application US/10043875

; Publication No. US20030054339A1

; GENERAL INFORMATION:

; APPLICANT: De Smet, Koenraad

; APPLICANT: Stuyver, Lieven

; TITLE OF INVENTION: Method for Detection of Drug-Induced Mutations in the HIV Reverse

; TITLE OF INVENTION: Transcriptase Gene

; FILE REFERENCE: 11362-0033-NPUS01 (INNS:033)

; CURRENT APPLICATION NUMBER: US/10/043,875

; CURRENT FILING DATE: 2002-04-03

; PRIOR APPLICATION NUMBER: 60/286,102

; PRIOR FILING DATE: 2001-04-24

; PRIOR APPLICATION NUMBER: EP 01870085.6

; PRIOR FILING DATE: 2001-04-20

; PRIOR APPLICATION NUMBER: EP 01870005.4

; PRIOR FILING DATE: 2001-01-11

; NUMBER OF SEQ ID NOS: 884

; SOFTWARE: PatentIn version 3.1

```
; SEQ ID NO 397
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus
US-10-043-875-397

Query Match      33.8%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 44;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      2 CATCCACCTGCTG 14
      ||||| |||
Db      13 CATCCACGTACTG 1

RESULT 92
US-10-043-875-422/c
; Sequence 422, Application US/10043875
; Publication No. US20030054339A1
; GENERAL INFORMATION:
; APPLICANT: De Smet, Koenraad
; APPLICANT: Stuyver, Lieven
; TITLE OF INVENTION: Method for Detection of Drug-Induced Mutations in the HIV Reverse
; TITLE OF INVENTION: Transcriptase Gene
; FILE REFERENCE: 11362-0033-NPUS01 (INNS:033)
; CURRENT APPLICATION NUMBER: US/10/043,875
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/286,102
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: EP 01870085.6
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: EP 01870005.4
; PRIOR FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 884
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 422
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus
US-10-043-875-422

Query Match      33.8%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 44;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      2 CATCCACCTGCTG 14
      ||||| |||
Db      13 CATCCACGTACTG 1

RESULT 93
US-10-311-645A-118
; Sequence 118, Application US/10311645A
; Publication No. US20040214302A1
; GENERAL INFORMATION:
; APPLICANT: Anthony, James
; APPLICANT: Lorincz, Attila
; APPLICANT: Williams, Inna
; APPLICANT: Troy, John
; APPLICANT: Tang, Yanglin
; TITLE OF INVENTION: DETECTION OF NUCLEIC ACIDS BY TYPE-SPECIFIC HYBRID CAPTURE METHOD
; FILE REFERENCE: 2629-4017US1
; CURRENT APPLICATION NUMBER: US/10/311,645A
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/US01/19353
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 09/594,839
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 118
; LENGTH: 13
; TYPE: DNA
```

```
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Nucleic acid probe: PZ-1
US-10-311-645A-118

Query Match      33.8%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 44;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      5 CCACCTGCTGTGT 17
      ||||| |||
Db      1 CCACCTCCTGCGT 13

RESULT 94
US-10-257-017B-145363/c
; Sequence 145363, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 145363
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0036590
US-10-257-017B-145363

Query Match      33.8%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 44;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1 CCATCCACCTGCT 13
      ||||| |||
Db      13 CCATCCGCTACT 1

RESULT 95
US-10-257-017B-145364
; Sequence 145364, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 145364
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0036590
US-10-257-017B-145364

Query Match      33.8%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 44;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1 CCATCCACCTGCT 13
      ||||| |||
Db      13 CCATCCGCTACT 1

RESULT 95
US-10-257-017B-145364
; Sequence 145364, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 145364
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0036590
US-10-257-017B-145364

Query Match      33.8%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 44;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCT 13  
|||||

Db 1 CCATCCGCCTACT 13

RESULT 96

US-09-771-933-166

; Sequence 166, Application US/09771933

; Publication No. US20030023387A1

; GENERAL INFORMATION:

; APPLICANT: Gill-Garrison, Rosalynn D

; APPLICANT: Martin, Christopher J

; APPLICANT: Sanchez-Felix, Manuel V

; TITLE OF INVENTION: Computer-assisted Means for Assessing Lifestyle Risk

; TITLE OF INVENTION: Factors

; FILE REFERENCE: 620-130

; CURRENT APPLICATION NUMBER: US/09/771,933

; CURRENT FILING DATE: 2001-01-30

; NUMBER OF SEQ ID NOS: 205

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 166

; LENGTH: 14

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Probe

US-09-771-933-166

Query Match 33.8%; Score 9.8; DB 1; Length 14;

Best Local Similarity 84.6%; Pred. No. 48;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TCCACCTGCTGTG 16  
|||||

Db 2 TCCACCTCCTGGG 14

RESULT 97

US-10-146-058-15

; Sequence 15, Application US/10146058

; Publication No. US20030040499A1

; GENERAL INFORMATION:

; APPLICANT: Schlingensiepen, Georg-Ferdinand

; APPLICANT: Brysch, Wolfgang

; APPLICANT: Schlingensiepen, Karl-Hermann

; APPLICANT: Schlingensiepen, Reimar

; APPLICANT: Bogdahn, Ulrich

; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of

; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta

; NUMBER OF SEQUENCES: 137

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Jacobson, Price, Holman & Stern

; STREET: 400 Seventh St. N.W.

; CITY: Washington D.C

; COUNTRY: U.S.A.

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/146,058

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/535,249

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 93 107 089.0

; FILING DATE: 30-APR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 93 107 849.7

; FILING DATE: 13-MAY-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Player, William E.

; REGISTRATION NUMBER: 31,409

; REFERENCE/DOCKET NUMBER: 10577/P58418

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)638-6666

; TELEFAX: (202) 393-5350

; TELEX: RCA 248593 IDEA UR

; INFORMATION FOR SEQ ID NO: 15:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 14 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: DNA (genomic)

; ANTI-SENSE: YES

US-10-146-058-15

Query Match 33.8%; Score 9.8; DB 1; Length 14;

Best Local Similarity 84.6%; Pred. No. 48;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 TGCTGTGTGACCT 22  
|||||

Db 1 TGCTGTGTGTACT 13

RESULT 98

US-10-043-875-394/c

; Sequence 394, Application US/10043875

; Publication No. US20030054339A1

; GENERAL INFORMATION:

; APPLICANT: De Smet, Koenraad

; APPLICANT: Stuyver, Lieven

; TITLE OF INVENTION: Method for Detection of Drug-Induced Mutations in the HIV Reverse

; TITLE OF INVENTION: Transcriptase Gene

; FILE REFERENCE: 11362-0033-NPUS01 (INNS:033)

; CURRENT APPLICATION NUMBER: US/10/043,875

; CURRENT FILING DATE: 2002-04-03

; PRIOR APPLICATION NUMBER: 60/286,102

; PRIOR FILING DATE: 2001-04-24

; PRIOR APPLICATION NUMBER: EP 01870085.6

; PRIOR FILING DATE: 2001-04-20

; PRIOR APPLICATION NUMBER: EP 01870005.4

; PRIOR FILING DATE: 2001-01-11

; NUMBER OF SEQ ID NOS: 884

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 394

; LENGTH: 14

; TYPE: DNA

; ORGANISM: Human immunodeficiency virus

US-10-043-875-394

Query Match 33.8%; Score 9.8; DB 1; Length 14;

Best Local Similarity 84.6%; Pred. No. 48;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTG 14  
|||||

Db 14 CATCCACGTACTG 2

RESULT 99

US-10-043-875-398/c

; Sequence 398, Application US/10043875

; Publication No. US20030054339A1

; GENERAL INFORMATION:

; APPLICANT: De Smet, Koenraad

; APPLICANT: Stuyver, Lieven

; TITLE OF INVENTION: Method for Detection of Drug-Induced Mutations in the HIV Reverse



```
; TITLE OF INVENTION: Transcriptase Gene
; FILE REFERENCE: 11362-0033-NPUS01 (INNS:033)
; CURRENT APPLICATION NUMBER: US/10/043,875
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/286,102
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: EP 01870085.6
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: EP 01870005.4
; PRIOR FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 884
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 398
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus
US-10-043-875-398

Query Match      33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 CATCCACCTGCTG 14
Db      14 CATCCACATACTG 2

RESULT 100
US-10-043-875-412/c
; Sequence 412, Application US/10043875
; Publication No. US20030054339A1
; GENERAL INFORMATION:
; APPLICANT: De Smet, Koenraad
; APPLICANT: Stuyver, Lieven
; TITLE OF INVENTION: Method for Detection of Drug-Induced Mutations in the HIV Reverse
; FILE REFERENCE: 11362-0033-NPUS01 (INNS:033)
; CURRENT APPLICATION NUMBER: US/10/043,875
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/286,102
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: EP 01870085.6
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: EP 01870005.4
; PRIOR FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 884
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 412
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus
US-10-043-875-412

Query Match      33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 CATCCACCTGCTG 14
Db      14 CATCCACGTACTG 2

RESULT 101
US-10-043-875-414/c
; Sequence 414, Application US/10043875
; Publication No. US20030054339A1
; GENERAL INFORMATION:
; APPLICANT: De Smet, Koenraad
; APPLICANT: Stuyver, Lieven
; TITLE OF INVENTION: Method for Detection of Drug-Induced Mutations in the HIV Reverse
; FILE REFERENCE: 11362-0033-NPUS01 (INNS:033)
; CURRENT APPLICATION NUMBER: US/10/043,875
```

```
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/286,102
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: EP 01870085.6
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: EP 01870005.4
; PRIOR FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 884
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 414
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus
US-10-043-875-414

Query Match      33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 CATCCACCTGCTG 14
Db      14 CATCCACGTACTG 2

RESULT 102
US-10-043-875-417/c
; Sequence 417, Application US/10043875
; Publication No. US20030054339A1
; GENERAL INFORMATION:
; APPLICANT: De Smet, Koenraad
; APPLICANT: Stuyver, Lieven
; TITLE OF INVENTION: Method for Detection of Drug-Induced Mutations in the HIV Reverse
; FILE REFERENCE: 11362-0033-NPUS01 (INNS:033)
; CURRENT APPLICATION NUMBER: US/10/043,875
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/286,102
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: EP 01870085.6
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: EP 01870005.4
; PRIOR FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 884
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 417
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus
US-10-043-875-417

Query Match      33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 CATCCACCTGCTG 14
Db      13 CATCCACATACTG 1

RESULT 103
US-10-043-875-421/c
; Sequence 421, Application US/10043875
; Publication No. US20030054339A1
; GENERAL INFORMATION:
; APPLICANT: De Smet, Koenraad
; APPLICANT: Stuyver, Lieven
; TITLE OF INVENTION: Method for Detection of Drug-Induced Mutations in the HIV Reverse
; FILE REFERENCE: 11362-0033-NPUS01 (INNS:033)
; CURRENT APPLICATION NUMBER: US/10/043,875
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/286,102
; PRIOR FILING DATE: 2001-04-24
```

```
; PRIOR APPLICATION NUMBER: EP 01870085.6
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: EP 01870005.4
; PRIOR FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 884
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 421
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus
US-10-043-875-421

Query Match      33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CATCCACCTGCTG 14
      ||||| | |||
Db      13 CATCCACGTACTG 1

RESULT 104
US-10-984-919-367
; Sequence 367, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/10/984,919
; PRIOR FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 367
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-367

Query Match      33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      11 GCTGTGTGACCTG 23
      ||||| | |||
Db      1 GCTGTGTCACCAG 13

RESULT 105
US-10-984-919-1153
; Sequence 1153, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
```

```
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1153
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-1153

Query Match      33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      10 TGCTGTGTGACCT 22
      ||||| | ||
Db      1 TGCTGTGTGTACT 13

RESULT 106
US-10-984-919-1469/c
; Sequence 1469, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1469
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-1469

Query Match      33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      12 CTGTGTGACCTGG 24
      |||| | |||
Db      13 CTGTCTGACATGG 1

Search completed: May 15, 2006, 15:06:05
Job time : 1 secs
```

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 15, 2006, 15:24:11 ; Search time 0.001 Seconds  
(without alignments)  
136.184 Million cell updates/sec

Title: US-09-904-968A-3-COPY  
Perfect score: 29  
Sequence: 1 ccattccactgtgtgtgacctggtgtaaat 29

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 0.5  
Searched: 124 seqs, 2348 residues

Total number of hits satisfying chosen parameters: 248

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 124 summaries

Database : pubnewdb:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID                       | Description       |
|------------|-------|-------------|--------|--------------------------|-------------------|
| 1          | 17.6  | 60.7        | 25     | 1 US-11-121-849-418301   | Sequence 418301,  |
| 2          | 16.8  | 57.9        | 20     | 1 US-10-310-914A-1382191 | Sequence 1382191, |
| 3          | 16.8  | 57.9        | 21     | 1 US-10-310-914A-289945  | Sequence 289945,  |
| 4          | 16.2  | 55.9        | 23     | 1 US-10-310-914A-739052  | Sequence 739052,  |
| 5          | 16    | 55.2        | 22     | 1 US-10-310-914A-738911  | Sequence 738911,  |
| 6          | 15.8  | 54.5        | 21     | 1 US-10-310-914A-1382178 | Sequence 1382178, |
| 7          | 15.4  | 53.1        | 19     | 1 US-11-101-244-1259291  | Sequence 1259291, |
| 8          | 15.4  | 53.1        | 19     | 1 US-11-083-784-1259291  | Sequence 1259291, |
| 9          | 15    | 51.7        | 19     | 1 US-10-310-914A-943748  | Sequence 943748,  |
| 10         | 15    | 51.7        | 20     | 1 US-10-310-914A-1142003 | Sequence 1142003, |
| 11         | 14.8  | 51.0        | 18     | 1 US-10-310-914A-1382190 | Sequence 1382190, |
| 12         | 14.8  | 51.0        | 19     | 1 US-11-101-244-561054   | Sequence 561054,  |
| 13         | 14.8  | 51.0        | 19     | 1 US-11-101-244-681930   | Sequence 681930,  |
| 14         | 14.8  | 51.0        | 19     | 1 US-11-101-244-807207   | Sequence 807207,  |
| 15         | 14.8  | 51.0        | 19     | 1 US-11-101-244-935230   | Sequence 935230,  |
| 16         | 14.8  | 51.0        | 19     | 1 US-11-101-244-1066344  | Sequence 1066344, |
| 17         | 14.8  | 51.0        | 19     | 1 US-11-101-244-1309698  | Sequence 1309698, |
| 18         | 14.8  | 51.0        | 19     | 1 US-11-083-784-561054   | Sequence 561054,  |
| 19         | 14.8  | 51.0        | 19     | 1 US-11-083-784-681930   | Sequence 681930,  |
| 20         | 14.8  | 51.0        | 19     | 1 US-11-083-784-807207   | Sequence 807207,  |
| 21         | 14.8  | 51.0        | 19     | 1 US-11-083-784-935230   | Sequence 935230,  |
| 22         | 14.8  | 51.0        | 19     | 1 US-11-083-784-1066344  | Sequence 1066344, |
| 23         | 14.8  | 51.0        | 19     | 1 US-11-083-784-1309698  | Sequence 1309698, |
| 24         | 14.8  | 51.0        | 21     | 1 US-10-310-914A-1382262 | Sequence 1382262, |
| 25         | 14.4  | 49.7        | 18     | 1 US-10-310-914A-753677  | Sequence 753677,  |
| 26         | 14.4  | 49.7        | 18     | 1 US-10-310-914A-776270  | Sequence 776270,  |
| 27         | 14.4  | 49.7        | 18     | 1 US-10-310-914A-846082  | Sequence 846082,  |
| 28         | 14.4  | 49.7        | 19     | 1 US-11-101-244-60143    | Sequence 60143, A |
| 29         | 14.4  | 49.7        | 19     | 1 US-11-101-244-732143   | Sequence 732143,  |
| 30         | 14.4  | 49.7        | 19     | 1 US-11-101-244-732234   | Sequence 732234,  |
| 31         | 14.4  | 49.7        | 19     | 1 US-11-101-244-1350412  | Sequence 1350412, |
| 32         | 14.4  | 49.7        | 19     | 1 US-11-101-244-1350424  | Sequence 1350424, |
| 33         | 14.4  | 49.7        | 19     | 1 US-11-083-784-60143    | Sequence 60143, A |

|     |      |      |    |                          |                   |
|-----|------|------|----|--------------------------|-------------------|
| 34  | 14.4 | 49.7 | 19 | 1 US-11-083-784-732143   | Sequence 732143,  |
| 35  | 14.4 | 49.7 | 19 | 1 US-11-083-784-732234   | Sequence 732234,  |
| 36  | 14.4 | 49.7 | 19 | 1 US-11-083-784-1350412  | Sequence 1350412, |
| 37  | 14.4 | 49.7 | 19 | 1 US-11-083-784-1350424  | Sequence 1350424, |
| 38  | 14.4 | 49.7 | 20 | 1 US-10-310-914A-1087566 | Sequence 1087566, |
| 39  | 14.2 | 49.0 | 19 | 1 US-11-101-244-169031   | Sequence 169031,  |
| 40  | 14.2 | 49.0 | 19 | 1 US-11-101-244-169132   | Sequence 169132,  |
| 41  | 14.2 | 49.0 | 19 | 1 US-11-101-244-169222   | Sequence 169222,  |
| 42  | 14.2 | 49.0 | 19 | 1 US-11-101-244-169323   | Sequence 169323,  |
| 43  | 14.2 | 49.0 | 19 | 1 US-11-101-244-179633   | Sequence 179633,  |
| 44  | 14.2 | 49.0 | 19 | 1 US-11-101-244-385863   | Sequence 385863,  |
| 45  | 14.2 | 49.0 | 19 | 1 US-11-101-244-491187   | Sequence 491187,  |
| 46  | 14.2 | 49.0 | 19 | 1 US-11-101-244-599457   | Sequence 599457,  |
| 47  | 14.2 | 49.0 | 19 | 1 US-11-101-244-762299   | Sequence 762299,  |
| 48  | 14.2 | 49.0 | 19 | 1 US-11-101-244-762404   | Sequence 762404,  |
| 49  | 14.2 | 49.0 | 19 | 1 US-11-101-244-767248   | Sequence 767248,  |
| 50  | 14.2 | 49.0 | 19 | 1 US-11-101-244-767320   | Sequence 767320,  |
| 51  | 14.2 | 49.0 | 19 | 1 US-11-101-244-1316239  | Sequence 1316239, |
| 52  | 14.2 | 49.0 | 19 | 1 US-11-101-244-1338912  | Sequence 1338912, |
| 53  | 14.2 | 49.0 | 19 | 1 US-11-101-244-1559238  | Sequence 1559238, |
| 54  | 14.2 | 49.0 | 19 | 1 US-11-083-784-169031   | Sequence 169031,  |
| 55  | 14.2 | 49.0 | 19 | 1 US-11-083-784-169132   | Sequence 169132,  |
| 56  | 14.2 | 49.0 | 19 | 1 US-11-083-784-169222   | Sequence 169222,  |
| 57  | 14.2 | 49.0 | 19 | 1 US-11-083-784-169323   | Sequence 169323,  |
| 58  | 14.2 | 49.0 | 19 | 1 US-11-083-784-179633   | Sequence 179633,  |
| 59  | 14.2 | 49.0 | 19 | 1 US-11-083-784-385863   | Sequence 385863,  |
| 60  | 14.2 | 49.0 | 19 | 1 US-11-083-784-491187   | Sequence 491187,  |
| 61  | 14.2 | 49.0 | 19 | 1 US-11-083-784-599457   | Sequence 599457,  |
| 62  | 14.2 | 49.0 | 19 | 1 US-11-083-784-762299   | Sequence 762299,  |
| 63  | 14.2 | 49.0 | 19 | 1 US-11-083-784-762404   | Sequence 762404,  |
| 64  | 14.2 | 49.0 | 19 | 1 US-11-083-784-767248   | Sequence 767248,  |
| 65  | 14.2 | 49.0 | 19 | 1 US-11-083-784-767320   | Sequence 767320,  |
| 66  | 14.2 | 49.0 | 19 | 1 US-11-083-784-1316239  | Sequence 1316239, |
| 67  | 14.2 | 49.0 | 19 | 1 US-11-083-784-1338912  | Sequence 1338912, |
| 68  | 14.2 | 49.0 | 19 | 1 US-11-083-784-1559238  | Sequence 1559238, |
| 69  | 13.8 | 47.6 | 19 | 1 US-10-898-311-111      | Sequence 111, App |
| 70  | 13.8 | 47.6 | 19 | 1 US-10-898-311-367      | Sequence 367, App |
| 71  | 13.8 | 47.6 | 19 | 1 US-10-310-914A-161892  | Sequence 161892,  |
| 72  | 13.8 | 47.6 | 19 | 1 US-10-310-914A-161893  | Sequence 161893,  |
| 73  | 13.8 | 47.6 | 19 | 1 US-10-310-914A-1323233 | Sequence 1323233, |
| 74  | 13.8 | 47.6 | 19 | 1 US-11-101-244-282638   | Sequence 282638,  |
| 75  | 13.8 | 47.6 | 19 | 1 US-11-101-244-403263   | Sequence 403263,  |
| 76  | 13.8 | 47.6 | 19 | 1 US-11-101-244-403331   | Sequence 403331,  |
| 77  | 13.8 | 47.6 | 19 | 1 US-11-101-244-672456   | Sequence 672456,  |
| 78  | 13.8 | 47.6 | 19 | 1 US-11-101-244-677906   | Sequence 677906,  |
| 79  | 13.8 | 47.6 | 19 | 1 US-11-101-244-847054   | Sequence 847054,  |
| 80  | 13.8 | 47.6 | 19 | 1 US-11-101-244-1035429  | Sequence 1035429, |
| 81  | 13.8 | 47.6 | 19 | 1 US-11-101-244-1436644  | Sequence 1436644, |
| 82  | 13.8 | 47.6 | 19 | 1 US-11-101-244-1436706  | Sequence 1436706, |
| 83  | 13.8 | 47.6 | 19 | 1 US-11-101-244-1467224  | Sequence 1467224, |
| 84  | 13.8 | 47.6 | 19 | 1 US-11-101-244-1568291  | Sequence 1568291, |
| 85  | 13.8 | 47.6 | 19 | 1 US-11-101-244-1568369  | Sequence 1568369, |
| 86  | 13.8 | 47.6 | 19 | 1 US-11-083-784-282638   | Sequence 282638,  |
| 87  | 13.8 | 47.6 | 19 | 1 US-11-083-784-403263   | Sequence 403263,  |
| 88  | 13.8 | 47.6 | 19 | 1 US-11-083-784-403331   | Sequence 403331,  |
| 89  | 13.8 | 47.6 | 19 | 1 US-11-083-784-672456   | Sequence 672456,  |
| 90  | 13.8 | 47.6 | 19 | 1 US-11-083-784-677906   | Sequence 677906,  |
| 91  | 13.8 | 47.6 | 19 | 1 US-11-083-784-847054   | Sequence 847054,  |
| 92  | 13.8 | 47.6 | 19 | 1 US-11-083-784-1035429  | Sequence 1035429, |
| 93  | 13.8 | 47.6 | 19 | 1 US-11-083-784-1436644  | Sequence 1436644, |
| 94  | 13.8 | 47.6 | 19 | 1 US-11-083-784-1436706  | Sequence 1436706, |
| 95  | 13.8 | 47.6 | 19 | 1 US-11-083-784-1467224  | Sequence 1467224, |
| 96  | 13.8 | 47.6 | 19 | 1 US-11-083-784-1568291  | Sequence 1568291, |
| 97  | 13.8 | 47.6 | 19 | 1 US-11-083-784-1568369  | Sequence 1568369, |
| 98  | 13.4 | 46.2 | 18 | 1 US-10-310-914A-606643  | Sequence 606643,  |
| 99  | 13.4 | 46.2 | 18 | 1 US-10-310-914A-1317194 | Sequence 1317194, |
| 100 | 13.4 | 46.2 | 19 | 1 US-10-310-914A-472976  | Sequence 472976,  |
| 101 | 13.4 | 46.2 | 19 | 1 US-10-310-914A-549957  | Sequence 549957,  |
| 102 | 13.4 | 46.2 | 19 | 1 US-11-101-244-821390   | Sequence 821390,  |
| 103 | 13.4 | 46.2 | 19 | 1 US-11-101-244-859101   | Sequence 859101,  |
| 104 | 13.4 | 46.2 | 19 | 1 US-11-101-244-1260137  | Sequence 1260137, |
| 105 | 13.4 | 46.2 | 19 | 1 US-11-101-244-1260202  | Sequence 1260202, |
| 106 | 13.4 | 46.2 | 19 | 1 US-11-101-244-1318311  | Sequence 1318311, |

Published Applications  
NA New

c 107 13.4 46.2 19 1 US-11-101-244-1544345 Sequence 1544345,  
108 13.4 46.2 19 1 US-11-083-784-821390 Sequence 821390,  
109 13.4 46.2 19 1 US-11-083-784-859101 Sequence 859101,  
110 13.4 46.2 19 1 US-11-083-784-1260137 Sequence 1260137,  
111 13.4 46.2 19 1 US-11-083-784-1260202 Sequence 1260202,  
c 112 13.4 46.2 19 1 US-11-083-784-1318311 Sequence 1318311,  
c 113 13.4 46.2 19 1 US-11-083-784-1544345 Sequence 1544345,  
114 13.2 45.5 18 1 US-10-310-914A-623917 Sequence 623917,  
115 13.2 45.5 18 1 US-10-310-914A-784062 Sequence 784062,  
116 13.2 45.5 18 1 US-10-310-914A-1081549 Sequence 1081549,  
c 117 13 44.8 18 1 US-10-310-914A-608562 Sequence 608562,  
118 13 44.8 18 1 US-10-310-914A-730768 Sequence 730768,  
c 119 12.8 44.1 18 1 US-10-310-914A-183276 Sequence 183276,  
c 120 12.8 44.1 18 1 US-10-310-914A-481748 Sequence 481748,  
c 121 12.8 44.1 18 1 US-10-310-914A-954247 Sequence 954247,  
122 10.8 37.2 14 1 US-10-880-315-224 Sequence 224, Appl  
c 123 9.8 33.8 13 1 US-11-269-003-81 Sequence 81, Appl  
c 124 9.8 33.8 14 1 US-11-176-026A-24 Sequence 24, Appl

ALIGNMENTS

RESULT 1  
US-11-121-849-418301  
; Sequence 418301, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; TITLE OF INVENTION: Microarrays  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 418301  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-418301

Query Match 60.7%; Score 17.6; DB 1; Length 25;  
Best Local Similarity 83.3%; Pred. No. 13;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTGACCTGGTAAA 28  
|| |||||  
Db 1 CCTGCTGCTGTGTACCTGGTACA 24

RESULT 2  
US-10-310-914A-1382191  
; Sequence 1382191, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1382191  
; LENGTH: 20  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1382191

Query Match 55.9%; Score 16.2; DB 1; Length 23;  
Best Local Similarity 61.9%; Pred. No. 19;  
Matches 13; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGTGACCT 22  
|| |||  
Db 3 CAGAAACCGUGUGUGACCU 23

RESULT 5  
US-10-310-914A-738911  
; Sequence 738911, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac

Query Match 57.9%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 65.0%; Pred. No. 19;  
Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
QY 5 CCACCTGCTGTGTGACCTGG 24  
|| |||  
Db 1 CCCCCUGUGUGGCCUGG 20  
RESULT 3  
US-10-310-914A-289945/c  
; Sequence 289945, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 289945  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-289945

Query Match 57.9%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 90.0%; Pred. No. 18;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 ACCTGCTGTGTGACCTGGTA 26  
| |||||  
Db 20 AGCTGCTGTGTGACCTGGGA 1

RESULT 4  
US-10-310-914A-739052  
; Sequence 739052, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 739052  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-739052

Query Match 55.9%; Score 16.2; DB 1; Length 23;  
Best Local Similarity 61.9%; Pred. No. 19;  
Matches 13; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

```

; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 738911
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-738911

Query Match          55.2%; Score 16; DB 1; Length 22;
Best Local Similarity 68.8%; Pred. No. 21;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCTGCTGTGTGACCT 22
Db |||:||||:||||:
5 ACCUGCUGUGUGACCU 20

RESULT 6
US-10-310-914A-1382178
; Sequence 1382178, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1382178
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1382178

Query Match          54.5%; Score 15.8; DB 1; Length 21;
Best Local Similarity 63.2%; Pred. No. 23;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTGACCTG 23
Db ||||:||||:||||:
3 CCCCCUGCUGUGUGGCCUG 21

RESULT 7
US-11-101-244-1259291/c
; Sequence 1259291, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
US-11-101-244-1259291/c

APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 738911
LENGTH: 22
TYPE: RNA
ORGANISM: Human
US-10-310-914A-738911

Query Match          55.2%; Score 16; DB 1; Length 22;
Best Local Similarity 68.8%; Pred. No. 21;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCTGCTGTGTGACCT 22
Db |||:||||:||||:
5 ACCUGCUGUGUGACCU 20

RESULT 6
US-10-310-914A-1382178
; Sequence 1382178, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1382178
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1382178

Query Match          54.5%; Score 15.8; DB 1; Length 21;
Best Local Similarity 63.2%; Pred. No. 23;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTGACCTG 23
Db ||||:||||:||||:
3 CCCCCUGCUGUGUGGCCUG 21

RESULT 7
US-11-101-244-1259291/c
; Sequence 1259291, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
US-11-101-244-1259291/c
```

```

; SEQ ID NO 1259291
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1259291

Query Match          53.1%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 28;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGTG 18
Db |||||:|||||:|||||
18 CATCCACCTGCTGTCTG 2

RESULT 8
US-11-083-784-1259291/c
; Sequence 1259291, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1259291
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1259291

Query Match          53.1%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 28;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGTG 18
Db |||||:|||||:|||||
18 CATCCACCTGCTGTCTG 2

RESULT 9
US-10-310-914A-943748
; Sequence 943748, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 943748
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-943748
```



```
Query Match          51.7%; Score 15; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 10 TGCTGTGTGACCTGG 24
Db 1 UGCUGUGUGACCUUG 15

RESULT 10
US-10-310-914A-1142003
; Sequence 1142003, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1142003
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1142003

Query Match          51.7%; Score 15; DB 1; Length 20;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 10 TGCTGTGTGACCTGG 24
Db 1 UGCUGUGUGACCUUG 15

RESULT 11
US-10-310-914A-1382190
; Sequence 1382190, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1382190
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1382190

Query Match          51.0%; Score 14.8; DB 1; Length 18;
Best Local Similarity 61.1%; Pred. No. 34;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCACCTGTGTGTGACCT 22
Db 1 CCCCCUGUGUGGCGCCU 18

RESULT 12
US-11-101-244-561054
; Sequence 561054, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
```

```
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 561054
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-561054

Query Match          51.0%; Score 14.8; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGTA 19
Db 2 CAUCUACCCGUGUGUGA 19

RESULT 13
US-11-101-244-681930
; Sequence 681930, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 681930
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-681930

Query Match          51.0%; Score 14.8; DB 1; Length 19;
Best Local Similarity 55.6%; Pred. No. 32;
Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 9 CTGCTGTGTGACCTGGTA 26
Db 2 CUCCUAUGUGACCUUGUA 19

RESULT 14
US-11-101-244-807207
; Sequence 807207, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
```

; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 807207  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-807207

Query Match 51.0%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 55.6%; Pred. No. 32;  
Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 9 CTGCTGTGTGACCTGGTA 26  
|:|:|:|:|:|:|:|:|:|:|:|:|:|  
Db 2 CUGCUAUGGCGCCUGGUA 19

RESULT 15  
US-11-101-244-935230  
; Sequence 935230, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 935230  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-935230

Query Match 51.0%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 61.1%; Pred. No. 32;  
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATCCACCTGTGTGTGA 19  
|:|:|:|:|:|:|:|:|:|:|:|:|:|  
Db 2 CCUCUACCUGCGUGUGUA 19

RESULT 16  
US-11-101-244-1066344  
; Sequence 1066344, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela

; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1066344  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1066344

Query Match 51.0%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 55.6%; Pred. No. 32;  
Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 9 CTGCTGTGTGACCTGGTA 26  
|:|:|:|:|:|:|:|:|:|:|:|:|:|  
Db 2 CUGCUGUCUGAACUGGUA 19

RESULT 17  
US-11-101-244-1309698  
; Sequence 1309698, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1309698  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1309698

Query Match 51.0%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 61.1%; Pred. No. 32;  
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 9 CTGCTGTGTGACCTGGTA 26  
|:|:|:|:|:|:|:|:|:|:|:|:|:|  
Db 2 CUGCUGCGUGAGCUGGUA 19

RESULT 18  
US-11-083-784-561054  
; Sequence 561054, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin

; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 561054  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-561054

Query Match 51.0%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 66.7%; Pred. No. 32;  
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGTGA 19  
||:| ||| ||:| ||:| ||:  
Db 2 CAUCUACCCGCGUGUGA 19

RESULT 19  
US-11-083-784-681930  
; Sequence 681930, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 681930  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-681930

Query Match 51.0%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 55.6%; Pred. No. 32;  
Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 9 CTGCTGTGTGACCTGGTA 26  
|: |: |:| ||| |:| |:|  
Db 2 CUCCUAUGUGACCCUGGUA 19

RESULT 20  
US-11-083-784-807207  
; Sequence 807207, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.

; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 807207  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-807207

Query Match 51.0%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 55.6%; Pred. No. 32;  
Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 9 CTGCTGTGTGACCTGGTA 26  
|: |: |:| ||| |:| |:|  
Db 2 CUGCUAUGUGGCCUGGUA 19

RESULT 21  
US-11-083-784-935230  
; Sequence 935230, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 935230  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-935230

Query Match 51.0%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 61.1%; Pred. No. 32;  
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGTGA 19  
|: |: |:| ||| |:| |:|  
Db 2 CCUCUACCCUGCUGUGA 19

RESULT 22  
US-11-083-784-1066344  
; Sequence 1066344, Application US/11083784

```

; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1066344
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1066344

Query Match          51.0%; Score 14.8; DB 1; Length 19;
Best Local Similarity 55.6%; Pred. No. 32;
Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 9 CTGCTGTGTGACCTGGTA 26
   |:|:|: |:|:|:|:|:|
Db 2 CUGCUGUCUGACUGGUA 19

RESULT 23
US-11-083-784-1309698
; Sequence 1309698, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1309698
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1309698

Query Match          51.0%; Score 14.8; DB 1; Length 19;
Best Local Similarity 61.1%; Pred. No. 32;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 9 CTGCTGTGTGACCTGGTA 26
   |:|:|: |:|:|:|:|:|
Db 2 CUGCUGCUGAGACUGGUA 19

US-11-083-784-1309698
; Sequence 1309698, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1309698
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1309698

Query Match          51.0%; Score 14.8; DB 1; Length 19;
Best Local Similarity 61.1%; Pred. No. 32;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 9 CTGCTGTGTGACCTGGTA 26
   |:|:|: |:|:|:|:|:|
Db 2 CUGCUGCUGAGACUGGUA 19
```

```

RESULT 24
US-10-310-914A-1382262
; Sequence 1382262, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1382262
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1382262

Query Match          51.0%; Score 14.8; DB 1; Length 21;
Best Local Similarity 61.1%; Pred. No. 29;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTGACCT 22
   |||:|:|:|:|:|:|:|
Db 4 CCCCUGCUGUGUGGCCU 21

RESULT 25
US-10-310-914A-753677
; Sequence 753677, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 753677
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-753677

Query Match          49.7%; Score 14.4; DB 1; Length 18;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTG 16
   |||:|:|:|:|:|:|
Db 3 CCAGCCACCUGCUGUG 18

RESULT 26
US-10-310-914A-776270
; Sequence 776270, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 776270
```





Qy 8 CCTGCTGTGTGACCTG 23  
||: ||: ||: ||: ||: ||:  
Db 1 CCUACUGUGUGACCCUG 16

```

RESULT 31
US-11-101-244-1350412
; Sequence 1350412, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1350412
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1350412

```

Query Match 49.7%; Score 14.4; DB 1; Length 19;  
Best Local Similarity 62.5%; Pred. No. 35;  
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy            2 CATCCACCTGCTGTGT 17  
               |||:|||||::|::|:  
Db            4 CAUCCACCUGCUGAU 19

```

RESULT 32
US-11-101-244-1350424
; Sequence 1350424, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1350424
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1350424

```

Query Match 49.7%; Score 14.4; DB 1; Length 19;  
Best Local Similarity 62.5%; Pred. No. 35;  
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGT 17

Db 2 CAUCCACCUGCUGAU 17

||:|||:||:|:

RESULT 33

US-11-083-784-60143

; Sequence 60143, Application US/11083784

; Publication No. US20050245475A1

; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.

; APPLICANT: Khvorova, Anastasia

; APPLICANT: Reynolds, Angela

; APPLICANT: Leake, Devin

; APPLICANT: Marshall, William

; APPLICANT: Scaringe, Stephen

; TITLE OF INVENTION: Functional and Hypo

; FILE REFERENCE: 13499US

; CURRENT APPLICATION NUMBER: US/11/083,

; CURRENT FILING DATE: 2005-03-18

; PRIOR APPLICATION NUMBER: US/10/714,333

; PRIOR FILING DATE: 2003-11-14

; PRIOR APPLICATION NUMBER: 60/502,050

; PRIOR FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: 60/426,137

; PRIOR FILING DATE: 2002-11-14

; NUMBER OF SEQ ID NOS: 1591911

; SOFTWARE: Proprietary

; SEQ ID NO 60143

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Homo sapiens

US-11-083-784-60143

Query Match 49.7%; Score 14.4; DB 1; Length 19;  
Best Local Similarity 62.5%; Pred. No. 35;  
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ACCTGCTGTGTGACCT 22  
|||:|:|:|:|:  
Db 2 ACUUGCUGUGACCU 17

```

RESULT 34
US-11-083-784-732143
; Sequence 732143, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 732143
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-732143

```

Query Match 49.7%; Score 14.4; DB 1; Length 19;  
Best Local Similarity 62.5%; Pred. No. 35;

...

Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
QY 8 CCTGCTGTGTGACCTG 23  
||:|:|:|:|:|:|  
Db 1 CCUACUGUGUGACCUG 16

RESULT 35  
US-11-083-784-732234  
; Sequence 732234, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 732234  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-732234

Query Match 49.7%; Score 14.4; DB 1; Length 19;  
Best Local Similarity 62.5%; Pred. No. 35;  
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGTGACCTG 23  
||:|:|:|:|:|:|  
Db 1 CCUACUGUGUGACCUG 16

RESULT 36  
US-11-083-784-1350412  
; Sequence 1350412, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1350412  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1350412

Query Match 49.7%; Score 14.4; DB 1; Length 19;  
Best Local Similarity 62.5%; Pred. No. 35;  
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGT 17  
||:|:|:|:|:|:|  
Db 4 CAUCCACCUGCUGUAU 19

RESULT 37  
US-11-083-784-1350424  
; Sequence 1350424, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1350424  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1350424

Query Match 49.7%; Score 14.4; DB 1; Length 19;  
Best Local Similarity 62.5%; Pred. No. 35;  
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGT 17  
||:|:|:|:|:|:|  
Db 2 CAUCCACCUGCUGUAU 17

RESULT 38  
US-10-310-914A-1087566  
; Sequence 1087566, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1087566  
; LENGTH: 20  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1087566

Query Match 49.7%; Score 14.4; DB 1; Length 20;  
Best Local Similarity 62.5%; Pred. No. 33;  
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 12 CTGTGTGACCTGGTAA 27

Db 3 CUGUGAGACCUGGUGA 18  
|:|:|:|:|:|:|:|:|  
RESULT 39  
US-11-101-244-169031  
; Sequence 169031, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 169031  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-169031  
Query Match 49.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 37;  
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 1 CCATCCACCTGCTGTGTGA 19  
||| |||||:| |:  
Db 1 CCACCCACCUGCAGAGUGA 19

Db 3 CUGUGAGACCUGGUGA 18  
|:|:|:|:|:|:|:|:|  
RESULT 40  
US-11-101-244-169132  
; Sequence 169132, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 169132  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-169132  
Query Match 49.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 37;  
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 1 CCATCCACCTGCTGTGTGA 19  
||| |||||:| |:  
Db 1 CCACCCACCUGCAGAGUGA 19

Db 3 CUGUGAGACCUGGUGA 18  
|:|:|:|:|:|:|:|:|  
RESULT 41  
US-11-101-244-169222  
; Sequence 169222, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 169222  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-169222  
Query Match 49.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 37;  
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 1 CCATCCACCTGCTGTGTGA 19  
||| |||||:| |:  
Db 1 CCACCCACCUGCAGAGUGA 19

Db 3 CUGUGAGACCUGGUGA 18  
|:~|:~|:~|:~|:~|:~|:~|  
RESULT 42  
US-11-101-244-169323  
; Sequence 169323, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 169323  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-169323  
Query Match 49.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 37;  
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 1 CCATCCACCTGCTGTGTGA 19  
||| |||||:| |:  
Db 1 CCACCCACCUGCAGAGUGA 19

Db 1 CCACCCACCUGCAGAGUGA 19  
|:~|:~|:~|:~|:~|:~|:~|  
RESULT 41  
US-11-101-244-169222  
; Sequence 169222, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 169222  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-169222  
Query Match 49.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 37;  
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 1 CCATCCACCTGCTGTGTGA 19  
||| |||||:| |:  
Db 1 CCACCCACCUGCAGAGUGA 19

Db 1 CCACCCACCUGCAGAGUGA 19  
|:~|:~|:~|:~|:~|:~|:~|  
RESULT 42  
US-11-101-244-169323  
; Sequence 169323, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 169323  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-169323  
Query Match 49.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 37;  
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 1 CCATCCACCTGCTGTGTGA 19  
||| |||||:| |:  
Db 1 CCACCCACCUGCAGAGUGA 19

RESULT 43  
US-11-101-244-179633  
; Sequence 179633, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 179633  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-179633

Query Match 49.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 52.6%; Pred. No. 37;  
Matches 10; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGTGACCTGGTA 26  
||:|:|:| ||:|:|  
Db 1 CCUACUGUGGCCCCUGCUA 19

RESULT 44  
US-11-101-244-385863  
; Sequence 385863, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 385863  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-385863

Query Match 49.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 37;  
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTGTGA 19  
|||:| ||| |:|:|  
Db 1 CCAUCGACCACCUGUGUA 19

RESULT 45  
US-11-101-244-491187  
; Sequence 491187, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491187  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-491187

Query Match 49.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 37;  
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTGTGA 19  
||| ||| |:|:|  
Db 1 CCACCCUCAUGCUGUGUA 19

RESULT 46  
US-11-101-244-599457  
; Sequence 599457, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 599457  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-599457

Query Match 49.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 57.9%; Pred. No. 37;  
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGTGACCTGGTA 26  
||:|:| |:|:|  
Db 1 CCUGUGGCUGACCUGGUA 19

RESULT 47  
US-11-101-244-762299  
; Sequence 762299, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13493US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 762299  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-762299

Query Match 49.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 57.9%; Pred. No. 37;  
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTGTGA 19  
|||: ||: ||: ||: ||: ||  
Db 1 CCAUUAACUUGCUGUGA 19

RESULT 48  
US-11-101-244-762404  
; Sequence 762404, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 762404  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-762404

Query Match 49.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 57.9%; Pred. No. 37;  
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTGTGA 19  
|||: ||: ||: ||: ||: ||  
Db 1 CCAUUAACUUGCUGUGA 19

RESULT 49

US-11-101-244-767248  
; Sequence 767248, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 767248  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-767248

Query Match 49.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 57.9%; Pred. No. 37;  
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGTGACCTGGTA 26  
|||: ||: ||: ||: ||: ||  
Db 1 CCUGGUGUGGCCUGGAA 19

RESULT 50  
US-11-101-244-767320  
; Sequence 767320, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 767320  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-767320

Query Match 49.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 57.9%; Pred. No. 37;  
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGTGACCTGGTA 26  
|||: ||: ||: ||: ||: ||  
Db 1 CCUGGUGUGGCCUGGAA 19

RESULT 51  
US-11-101-244-1316239



; Sequence 1316239, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1316239  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1316239

Query Match 49.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 37;  
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 8 CCTGCTGTGTGACCTGGTA 26  
||:|:|:|:|:|:|:|:|:|:|  
Db 1 CCUGCUGGGUGACGUGGAA 19

RESULT 52  
US-11-101-244-1338912  
; Sequence 1338912, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1338912  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1338912

Query Match 49.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 37;  
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGTA 19  
|||:|:|:|:|:|:|:|:|:|:|  
Db 1 CCAUCCACCUGACUGUGA 19

RESULT 53  
US-11-101-244-1559238  
; Sequence 1559238, Application US/11101244

; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1559238  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1559238

Query Match 49.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 52.6%; Pred. No. 37;  
Matches 10; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 8 CCTGCTGTGTGACCTGGTA 26  
||:|:|:|:|:|:|:|:|:|:|  
Db 1 CCUGCUGUGUCAUCUGUUA 19

RESULT 54  
US-11-083-784-169031  
; Sequence 169031, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 169031  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-169031

Query Match 49.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 37;  
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGTA 19  
|||:|:|:|:|:|:|:|:|:|:|  
Db 1 CCACCACCGACAGUGA 19

RESULT 55  
US-11-083-784-169132

; Sequence 169132, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 169132  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-169132

Query Match 49.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 37;  
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTGTGA 19  
||| |||||:|:|:|  
Db 1 CCACCCACCUGCAGAGUGA 19

RESULT 56

US-11-083-784-169222  
; Sequence 169222, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 169222  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-169222

Query Match 49.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 37;  
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTGTGA 19  
||| |||||:|:|:|  
Db 1 CCACCCACCUGCAGAGUGA 19

RESULT 57  
US-11-083-784-169323  
; Sequence 169323, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 169323  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-169323

Query Match 49.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 37;  
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTGTGA 19  
||| |||||:|:|:|  
Db 1 CCACCCACCUGCAGAGUGA 19

RESULT 58

US-11-083-784-179633  
; Sequence 179633, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 179633  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-179633

Query Match 49.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 52.6%; Pred. No. 37;  
Matches 10; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGTGACCTGGTA 26



Query Match 49.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 57.9%; Pred. No. 37;  
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGTGA 19  
|||: ||: ||: ||: ||: ||: ||  
Db 1 CCAUUAACUUGCUGUGUGA 19

RESULT 63  
US-11-083-784-762404  
; Sequence 762404, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 762404  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-762404

Query Match 49.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 57.9%; Pred. No. 37;  
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGTGA 19  
|||: ||: ||: ||: ||: ||: ||  
Db 1 CCAUUAACUUGCUGUGUGA 19

RESULT 64  
US-11-083-784-767248  
; Sequence 767248, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 767248  
; LENGTH: 19

; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-767248

Query Match 49.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 57.9%; Pred. No. 37;  
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 8 CCTGCTGTGTGACCTGGTA 26  
||: ||: ||: ||: ||: ||: ||  
Db 1 CCUGGUGUGGCCUGGAA 19

RESULT 65  
US-11-083-784-767320  
; Sequence 767320, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 767320  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-767320

Query Match 49.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 57.9%; Pred. No. 37;  
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 8 CCTGCTGTGTGACCTGGTA 26  
||: ||: ||: ||: ||: ||: ||  
Db 1 CCUGGUGUGGCCUGGAA 19

RESULT 66  
US-11-083-784-1316239  
; Sequence 1316239, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911

; SOFTWARE: Proprietary  
; SEQ ID NO 1316239  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1316239

Query Match 49.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 37;  
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 8 CCTGCTGTGTGACCTGGTA 26  
||:||||:|:||||:|  
Db 1 CCUGCUGGGUGACGUGGAA 19

RESULT 67

US-11-083-784-1338912  
; Sequence 1338912, Application US/11083784  
; Publication No. US20050245475A1

; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US

; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1338912

; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1338912

Query Match 49.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 37;  
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGTA 19  
|||:|||||:|:|  
Db 1 CCAUCCACCUAACUGUGA 19

RESULT 68

US-11-083-784-1559238  
; Sequence 1559238, Application US/11083784  
; Publication No. US20050245475A1

; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US

; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1559238  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1559238

Query Match 49.0%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 52.6%; Pred. No. 37;  
Matches 10; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 8 CCTGCTGTGTGACCTGGTA 26  
||:||||:|:||||:|  
Db 1 CCUGCUGUGUCAUCUGUUA 19

RESULT 69

US-10-898-311-111  
; Sequence 111, Application US/10898311  
; Publication No. US20050277608A1

; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: Guerdiolini, Roberto  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Vitamin D Receptor Gene  
; FILE REFERENCE: 400/200 (MBHB04-586)  
; CURRENT APPLICATION NUMBER: US/10/898,311  
; CURRENT FILING DATE: 2004-07-23  
; PRIOR APPLICATION NUMBER: PCT/US04/16390  
; PRIOR FILING DATE: 2004-05-24  
; PRIOR APPLICATION NUMBER: PCT/US04/13456  
; PRIOR FILING DATE: 2004-04-30  
; PRIOR APPLICATION NUMBER: US 10/826,966  
; PRIOR FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: US 10/780,447  
; PRIOR FILING DATE: 2004-02-13  
; PRIOR APPLICATION NUMBER: US 10/757,803  
; PRIOR FILING DATE: 2004-01-14  
; PRIOR APPLICATION NUMBER: US 60/362,016  
; PRIOR FILING DATE: 2002-03-06  
; PRIOR APPLICATION NUMBER: US 60/292,217  
; PRIOR FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: US 60/306,883  
; PRIOR FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 60/311,865  
; PRIOR FILING DATE: 2001-08-13  
; PRIOR APPLICATION NUMBER: US 10/727,780  
; PRIOR FILING DATE: 2003-12-03  
; Remaining prior Application data removed - See File Wrapper or PALM.

; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 111  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r  
US-10-898-311-111

Query Match 47.6%; Score 13.8; DB 1; Length 19;  
Best Local Similarity 76.5%; Pred. No. 40;  
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTGACC 21  
|||:||||:|:|  
Db 1 CCACCUGCUGAGAGACC 17

RESULT 70



US-10-898-311-367/c  
; Sequence 367, Application US/10898311  
; Publication No. US20050277608A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: Guerdiolini, Roberto  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Vitamin D Receptor Gene  
; TITLE OF INVENTION: Expression Using Short Interfering Nucleic Acid (siNA)  
; FILE REFERENCE: 400/200 (MBHB04-586)  
; CURRENT APPLICATION NUMBER: US/10/898,311  
; CURRENT FILING DATE: 2004-07-23  
; PRIOR APPLICATION NUMBER: PCT/US04/16390  
; PRIOR FILING DATE: 2004-05-24  
; PRIOR APPLICATION NUMBER: PCT/US04/13456  
; PRIOR FILING DATE: 2004-04-30  
; PRIOR APPLICATION NUMBER: US 10/826,966  
; PRIOR FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: US 10/780,447  
; PRIOR FILING DATE: 2004-02-13  
; PRIOR APPLICATION NUMBER: US 10/757,803  
; PRIOR FILING DATE: 2004-01-14  
; PRIOR APPLICATION NUMBER: US 60/362,016  
; PRIOR FILING DATE: 2002-03-06  
; PRIOR APPLICATION NUMBER: US 60/292,217  
; PRIOR FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: US 60/306,883  
; PRIOR FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 60/311,865  
; PRIOR FILING DATE: 2001-08-13  
; PRIOR APPLICATION NUMBER: US 10/727,780  
; PRIOR FILING DATE: 2003-12-03  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 638  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 367  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region  
US-10-898-311-367

Query Match 47.6%; Score 13.8; DB 1; Length 19;  
Best Local Similarity 88.2%; Pred. No. 40;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGAC 21  
| | | | | | | | | | | | | | |  
Db 19 CCACCTGCTGAGAGACC 3

RESULT 71  
US-10-310-914A-161892/c  
; Sequence 161892, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 161892  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-161892  
Query Match 47.6%; Score 13.8; DB 1; Length 19;

Best Local Similarity 88.2%; Pred. No. 40;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 8 CCTGCTGTGTGACCTGG 24  
| | | | | | | | | | | | | | |  
Db 18 CCTGCTGTGTGGCTTGG 2  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 161893  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-161893

Query Match 47.6%; Score 13.8; DB 1; Length 19;  
Best Local Similarity 88.2%; Pred. No. 40;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CCTGCTGTGTGACCTGG 24  
| | | | | | | | | | | | | | |  
Db 18 CCTGCTGTGTGGCTTGG 2

RESULT 73  
US-10-310-914A-1323233/c  
; Sequence 1323233, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1323233  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1323233  
Query Match 47.6%; Score 13.8; DB 1; Length 19;  
Best Local Similarity 88.2%; Pred. No. 40;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGTG 18  
| | | | | | | | | | | | | | |  
Db 17 CATTACCAGCTGTGTG 1

RESULT 74  
US-11-101-244-282638  
; Sequence 282638, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia

```
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 282638
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-282638
```

```
Query Match      47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 58.8%; Pred. No. 40;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 CCATCCACCTGCTGTGT 17
      |||:| | |:| |:| |:|
Db      1 CCAUCCUGCGUGUGU 17
```

```
RESULT 75
US-11-101-244-403263
; Sequence 403263, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 403263
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-403263
```

```
Query Match      47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 58.8%; Pred. No. 40;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 CCATCCACCTGCTGTGT 17
      |||:| | |:| |:| |:|
Db      1 CCAUCAACCGUGUGU 17
```

```
RESULT 76
US-11-101-244-403331
; Sequence 403331, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
```

```
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 403331
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-403331
```

```
Query Match      47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 58.8%; Pred. No. 40;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 CCATCCACCTGCTGTGT 17
      |||:| | |:| |:| |:|
Db      2 CCAUCAACCGUGUGU 18
```

```
RESULT 77
US-11-101-244-672456
; Sequence 672456, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 672456
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-672456
```

```
Query Match      47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 58.8%; Pred. No. 40;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      13 TGTGTGACCTGGTAAAT 29
      :| |:| |:| |:| |:|
Db      1 UGUGUGAGCUGGAAU 17
```

```
RESULT 78
US-11-101-244-677906
; Sequence 677906, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
```

```
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 677906
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-677906
```

```
Query Match      47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 52.9%; Pred. No. 40;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      13 TGTGTGACCTGCTGTAAT 29
      :|:|:|:|:|:|:|:|:|:|:|:|:
Db      1 UGUGUGUCCUUGUAAAU 17
```

```
RESULT 79
US-11-101-244-847054/c
; Sequence 847054, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 847054
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-847054
```

```
Query Match      47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 40;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      2 CATCCACCTGCTGTGTG 18
      ||||| ||| ||||| |||
Db      18 CATCCTCCTCCTGTGTG 2
```

```
RESULT 80
US-11-101-244-1035429/c
; Sequence 1035429, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
```

```
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1035429
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1035429
```

```
Query Match      47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 40;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      3 ATCCACCTGCTGTGTGA 19
      ||||| ||||| |||||
Db      17 ATCCACCTGCAATGTGA 1
```

```
RESULT 81
US-11-101-244-1436644/c
; Sequence 1436644, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1436644
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1436644
```

```
Query Match      47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 40;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      2 CATCCACCTGCTGTGTG 18
      ||||| ||||| ||||| |||
Db      18 CATCCACCTGCTCTTTG 2
```

```
RESULT 82
US-11-101-244-1436706/c
; Sequence 1436706, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
```

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1436706  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1436706

Query Match 47.6%; Score 13.8; DB 1; Length 19;  
Best Local Similarity 88.2%; Pred. No. 40;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCTGTGTG 18  
||| ||||| |||  
Db 17 CATCCACCTGCCTTTG 1

RESULT 83  
US-11-101-244-1467224  
; Sequence 1467224, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1467224  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1467224

Query Match 47.6%; Score 13.8; DB 1; Length 19;  
Best Local Similarity 58.8%; Pred. No. 40;  
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 7 ACCTGCTGTGTGACCTG 23  
||| ||||| |||  
Db 3 ACCUGCUGUGACUUG 19

RESULT 84  
US-11-101-244-1568291  
; Sequence 1568291, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
;

; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1568291  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1568291

Query Match 47.6%; Score 13.8; DB 1; Length 19;  
Best Local Similarity 64.7%; Pred. No. 40;  
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTGT 17  
||| ||||| |||  
Db 1 CCAGCCACCUCUGUGU 17

RESULT 85  
US-11-101-244-1568369  
; Sequence 1568369, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1568369  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1568369

Query Match 47.6%; Score 13.8; DB 1; Length 19;  
Best Local Similarity 64.7%; Pred. No. 40;  
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTGT 17  
||| ||||| |||  
Db 3 CCAGCCACCUCUGUGU 19

RESULT 86  
US-11-083-784-282638  
; Sequence 282638, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
;

```

; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 282638
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-282638

Query Match      47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 58.8%; Pred. No. 40;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCATCCACCTGCTGTGT 17
      |||:|||:|||:|||:
Db      1 CCAUCCUGCUGCUGUGU 17

RESULT 87
US-11-083-784-403263
; Sequence 403263, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 403263
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-403263

Query Match      47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 58.8%; Pred. No. 40;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCATCCACCTGCTGTGT 17
      |||:|||:|||:|||:
Db      1 CCAUCCUGCUGCUGUGU 17

RESULT 88
US-11-083-784-403331
; Sequence 403331, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William

```

```

; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 403331
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-403331

Query Match      47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 58.8%; Pred. No. 40;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCATCCACCTGCTGTGT 17
      |||:|||:|||:|||:
Db      2 CCAUCAACCGUCUGUCU 18

RESULT 89
US-11-083-784-672456
; Sequence 672456, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 672456
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-672456

Query Match      47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 58.8%; Pred. No. 40;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      13 TGTGTGACCTGGTAAAT 29
      :|:|:|||:|||:|||:
Db      1 UGUGUGAGCUGGGAUU 17

RESULT 90
US-11-083-784-677906
; Sequence 677906, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia

```



```

; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 677906
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-677906

Query Match          47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 52.9%; Pred. No. 40;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 13 TGTGTGACCTGGTAAAT 29
      :||:||||:||||:
Db 1 UGUGUGUCCUUGUAAAU 17

RESULT 91
US-11-083-784-847054/c
; Sequence 847054, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 847054
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-847054

Query Match          47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 40;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGTG 18
      ||||| ||| |||||
Db 18 CATCCTCCTCCTGTGTG 2

RESULT 92
US-11-083-784-1035429/c
; Sequence 1035429, Application US/11083784
; Publication No. US20050245475A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1035429
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1035429

Query Match          47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 40;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATCCACCTGCTGTGTGA 19
      ||||| ||||| |||||
Db 17 ATCCACCTGCAATGTGA 1

RESULT 93
US-11-083-784-1436644/c
; Sequence 1436644, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1436644
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1436644

Query Match          47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 40;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGTG 18
      ||||| ||||| |||||
Db 18 CATCCACCTGCTCTTTG 2

RESULT 94

```

US-11-083-784-1436706/c  
; Sequence 1436706, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1436706  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1436706

Query Match 47.6%; Score 13.8; DB 1; Length 19;  
Best Local Similarity 88.2%; Pred. No. 40;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGTG 18  
|||||  
Db 17 CATCCACCTGCTCTTTG 1

RESULT 95

US-11-083-784-1467224  
; Sequence 1467224, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1467224  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1467224

Query Match 47.6%; Score 13.8; DB 1; Length 19;  
Best Local Similarity 58.8%; Pred. No. 40;  
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 7 ACCTGCTGTGTGACCTG 23  
|||:|:|:|:|:|:|  
Db 3 ACCUGCUGUGACUUG 19

RESULT 96

US-11-083-784-1568291  
; Sequence 1568291, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1568291  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1568291

Query Match 47.6%; Score 13.8; DB 1; Length 19;  
Best Local Similarity 64.7%; Pred. No. 40;  
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGT 17  
||| |||||:|:|:|  
Db 1 CCAGCCACCUCUGUGU 17

RESULT 97

US-11-083-784-1568369  
; Sequence 1568369, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1568369  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1568369

Query Match 47.6%; Score 13.8; DB 1; Length 19;  
Best Local Similarity 64.7%; Pred. No. 40;  
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGT 17  
||| |||||: |:|:|:  
Db 3 CCAGCCACCUCUGUGU 19

RESULT 98  
US-10-310-914A-606643/c  
; Sequence 606643, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 606643  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-606643

Query Match 46.2%; Score 13.4; DB 1; Length 18;  
Best Local Similarity 93.3%; Pred. No. 47;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 GTGTGACCTGGTAAA 28  
| ||||| |||||  
Db 15 GAGTGACCTGGTAAA 1

RESULT 99  
US-10-310-914A-1317194  
; Sequence 1317194, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1317194  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1317194

Query Match 46.2%; Score 13.4; DB 1; Length 18;  
Best Local Similarity 73.3%; Pred. No. 47;  
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 CACCTGCTGTGTGAC 20  
|||:|:|:|:|:  
Db 1 CACCUGCUGGUGAC 15

RESULT 100  
US-10-310-914A-472976  
; Sequence 472976, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 472976  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-472976

Query Match 46.2%; Score 13.4; DB 1; Length 19;  
Best Local Similarity 60.0%; Pred. No. 44;  
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 10 TGCTGTGTGACCTGG 24  
:|:|:|:|:|:|:  
Db 1 UGCUCUGUGACCUUG 15

RESULT 101  
US-10-310-914A-549957  
; Sequence 549957, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 549957  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-549957

Query Match 46.2%; Score 13.4; DB 1; Length 19;  
Best Local Similarity 60.0%; Pred. No. 44;  
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 10 TGCTGTGTGACCTGG 24  
:|:|:|:|:|:|:  
Db 4 UGCUCUGUGAGCUGG 18

RESULT 102  
US-11-101-244-821390  
; Sequence 821390, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 821390  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens

```
US-11-101-244-821390
Query Match      46.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 60.0%; Pred. No. 44;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      15 TGTGACCTGGTAAAT 29
      |:|||||:|:||||:
Db      3 UGUGACCUGUUAUU 17

RESULT 103
US-11-101-244-859101
; Sequence 859101, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 859101
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-859101

Query Match      46.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 60.0%; Pred. No. 44;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      9 CTGCTGTGTGACCTG 23
      |:||||:|:||||:|
Db      2 CUGCUGUCUGACCG 16

RESULT 104
US-11-101-244-1260137
; Sequence 1260137, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1260137
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1260137
```

```
US-11-101-244-821390
Query Match      46.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 73.3%; Pred. No. 44;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      14 GTGTGACCTGGTAAA 28
      |:|||||:|:||||:
Db      2 GAGUGACCUGGUAAA 16

RESULT 105
US-11-101-244-1260202
; Sequence 1260202, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1260202
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1260202

Query Match      46.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 73.3%; Pred. No. 44;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      14 GTGTGACCTGGTAAA 28
      |:|||||:|:||||:
Db      3 GAGUGACCUGGUAAA 17

RESULT 106
US-11-101-244-1318311/c
; Sequence 1318311, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1318311
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1318311
```

Query Match 46.2%; Score 13.4; DB 1; Length 19;  
Best Local Similarity 93.3%; Pred. No. 44;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCCACCTGCTGTGTG 18  
Db 18 TCCACCTGCTGTTTG 4

RESULT 107  
US-11-101-244-1544345/c  
; Sequence 1544345, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1544345  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1544345

Query Match 46.2%; Score 13.4; DB 1; Length 19;  
Best Local Similarity 93.3%; Pred. No. 44;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGTGACCT 22  
Db 16 CCTGCTGTGTACCT 2

RESULT 108  
US-11-083-784-821390  
; Sequence 821390, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 821390  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-821390

Query Match 46.2%; Score 13.4; DB 1; Length 19;  
Best Local Similarity 60.0%; Pred. No. 44;  
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 15 TGTGACCTGGTAAAT 29  
Db 3 UGUGACCUGUUAUU 17

RESULT 109  
US-11-083-784-859101  
; Sequence 859101, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 859101  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-859101

Query Match 46.2%; Score 13.4; DB 1; Length 19;  
Best Local Similarity 60.0%; Pred. No. 44;  
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTGCTGTGTGACCTG 23  
Db 2 CUGCUGUCUGACCUG 16

RESULT 110  
US-11-083-784-1260137  
; Sequence 1260137, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1260137  
; LENGTH: 19



```
;
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-1260137

Query Match      46.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 73.3%; Pred. No. 44;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      14 GTGTGACCTGGTAA 28
Db      2 GAGUGACCUUGUAAA 16

RESULT 111
US-11-083-784-1260202
; Sequence 1260202, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1260202
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1260202

Query Match      46.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 73.3%; Pred. No. 44;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      14 GTGTGACCTGGTAA 28
Db      3 GAGUGACCUUGUAAA 17

RESULT 112
US-11-083-784-1318311/c
; Sequence 1318311, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
```

```
;
;   SOFTWARE: Proprietary
;   SEQ ID NO 1318311
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-1318311

Query Match      46.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 44;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 TCCACCTGCTGTGTG 18
Db      18 TCCACCTGCTGTTTG 4

RESULT 113
US-11-083-784-1544345/c
; Sequence 1544345, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1544345
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1544345

Query Match      46.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 44;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      8 CCTGCTGTGTGACCT 22
Db      16 CCTGCTGTGTAACCT 2

RESULT 114
US-10-310-914A-623917
; Sequence 623917, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 623917
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-623917
```



Query Match 44.1%; Score 12.8; DB 1; Length 18;  
Best Local Similarity 87.5%; Pred. No. 53;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGT 17  
Db 16 CCTCCACCTGCTGGT 1

RESULT 120  
US-10-310-914A-481748/c  
; Sequence 481748, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 481748  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-481748

Query Match 44.1%; Score 12.8; DB 1; Length 18;  
Best Local Similarity 87.5%; Pred. No. 53;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 CTGCTGTGTGACCTGG 24  
Db 17 CTGCTGTGTGACCAGG 2

RESULT 121  
US-10-310-914A-954247/c  
; Sequence 954247, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 954247  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-954247

Query Match 44.1%; Score 12.8; DB 1; Length 18;  
Best Local Similarity 87.5%; Pred. No. 53;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 CTGCTGTGTGACCTGG 24  
Db 18 CAGCTGTGTGACCGGG 3

RESULT 122  
US-10-880-315-224  
; Sequence 224, Application US/10880315  
; Publication No. US20050288497A1  
; GENERAL INFORMATION:  
; APPLICANT: Hwang, Yuchi

; APPLICANT: Chen, Kuang-Den  
; APPLICANT: Chang, Chingwei  
; APPLICANT: Chen, Jui-Lin  
; APPLICANT: Chen, Ding-Shinn  
; APPLICANT: Chen, Pei-Jer  
; APPLICANT: Lai, Ming-Yang  
; TITLE OF INVENTION: RESPONSIVENESS TO THERAPY FOR LIVER  
; FILE REFERENCE: 14720-004001  
; CURRENT APPLICATION NUMBER: US/10/880,315  
; CURRENT FILING DATE: 2004-06-29  
; NUMBER OF SEQ ID NOS: 230  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 224  
; LENGTH: 14  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-10-880-315-224

Query Match 37.2%; Score 10.8; DB 1; Length 14;  
Best Local Similarity 85.7%; Pred. No. 1.1e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 TGCTGTGTGACCTG 23  
Db 1 TGGTGTGTGTCCTG 14

RESULT 123  
US-11-269-003-81/c  
; Sequence 81, Application US/11269003  
; Publication No. US20060051809A1  
; GENERAL INFORMATION:  
; APPLICANT: Nazarenko, Irina  
; APPLICANT: Lorincz, Attila  
; APPLICANT: Eder, Paul  
; APPLICANT: Lowe, Brian  
; APPLICANT: Mallonee, Richard  
; APPLICANT: Thai, Ha  
; TITLE OF INVENTION: DETECTION OF NUCLEIC ACIDS BY TARGET-SPECIFIC HYBRID CAPTURE  
; FILE REFERENCE: 2629-4066  
; CURRENT APPLICATION NUMBER: US/11/269,003  
; CURRENT FILING DATE: 2005-11-07  
; PRIOR APPLICATION NUMBER: US 11/005,617  
; PRIOR FILING DATE: 2004-12-06  
; PRIOR APPLICATION NUMBER: US 10/971,251  
; PRIOR FILING DATE: 2004-10-20  
; PRIOR APPLICATION NUMBER: US 09/594,839  
; PRIOR FILING DATE: 2000-06-15  
; NUMBER OF SEQ ID NOS: 129  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 81  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: HPV  
US-11-269-003-81

Query Match 33.8%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 1.4e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGT 17  
Db 13 CCACCTCCTGCGT 1

RESULT 124  
US-11-176-026A-24/c  
; Sequence 24, Application US/11176026A  
; Publication No. US20060069074A1

```
; GENERAL INFORMATION:
; APPLICANT: Lemanske, Robert
; APPLICANT: Sorkness, Christine
; APPLICANT: Chinchilli, Vernon
; APPLICANT: Liu, Wenlei
; APPLICANT: Phillips, Brenda
; APPLICANT: Zeiger, Robert
; APPLICANT: Heldt, Gregory
; APPLICANT: Martinez, Fernando
; APPLICANT: Klimecki, Walter
; APPLICANT: Guilbert, Theresa
; APPLICANT: Morgan, Wayne
; APPLICANT: Szeffler, Stanley
; APPLICANT: Larsen, Gary
; APPLICANT: Taussig, Lynn
; APPLICANT: Spahn, Joseph
; APPLICANT: Strunk, Robert
; APPLICANT: Bacharier, Leonard
; APPLICANT: Bloomberg, Gordon
; TITLE OF INVENTION: GENETIC PREDICTOR OF EFFICACY OF ANTI-ASTHMATIC AGENT FOR
; TITLE OF INVENTION: IMPROVING PULMONARY FUNCTION
; FILE REFERENCE: 960296.00195
; CURRENT APPLICATION NUMBER: US/11/176,026A
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: US 60/585,872
; PRIOR FILING DATE: 2004-07-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA FAM probe sequence for -47 SNP.
US-11-176-026A-24

Query Match      33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 TCCACCTGCTGTG 16
      ||| ||||| |
Db      14 TCCGCCTGCTGAG 2

Search completed: May 15, 2006, 15:24:12
Job time : 1 secs
```

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM nucleic - nucleic search, using sw model  
Run on: May 15, 2006, 15:03:38 ; Search time 0.001 Seconds  
(without alignments)  
322.538 Million cell updates/sec

Title: US-09-904-968A-3-COPY  
Perfect score: 29  
Sequence: 1 ccattccacctgtgtgtgaccttgtaaat 29  
Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 0.5  
Searched: 446 seqs, 5561 residues

N-Geneseq

Total number of hits satisfying chosen parameters: 892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 448 summaries

Database : ngsdb:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
|------------|-------|---------------|--------|----|-------------|
| 1          | 29    | 100.0         | 29     | 1  | AD30229     |
| 2          | 15.6  | 53.8          | 22     | 1  | AD42395     |
| 3          | 15.2  | 52.4          | 21     | 1  | AAZ77065    |
| 4          | 14.8  | 51.0          | 20     | 1  | AAZ74984    |
| 5          | 14.8  | 51.0          | 20     | 1  | ADY78981    |
| 6          | 14.2  | 49.0          | 20     | 1  | AAZ85859    |
| 7          | 14.2  | 49.0          | 20     | 1  | AAZ11144    |
| 8          | 14.2  | 49.0          | 20     | 1  | AAA71269    |
| 9          | 14.2  | 49.0          | 20     | 1  | AAF31967    |
| 10         | 14.2  | 49.0          | 20     | 1  | AAC92946    |
| 11         | 14.2  | 49.0          | 20     | 1  | ABQ83060    |
| 12         | 14.2  | 49.0          | 20     | 1  | ADA95533    |
| 13         | 14.2  | 49.0          | 20     | 1  | ADD66206    |
| 14         | 14.2  | 49.0          | 20     | 1  | ADO50763    |
| 15         | 14.2  | 49.0          | 20     | 1  | ADT98004    |
| 16         | 13.8  | 47.6          | 17     | 1  | ADP09253    |
| 17         | 13.4  | 46.2          | 18     | 1  | ADZ20529    |
| 18         | 13.4  | 46.2          | 19     | 1  | AAZ72126    |
| 19         | 13.4  | 46.2          | 19     | 1  | ADV60526    |
| 20         | 13.2  | 45.5          | 18     | 1  | AAZ44771    |
| 21         | 13    | 44.8          | 15     | 1  | AAS99971    |
| 22         | 12.8  | 44.1          | 17     | 1  | AAT80089    |
| 23         | 12.8  | 44.1          | 17     | 1  | ABV90926    |
| 24         | 12.8  | 44.1          | 17     | 1  | ABV90925    |
| 25         | 12.8  | 44.1          | 18     | 1  | AAT96932    |
| 26         | 12.8  | 44.1          | 18     | 1  | AAX63330    |
| 27         | 12.4  | 42.8          | 15     | 1  | ADW64053    |
| 28         | 12.4  | 42.8          | 17     | 1  | ABN02182    |
| 29         | 12.4  | 42.8          | 17     | 1  | ABN02180    |
| 30         | 12.4  | 42.8          | 17     | 1  | ABN02179    |
| 31         | 12.4  | 42.8          | 17     | 1  | ABN02181    |
| 32         | 12.4  | 42.8          | 17     | 1  | ABT39421    |
| 33         | 12.4  | 42.8          | 17     | 1  | ABT39428    |



|       |     |      |    |   |           |                    |
|-------|-----|------|----|---|-----------|--------------------|
| 107   | 10  | 34.5 | 12 | 1 | ABI05465  | Oligonucleotide pr |
| C 108 | 10  | 34.5 | 12 | 1 | ADQ30383  | Human VR1 exon 1d  |
| C 109 | 10  | 34.5 | 12 | 1 | ADQ30420  | Human VR1 exon 1d  |
| 110   | 10  | 34.5 | 13 | 1 | ABC35433  | Oligonucleotide SE |
| C 111 | 10  | 34.5 | 13 | 1 | ABF12886  | Oligonucleotide SE |
| C 112 | 10  | 34.5 | 13 | 1 | ABC14106  | Oligonucleotide SE |
| C 113 | 10  | 34.5 | 13 | 1 | ABC14104  | Oligonucleotide SE |
| 114   | 10  | 34.5 | 13 | 1 | ABH01641  | Oligonucleotide SE |
| 115   | 10  | 34.5 | 13 | 1 | ABC14107  | Oligonucleotide SE |
| C 116 | 10  | 34.5 | 13 | 1 | ABC35432  | Oligonucleotide SE |
| 117   | 10  | 34.5 | 13 | 1 | ABF12887  | Oligonucleotide SE |
| C 118 | 10  | 34.5 | 13 | 1 | ABH01640  | Oligonucleotide SE |
| 119   | 10  | 34.5 | 13 | 1 | ABC14105  | Oligonucleotide SE |
| 120   | 10  | 34.5 | 13 | 1 | ADE14132  | Optineurin promote |
| 121   | 10  | 34.5 | 14 | 1 | AAV92770  | Human A-raf target |
| 122   | 10  | 34.5 | 14 | 1 | AAZ64774  | Substrate for hair |
| 123   | 10  | 34.5 | 14 | 1 | AAZ37042  | Probe targeted to  |
| 124   | 10  | 34.5 | 14 | 1 | ABX01611  | Hepatitis C virus  |
| 125   | 10  | 34.5 | 14 | 1 | ABE76535  | Hepatitis C virus  |
| 126   | 9.8 | 33.8 | 13 | 1 | AAA06015  | CFTR gene analysis |
| C 127 | 9.8 | 33.8 | 13 | 1 | ABF45366  | Oligonucleotide SE |
| 128   | 9.8 | 33.8 | 13 | 1 | ABF45367  | Oligonucleotide SE |
| 129   | 9.8 | 33.8 | 13 | 1 | ABK28875  | HPV blocker probe  |
| C 130 | 9.8 | 33.8 | 13 | 1 | ABZ34180  | HIV-1 reverse tran |
| C 131 | 9.8 | 33.8 | 13 | 1 | ABZ34155  | HIV-1 reverse tran |
| 132   | 9.8 | 33.8 | 13 | 1 | ADF48833  | DNA array associat |
| 133   | 9.8 | 33.8 | 14 | 1 | AAQ78366  | Antisense oligonuc |
| 134   | 9.8 | 33.8 | 14 | 1 | AAV48778  | ErbB-2 gene antis  |
| C 135 | 9.8 | 33.8 | 14 | 1 | ABZ34156  | HIV-1 reverse tran |
| C 136 | 9.8 | 33.8 | 14 | 1 | ABZ34175  | HIV-1 reverse tran |
| C 137 | 9.8 | 33.8 | 14 | 1 | ABZ34152  | HIV-1 reverse tran |
| C 138 | 9.8 | 33.8 | 14 | 1 | ABZ34170  | HIV-1 reverse tran |
| C 139 | 9.8 | 33.8 | 14 | 1 | ABZ34179  | HIV-1 reverse tran |
| C 140 | 9.8 | 33.8 | 14 | 1 | ABZ34172  | HIV-1 reverse tran |
| 141   | 9.8 | 33.8 | 14 | 1 | AEA60845  | Blood fluke Sjpp 5 |
| 142   | 9.4 | 32.4 | 11 | 1 | AAZ18959  | Murine MRL SAGE ta |
| C 143 | 9.4 | 32.4 | 11 | 1 | AAZ18744  | Murine C57BL/6 SAG |
| C 144 | 9.4 | 32.4 | 11 | 1 | AAA96508  | Consensus sequence |
| 145   | 9.4 | 32.4 | 11 | 1 | ABQ86330  | Human skin stress/ |
| 146   | 9.4 | 32.4 | 11 | 1 | ABV64871  | Human skin EST 265 |
| 147   | 9.4 | 32.4 | 11 | 1 | ABV66455  | Human skin EST 424 |
| 148   | 9.4 | 32.4 | 11 | 1 | ABV67092  | Human skin EST 487 |
| 149   | 9.4 | 32.4 | 11 | 1 | ABV70439  | Human skin EST 822 |
| 150   | 9.4 | 32.4 | 11 | 1 | ABV63018  | Human skin EST 804 |
| 151   | 9.4 | 32.4 | 11 | 1 | ABV65196  | Human skin EST 298 |
| 152   | 9.4 | 32.4 | 11 | 1 | ABV67859  | Human skin EST 564 |
| 153   | 9.4 | 32.4 | 11 | 1 | ADQ34760  | Human facial skin- |
| 154   | 9.4 | 32.4 | 11 | 1 | ADQ33707  | Human facial skin- |
| 155   | 9.4 | 32.4 | 12 | 1 | AAZ48741  | PCR primer for hum |
| 156   | 9.4 | 32.4 | 12 | 1 | AAQ04006  | Primer used in det |
| 157   | 9.4 | 32.4 | 12 | 1 | AAV40900  | Primer CBFMYHA:10  |
| 158   | 9.4 | 32.4 | 12 | 1 | AAA06782  | VEGF derived short |
| 159   | 9.4 | 32.4 | 12 | 1 | AAA06783  | VEGF derived short |
| 160   | 9.4 | 32.4 | 12 | 1 | ABH86901  | Oligonucleotide pr |
| 161   | 9.4 | 32.4 | 12 | 1 | AAD54083  | HNFI-131-1 gene SN |
| C 162 | 9.4 | 32.4 | 12 | 1 | AAL51397  | Human polyamine ox |
| C 163 | 9.4 | 32.4 | 13 | 1 | AAAS4184  | 5' exon-intron jun |
| C 164 | 9.4 | 32.4 | 13 | 1 | ABC87602  | Oligonucleotide SE |
| C 165 | 9.4 | 32.4 | 13 | 1 | ABC87603  | Oligonucleotide SE |
| C 166 | 9.4 | 32.4 | 13 | 1 | ACC70395  | Cytoprotective res |
| 167   | 9   | 31.0 | 10 | 1 | AAZ79202  | Human dendritic ce |
| 168   | 9   | 31.0 | 10 | 1 | AAZ78009  | Human dendritic ce |
| 169   | 9   | 31.0 | 10 | 1 | AAZ78129  | Human dendritic ce |
| C 170 | 9   | 31.0 | 10 | 1 | AAZ85467  | Metastatic breast  |
| C 171 | 9   | 31.0 | 10 | 1 | AAZ86332  | Metastatic breast  |
| 172   | 9   | 31.0 | 10 | 1 | AAZ81042  | Metastatic breast  |
| 173   | 9   | 31.0 | 10 | 1 | AAZ82620  | Metastatic breast  |
| C 174 | 9   | 31.0 | 10 | 1 | AAH63185  | Human colon epithe |
| 175   | 9   | 31.0 | 10 | 1 | AAAS57316 | Human CHRN2 allel  |
| 176   | 9   | 31.0 | 10 | 1 | AAH32728  | LPS activated huma |
| 177   | 9   | 31.0 | 10 | 1 | ABA81652  | Human phospholipid |
| 178   | 9   | 31.0 | 10 | 1 | AAF35559  | Yeast NORF gene SA |
| 179   | 9   | 31.0 | 10 | 1 | AAF34581  | Yeast NORF gene SA |

|       |     |      |    |   |          |                    |
|-------|-----|------|----|---|----------|--------------------|
| C 180 | 9   | 31.0 | 10 | 1 | AAF37646 | Yeast NORF gene SA |
| C 181 | 9   | 31.0 | 10 | 1 | ABL52170 | Human PER1 preferr |
| 182   | 9   | 31.0 | 10 | 1 | AAS94664 | Human PLTP gene al |
| 183   | 9   | 31.0 | 10 | 1 | AAL39779 | SMOH polymorphism  |
| 184   | 9   | 31.0 | 10 | 1 | ADE14133 | Optineurin promote |
| 185   | 9   | 31.0 | 10 | 1 | ADQ30369 | Human VR1 exon 1d  |
| 186   | 9   | 31.0 | 11 | 1 | AAI19836 | Transcription fact |
| C 187 | 9   | 31.0 | 11 | 1 | AAA16595 | Human MN gene 5' d |
| C 188 | 9   | 31.0 | 11 | 1 | AAA52514 | Human MN gene intr |
| C 189 | 9   | 31.0 | 11 | 1 | ABQ86329 | Human skin stress/ |
| C 190 | 9   | 31.0 | 11 | 1 | ABV62312 | Human skin EST 98. |
| 191   | 9   | 31.0 | 11 | 1 | ABV69491 | Human skin EST 727 |
| C 192 | 9   | 31.0 | 11 | 1 | ABV69733 | Human skin EST 751 |
| C 193 | 9   | 31.0 | 11 | 1 | ABL91944 | Human Pan-Endothel |
| C 194 | 9   | 31.0 | 11 | 1 | ABX71869 | DNA tag used to id |
| C 195 | 9   | 31.0 | 11 | 1 | ADK41823 | Human MN gene intr |
| C 196 | 9   | 31.0 | 12 | 1 | ABH83073 | Oligonucleotide pr |
| C 197 | 9   | 31.0 | 12 | 1 | ABH64669 | Oligonucleotide pr |
| 198   | 9   | 31.0 | 12 | 1 | ABI17481 | Oligonucleotide pr |
| C 199 | 9   | 31.0 | 12 | 1 | ABI77789 | Oligonucleotide pr |
| C 200 | 9   | 31.0 | 12 | 1 | ABI74143 | Oligonucleotide pr |
| 201   | 9   | 31.0 | 12 | 1 | ABI17480 | Oligonucleotide pr |
| C 202 | 9   | 31.0 | 12 | 1 | ABH73202 | Oligonucleotide pr |
| 203   | 9   | 31.0 | 12 | 1 | ABI56716 | Oligonucleotide pr |
| 204   | 9   | 31.0 | 12 | 1 | AAL44624 | Muscle creatine ki |
| C 205 | 9   | 31.0 | 12 | 1 | ADF78489 | Chromosomal abnorm |
| C 206 | 9   | 31.0 | 12 | 1 | ADO08498 | Human papillomavir |
| C 207 | 9   | 31.0 | 12 | 1 | ADR98065 | Human SNP TSC12610 |
| C 208 | 9   | 31.0 | 12 | 1 | ADS08752 | Human DNA PCR prim |
| C 209 | 8.8 | 30.3 | 12 | 1 | AAQ86030 | IT10C3 coding regi |
| 210   | 8.8 | 30.3 | 12 | 1 | AAQ88466 | Human mitochondria |
| 211   | 8.8 | 30.3 | 12 | 1 | AAAS9759 | Bacteriophage M13m |
| C 212 | 8.8 | 30.3 | 12 | 1 | ABI24861 | Oligonucleotide pr |
| 213   | 8.8 | 30.3 | 12 | 1 | ABI11597 | Oligonucleotide pr |
| C 214 | 8.8 | 30.3 | 12 | 1 | ABI10363 | Oligonucleotide pr |
| C 215 | 8.8 | 30.3 | 12 | 1 | ABH87537 | Oligonucleotide pr |
| C 216 | 8.8 | 30.3 | 12 | 1 | ABIS2832 | Oligonucleotide pr |
| 217   | 8.8 | 30.3 | 12 | 1 | ABI39693 | Oligonucleotide pr |
| C 218 | 8.8 | 30.3 | 12 | 1 | ABH80092 | Oligonucleotide pr |
| 219   | 8.8 | 30.3 | 12 | 1 | ABH77417 | Oligonucleotide pr |
| C 220 | 8.8 | 30.3 | 12 | 1 | ABH83668 | Oligonucleotide pr |
| 221   | 8.8 | 30.3 | 12 | 1 | ABH87588 | Oligonucleotide pr |
| C 222 | 8.8 | 30.3 | 12 | 1 | ABI40468 | Oligonucleotide pr |
| C 223 | 8.8 | 30.3 | 12 | 1 | ABI60766 | Oligonucleotide pr |
| 224   | 8.8 | 30.3 | 12 | 1 | ABI62806 | Oligonucleotide pr |
| 225   | 8.8 | 30.3 | 12 | 1 | ABI17729 | Oligonucleotide pr |
| C 226 | 8.8 | 30.3 | 12 | 1 | ABH94984 | Oligonucleotide pr |
| C 227 | 8.8 | 30.3 | 12 | 1 | ABI26645 | Oligonucleotide pr |
| 228   | 8.8 | 30.3 | 12 | 1 | ABI39600 | Oligonucleotide pr |
| C 229 | 8.8 | 30.3 | 12 | 1 | ABI59140 | Oligonucleotide pr |
| 230   | 8.8 | 30.3 | 12 | 1 | ABI60733 | Oligonucleotide pr |
| 231   | 8.8 | 30.3 | 12 | 1 | ABI26571 | Oligonucleotide pr |
| 232   | 8.8 | 30.3 | 12 | 1 | ABH77044 | Oligonucleotide pr |
| C 233 | 8.8 | 30.3 | 12 | 1 | ABH46669 | Oligonucleotide pr |
| 234   | 8.8 | 30.3 | 12 | 1 | ACD28673 | Human acid sphingo |
| 235   | 8.8 | 30.3 | 12 | 1 | ADE13943 | Optineurin promote |
| C 236 | 8.8 | 30.3 | 12 | 1 | ABZ77024 | Bovine DGAT exon-1 |
| C 237 | 8.8 | 30.3 | 12 | 1 | ADZ24155 | Human SNP detectio |
| C 238 | 8.6 | 29.7 | 11 | 1 | ADS77727 | Breast cancer dete |
| C 239 | 8.6 | 29.7 | 11 | 1 | ADS77874 | Breast cancer dete |
| C 240 | 8.6 | 29.7 | 11 | 1 | ADS77394 | Breast cancer dete |
| 241   | 8.6 | 29.7 | 12 | 1 | AAD44125 | PCR primer #6 desi |
| 242   | 8.4 | 29.0 | 10 | 1 | AAQ97150 | HIV-1 NL4-3 LTR nu |
| C 243 | 8.4 | 29.0 | 10 | 1 | AAQ96785 | HIV-1 NL4-3 nef ge |
| 244   | 8.4 | 29.0 | 10 | 1 | AAQ97151 | HIV-1 NL4-3 LTR nu |
| C 245 | 8.4 | 29.0 | 10 | 1 | AAQ96482 | HIV-1 NL4-3 nef ge |
| 246   | 8.4 | 29.0 | 10 | 1 | AAQ97149 | HIV-1 NL4-3 LTR nu |
| C 247 | 8.4 | 29.0 | 10 | 1 | AAV34960 | Synthetic Agaricus |
| 248   | 8.4 | 29.0 | 10 | 1 | AAV03254 | Homo sapiens mutan |
| C 249 | 8.4 | 29.0 | 10 | 1 | AAI18637 | p53 serial analysi |
| C 250 | 8.4 | 29.0 | 10 | 1 | AAZ11274 | Splice donor site  |
| 251   | 8.4 | 29.0 | 10 | 1 | AAZ78697 | Human dendritic ce |
| C 252 | 8.4 | 29.0 | 10 | 1 | AAZ77846 | Human dendritic ce |

|       |     |      |    |   |           |                    |       |     |      |    |   |          |                     |
|-------|-----|------|----|---|-----------|--------------------|-------|-----|------|----|---|----------|---------------------|
| 253   | 8.4 | 29.0 | 10 | 1 | AAZ79150  | Human dendritic ce | 326   | 8.4 | 29.0 | 11 | 1 | ABV68983 | Human skin EST 676  |
| 254   | 8.4 | 29.0 | 10 | 1 | AAZ84055  | Metastatic breast  | c 327 | 8.4 | 29.0 | 11 | 1 | ABV67130 | Human skin EST 491  |
| 255   | 8.4 | 29.0 | 10 | 1 | AAZ81988  | Metastatic breast  | 328   | 8.4 | 29.0 | 11 | 1 | ABV67225 | Human skin EST 501  |
| c 256 | 8.4 | 29.0 | 10 | 1 | AAZ83343  | Metastatic breast  | c 329 | 8.4 | 29.0 | 11 | 1 | ABV67773 | Human skin EST 555  |
| c 257 | 8.4 | 29.0 | 10 | 1 | AAZ83792  | Metastatic breast  | c 330 | 8.4 | 29.0 | 11 | 1 | ABV62764 | Human skin EST 550  |
| 258   | 8.4 | 29.0 | 10 | 1 | AAZ86544  | Metastatic breast  | c 331 | 8.4 | 29.0 | 11 | 1 | ABV62815 | Human skin EST 601  |
| 259   | 8.4 | 29.0 | 10 | 1 | AAZ81303  | Metastatic breast  | 332   | 8.4 | 29.0 | 11 | 1 | ABV69214 | Human skin EST 700  |
| 260   | 8.4 | 29.0 | 10 | 1 | AAC74087  | Human dendritic ce | c 333 | 8.4 | 29.0 | 11 | 1 | ABV70185 | Human skin EST 797  |
| c 261 | 8.4 | 29.0 | 10 | 1 | AAC73981  | Human dendritic ce | c 334 | 8.4 | 29.0 | 11 | 1 | ABV70837 | Human skin EST 862  |
| c 262 | 8.4 | 29.0 | 10 | 1 | AAA56364  | Human macrophage g | 335   | 8.4 | 29.0 | 11 | 1 | ABV65404 | Human skin EST 319  |
| c 263 | 8.4 | 29.0 | 10 | 1 | AAZ91928  | PCR primer for mur | c 336 | 8.4 | 29.0 | 11 | 1 | ABV66252 | Human skin EST 403  |
| 264   | 8.4 | 29.0 | 10 | 1 | AAH18978  | UCP3 polymorphism  | 337   | 8.4 | 29.0 | 11 | 1 | ABV67008 | Human skin EST 479  |
| 265   | 8.4 | 29.0 | 10 | 1 | AAH19943  | Mouse Treg immunor | c 338 | 8.4 | 29.0 | 11 | 1 | ABV69518 | Human skin EST 730  |
| 266   | 8.4 | 29.0 | 10 | 1 | AAI67394  | Human FKBP8 gene p | 339   | 8.4 | 29.0 | 11 | 1 | ABV70736 | Human skin EST 852  |
| 267   | 8.4 | 29.0 | 10 | 1 | AAH63201  | Human colon epithe | 340   | 8.4 | 29.0 | 11 | 1 | ABV66438 | Human skin EST 422  |
| 268   | 8.4 | 29.0 | 10 | 1 | AAH63192  | Human colon epithe | c 341 | 8.4 | 29.0 | 11 | 1 | ABV67400 | Human skin EST 518  |
| 269   | 8.4 | 29.0 | 10 | 1 | AAH63266  | Human colon epithe | 342   | 8.4 | 29.0 | 11 | 1 | ABV67423 | Human skin EST 520  |
| 270   | 8.4 | 29.0 | 10 | 1 | AAH63751  | Human ubiquitously | c 343 | 8.4 | 29.0 | 11 | 1 | ABV70236 | Human skin EST 802  |
| 271   | 8.4 | 29.0 | 10 | 1 | AAH32787  | LPS activated huma | c 344 | 8.4 | 29.0 | 11 | 1 | ABV63416 | Human skin EST 120  |
| 272   | 8.4 | 29.0 | 10 | 1 | AAH41694  | Anti-PEP gene cons | c 345 | 8.4 | 29.0 | 11 | 1 | ABV64243 | Human skin EST 202  |
| c 273 | 8.4 | 29.0 | 10 | 1 | ABA06109  | Human normal hepat | c 346 | 8.4 | 29.0 | 11 | 1 | ABV67475 | Human skin EST 526  |
| 274   | 8.4 | 29.0 | 10 | 1 | AAF69625  | Human IL4Ra1pha ge | c 347 | 8.4 | 29.0 | 11 | 1 | ABV71664 | Human skin EST 945  |
| c 275 | 8.4 | 29.0 | 10 | 1 | AAF34164  | Yeast NORF gene SA | 348   | 8.4 | 29.0 | 11 | 1 | ABV67586 | Human skin EST 537  |
| 276   | 8.4 | 29.0 | 10 | 1 | AAF35667  | Yeast NORF gene SA | c 349 | 8.4 | 29.0 | 11 | 1 | ABV68554 | Human skin EST 634  |
| c 277 | 8.4 | 29.0 | 10 | 1 | AAF35804  | Yeast NORF gene SA | 350   | 8.4 | 29.0 | 11 | 1 | AAD40434 | Bovine DGAT1 gene   |
| c 278 | 8.4 | 29.0 | 10 | 1 | AAF44017  | Yeast NORF gene SA | 351   | 8.4 | 29.0 | 11 | 1 | ABV78654 | RXR binding site f  |
| c 279 | 8.4 | 29.0 | 10 | 1 | AAF43467  | Yeast NORF gene SA | c 352 | 8.4 | 29.0 | 11 | 1 | ADG13667 | Human EGFR Amberzy  |
| 280   | 8.4 | 29.0 | 10 | 1 | AAF34829  | Yeast NORF gene SA | c 353 | 8.4 | 29.0 | 11 | 1 | ADK41836 | Human MN gene intr  |
| 281   | 8.4 | 29.0 | 10 | 1 | AAF35820  | Yeast NORF gene SA | c 354 | 8.4 | 29.0 | 11 | 1 | ADQ35801 | Human hair-bearing  |
| c 282 | 8.4 | 29.0 | 10 | 1 | AAF35485  | Yeast NORF gene SA | 355   | 8.4 | 29.0 | 11 | 1 | ADQ35910 | Human hair-bearing  |
| 283   | 8.4 | 29.0 | 10 | 1 | ABL42879  | Human maturation/a | c 356 | 8.4 | 29.0 | 11 | 1 | ADQ35843 | Human hair-bearing  |
| 284   | 8.4 | 29.0 | 10 | 1 | ABL42726  | Human maturation/a | 357   | 8.4 | 29.0 | 11 | 1 | ADQ33204 | Human facial skin-  |
| 285   | 8.4 | 29.0 | 10 | 1 | ABL42777  | Human maturation/a | c 358 | 8.4 | 29.0 | 11 | 1 | ADQ33521 | Human facial skin-  |
| 286   | 8.4 | 29.0 | 10 | 1 | ABL42899  | Human maturation/a | c 359 | 8.4 | 29.0 | 11 | 1 | ADQ33660 | Human facial skin-  |
| c 287 | 8.4 | 29.0 | 10 | 1 | ABL39528  | Human ETFB primer- | 360   | 8.4 | 29.0 | 11 | 1 | ADQ33652 | Human facial skin-  |
| c 288 | 8.4 | 29.0 | 10 | 1 | ABV84850  | Human mitochondria | c 361 | 8.4 | 29.0 | 11 | 1 | ADQ34937 | Human facial skin-  |
| c 289 | 8.4 | 29.0 | 10 | 1 | ABK09446  | Human NPR1 gene al | c 362 | 8.4 | 29.0 | 11 | 1 | ADQ32556 | Human facial skin-  |
| c 290 | 8.4 | 29.0 | 10 | 1 | ABK09921  | P2RY1 gene allele- | 363   | 8.4 | 29.0 | 11 | 1 | ADQ33878 | Human facial skin-  |
| c 291 | 8.4 | 29.0 | 10 | 1 | ABK09919  | P2RY1 gene allele- | 364   | 8.4 | 29.0 | 11 | 1 | ADQ32289 | Human facial skin-  |
| c 292 | 8.4 | 29.0 | 10 | 1 | ABS64264  | Tachykinin recepto | 365   | 8.4 | 29.0 | 11 | 1 | ADQ32669 | Human facial skin-  |
| c 293 | 8.4 | 29.0 | 10 | 1 | ABS64271  | Tachykinin recepto | c 366 | 8.4 | 29.0 | 11 | 1 | ADQ34474 | Human facial skin-  |
| 294   | 8.4 | 29.0 | 10 | 1 | AAS99384  | Aldehyde dehydroge | c 367 | 8.4 | 29.0 | 12 | 1 | AAQ52115 | Breast cancer spec  |
| 295   | 8.4 | 29.0 | 10 | 1 | AAD47793  | Human GNB3 gene po | c 368 | 8.4 | 29.0 | 12 | 1 | AAV32307 | Random primed reve  |
| c 296 | 8.4 | 29.0 | 10 | 1 | ACC69006  | AMP protocol HpaII | c 369 | 8.4 | 29.0 | 12 | 1 | AAV32258 | Random primed reve  |
| c 297 | 8.4 | 29.0 | 10 | 1 | ABT14241  | Nucleic acid PCR a | c 370 | 8.4 | 29.0 | 12 | 1 | AAV32253 | Random primed reve  |
| c 298 | 8.4 | 29.0 | 10 | 1 | ADE14194  | Optineurin promote | c 371 | 8.4 | 29.0 | 12 | 1 | AAZ41830 | Organic material d  |
| c 299 | 8.4 | 29.0 | 10 | 1 | AAL51289  | SAGE transcript ta | 372   | 8.4 | 29.0 | 12 | 1 | AAZ41780 | Organic material d  |
| c 300 | 8.4 | 29.0 | 10 | 1 | ADL96345  | CD15+ myeloid cell | 373   | 8.4 | 29.0 | 12 | 1 | AAZ41564 | Microbe detection   |
| c 301 | 8.4 | 29.0 | 10 | 1 | ADG13687  | Human EGFR Amberzy | c 374 | 8.4 | 29.0 | 12 | 1 | AAZ41614 | Microbe detection   |
| 302   | 8.4 | 29.0 | 10 | 1 | ADH14437  | Human retinoblasto | c 375 | 8.4 | 29.0 | 12 | 1 | AAF74730 | Human smoothelein v |
| c 303 | 8.4 | 29.0 | 10 | 1 | ADK12825  | Human glioma endot | c 376 | 8.4 | 29.0 | 12 | 1 | AAS01805 | Human smoothelein g |
| c 304 | 8.4 | 29.0 | 10 | 1 | ADR27959  | Murine VE-statin e | c 377 | 8.4 | 29.0 | 12 | 1 | AAC97965 | Primer used to ill  |
| c 305 | 8.4 | 29.0 | 10 | 1 | ADS78008  | Breast cancer dete | 378   | 8.4 | 29.0 | 12 | 1 | AAC97915 | Primer used to ill  |
| c 306 | 8.4 | 29.0 | 10 | 1 | ADS76235  | Breast cancer dete | 379   | 8.4 | 29.0 | 12 | 1 | ABI29917 | Oligonucleotide pr  |
| 307   | 8.4 | 29.0 | 10 | 1 | ADS76988  | Breast cancer dete | c 380 | 8.4 | 29.0 | 12 | 1 | ABH85587 | Oligonucleotide pr  |
| c 308 | 8.4 | 29.0 | 10 | 1 | ADS77286  | Breast cancer dete | c 381 | 8.4 | 29.0 | 12 | 1 | ABI59162 | Oligonucleotide pr  |
| 309   | 8.4 | 29.0 | 10 | 1 | ADS76987  | Breast cancer dete | c 382 | 8.4 | 29.0 | 12 | 1 | ABH74750 | Oligonucleotide pr  |
| 310   | 8.4 | 29.0 | 10 | 1 | ADU19159  | Hypoxia-related tu | 383   | 8.4 | 29.0 | 12 | 1 | ABH75922 | Oligonucleotide pr  |
| c 311 | 8.4 | 29.0 | 10 | 1 | ADU19427  | Hypoxia-related tu | 384   | 8.4 | 29.0 | 12 | 1 | ABI26643 | Oligonucleotide pr  |
| 312   | 8.4 | 29.0 | 11 | 1 | AAV55915  | CYP1B1 gene exon I | 385   | 8.4 | 29.0 | 12 | 1 | ABI53560 | Oligonucleotide pr  |
| 313   | 8.4 | 29.0 | 11 | 1 | AAZ18975  | Murine MRL SAGE ta | 386   | 8.4 | 29.0 | 12 | 1 | ABI59024 | Oligonucleotide pr  |
| 314   | 8.4 | 29.0 | 11 | 1 | AAZ18803  | Murine C57BL/6 SAG | c 387 | 8.4 | 29.0 | 12 | 1 | ABI60693 | Oligonucleotide pr  |
| c 315 | 8.4 | 29.0 | 11 | 1 | AAA16608  | Human MN gene 3' a | 388   | 8.4 | 29.0 | 12 | 1 | ABI18617 | Oligonucleotide pr  |
| c 316 | 8.4 | 29.0 | 11 | 1 | AAA52527  | Human MN gene intr | 389   | 8.4 | 29.0 | 12 | 1 | ABH71661 | Oligonucleotide pr  |
| 317   | 8.4 | 29.0 | 11 | 1 | AAF75228  | Human RXR binding  | 390   | 8.4 | 29.0 | 12 | 1 | ABH77312 | Oligonucleotide pr  |
| c 318 | 8.4 | 29.0 | 11 | 1 | ABQ86838  | Human skin stress/ | 391   | 8.4 | 29.0 | 12 | 1 | ABI18206 | Oligonucleotide pr  |
| c 319 | 8.4 | 29.0 | 11 | 1 | ABQ86763  | Human skin stress/ | 392   | 8.4 | 29.0 | 12 | 1 | ABI43158 | Oligonucleotide pr  |
| 320   | 8.4 | 29.0 | 11 | 1 | ABQ86590  | Human skin stress/ | c 393 | 8.4 | 29.0 | 12 | 1 | ABI69159 | Oligonucleotide pr  |
| c 321 | 8.4 | 29.0 | 11 | 1 | ABQ87167  | Human skin stress/ | c 394 | 8.4 | 29.0 | 12 | 1 | ABH81976 | Oligonucleotide pr  |
| 322   | 8.4 | 29.0 | 11 | 1 | ABQ87430  | Human skin stress/ | c 395 | 8.4 | 29.0 | 12 | 1 | ABI69157 | Oligonucleotide pr  |
| 323   | 8.4 | 29.0 | 11 | 1 | ABQ86674  | Human skin stress/ | c 396 | 8.4 | 29.0 | 12 | 1 | ABI80903 | Oligonucleotide pr  |
| 324   | 8.4 | 29.0 | 11 | 1 | ABV63315  | Human skin EST 110 | c 397 | 8.4 | 29.0 | 12 | 1 | ABH97813 | Oligonucleotide pr  |
| c 325 | 8.4 | 29.0 | 11 | 1 | ABV666003 | Human skin EST 378 | c 398 | 8.4 | 29.0 | 12 | 1 | ABH93473 | Oligonucleotide pr  |

399 8.4 29.0 12 1 ABI43157 Oligonucleotide pr  
400 8.4 29.0 12 1 ABI72787 Oligonucleotide pr  
401 8.4 29.0 12 1 ABI05466 Oligonucleotide pr  
402 8.4 29.0 12 1 ABI13967 Oligonucleotide pr  
c 403 8.4 29.0 12 1 ABI16340 Oligonucleotide pr  
404 8.4 29.0 12 1 ABH69681 Oligonucleotide pr  
405 8.4 29.0 12 1 ABI37541 Oligonucleotide pr  
c 406 8.4 29.0 12 1 ABH77664 Oligonucleotide pr  
407 8.4 29.0 12 1 ABH86388 Oligonucleotide pr  
c 408 8.4 29.0 12 1 ABH74692 Oligonucleotide pr  
409 8.4 29.0 12 1 ABI02272 Oligonucleotide pr  
410 8.4 29.0 12 1 ABI77388 Oligonucleotide pr  
c 411 8.4 29.0 12 1 ABH97611 Oligonucleotide pr  
412 8.4 29.0 12 1 ABH84024 Oligonucleotide pr  
c 413 8.4 29.0 12 1 ABH85692 Oligonucleotide pr  
c 414 8.4 29.0 12 1 ABI53806 Oligonucleotide pr  
415 8.4 29.0 12 1 ABI19386 Oligonucleotide pr  
416 8.4 29.0 12 1 ABH69682 Oligonucleotide pr  
417 8.4 29.0 12 1 ABI29310 Oligonucleotide pr  
418 8.4 29.0 12 1 ABH84793 Oligonucleotide pr  
c 419 8.4 29.0 12 1 ABI73341 Oligonucleotide pr  
c 420 8.4 29.0 12 1 ABI59818 Oligonucleotide pr  
421 8.4 29.0 12 1 ABK72569 Human OPA1 gene, e  
422 8.4 29.0 12 1 ABK72535 Rice seed bZIP tra  
c 423 8.4 29.0 12 1 AAL42695 Rice seed bZIP tra  
c 424 8.4 29.0 12 1 AAL42645 Beta-lactamase pro  
425 8.4 29.0 12 1 ABK29928 Beta-lactamase pro  
426 8.4 29.0 12 1 ABK30092 Beta-lactamase pro  
427 8.4 29.0 12 1 ABA91368 DNA encoding neuro  
428 8.4 29.0 12 1 ADE85925 Immunostimulatory  
c 429 8.4 29.0 12 1 ADF78662 Chromosomal abnorm  
c 430 8.4 29.0 12 1 ADF78486 Chromosomal abnorm  
431 8.4 29.0 12 1 ABZ72938 Rod opsin hammethe  
432 8.4 29.0 12 1 ADM56049 Antibacterial pept  
c 433 8.4 29.0 12 1 ADM56293 Mouse SLC26A6 anio  
434 8.4 29.0 12 1 AEB80299 Organic waste trea  
c 435 8.4 29.0 12 1 ADM76195 NEPHA gene transcr  
c 436 8.4 29.0 12 1 ADQ30184 Murine VR1 exon 1d  
c 437 8.4 29.0 12 1 ADQ30185 Murine VR1 exon 1d  
c 438 8.4 29.0 12 1 ADQ30343 Human VR1 exon 1d  
c 439 8.4 29.0 12 1 ADR32504 Human nicking agen  
c 440 8.4 29.0 12 1 ADR98238 Human chromosome 2  
c 441 8.4 29.0 12 1 ADR98062 Human SNP TSC04700  
c 442 8.4 29.0 12 1 ADS08925 Human DNA PCR prim  
c 443 8.4 29.0 12 1 ADS08749 Human DNA PCR prim  
444 8.4 29.0 12 1 ADZ15183 PCR primer used to  
445 8.4 29.0 12 1 ADZ24372 Human SNP detectio  
446 8.4 29.0 12 1 AEA50022 Construct Fc-pcDNA  
447 7.4 25.5 10 1 ABK09921 p2RY1 gene allele-  
c 448 7.4 25.5 10 1 ADU19159 Hypoxia-related tu

ALIGNMENTS

RESULT 1  
AAD30229  
ID AAD30229 standard; DNA; 29 BP.  
XX  
AC AAD30229;  
XX  
DT 17-MAY-2002 (first entry)  
XX  
DE BPF14 PCR primer, to generate human PKD1 gene long range templates.  
XX  
KW Human; PKD1 gene; autosomal dominant polycystic kidney disease; ADPKD;  
KW acquired cystic disease; transgenic animal; PCR primer; ss.  
XX Homo sapiens.  
XX WO200206529-A2.  
PN  
XX 24-JAN-2002.

XX 13-JUL-2001; 2001WO-US022035.  
PF  
XX 13-JUL-2000; 2000US-0218261P.  
PR 13-APR-2001; 2001US-0283691P.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
XX Germino GG, Watnick TJ, Phakdeekitcharoen B;  
PI WPI; 2002-179805/23.  
XX  
DR Novel primer for diagnosing polycystic kidney disease-associated  
XX disorder, comprises regions having sequence that selectively hybridizes  
PT to polycystic kidney disease gene sequence.  
PT  
XX  
PS Claim 6; Page 98; 192pp; English.  
XX  
CC The present invention relates to compositions and methods useful for the  
CC identification and detection of polycystic kidney disease (PKD1) gene  
CC mutations. The invention also relates to primers comprising a 5' region  
CC having a sequence that selectively hybridises to a PKD1 gene sequence and  
CC optionally, to a PKD1 homologue sequence and an adjacent 3' region having  
CC a sequence that selectively hybridises to a PKD1 gene sequence and not to  
CC a PKD1 homologue sequence. Primer pairs of the invention are useful for  
CC detecting the presence or absence of a mutation in a PKD1 polynucleotide  
CC in a sample, for identifying a subject at risk for a PKD1-associated  
CC disorder such as autosomal dominant polycystic kidney disease (ADPKD) or  
CC acquired cystic disease and for diagnosing a PKD1- associated disorder in  
CC a subject. They are useful for selectively amplifying a region of a PKD1  
CC gene. PKD1 DNA fragments are useful detecting the presence of a mutant  
CC PKD1 polynucleotide in a sample, as a probe for an amplification  
CC reaction, in hybridisation or amplification assays of biological samples  
CC to detect abnormalities of PKD1 expression and for engineering transgenic  
CC animals. The present sequence is a PCR primer used to generate human PKD1  
CC gene long range templates (exon 1-34)  
XX  
SQ Sequence 29 BP; 6 A; 9 C; 6 G; 8 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 29; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 0.047;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CCATCCACCTGCTGTGTGACCTGGTAAAT 29  
Db 1 CCATCCACCTGCTGTGTGACCTGGTAAAT 29  
  
RESULT 2  
AAD42395  
ID AAD42395 standard; DNA; 22 BP.  
XX  
AC AAD42395;  
XX  
DT 04-NOV-2002 (first entry)  
XX  
DE Oxred 2C primer used to sequence human cytochrome p450 reductase DNA.  
XX  
KW 11 alpha hydroxylase; enzyme; sitosterol; eplerenone; cell therapy;  
KW steroid bioconversion; antiinflammatory; antiarthritic; cytostatic;  
KW cardiant; human; cytochrome p450 reductase; primer; ss.  
XX Homo sapiens.  
OS  
XX WO200246386-A2.  
PN  
XX 13-JUN-2002.  
XX  
PF 26-OCT-2001; 2001WO-US051070.  
XX  
PR 30-OCT-2000; 2000US-0244300P.  
XX (PHAA ) PHARMACIA CORP.  
PA

PA (BOLT/) BOLTON S.  
PA (CLAY/) CLAYTON R.  
PA (EAST/) EASTON A.  
PA (ENGE/) ENGEL L.  
PA (MESS/) MESSING D.  
XX  
PI Bolton S, Clayton R, Easton A, Engel L, Messing D;  
XX  
DR WPI; 2002-547772/58.  
XX  
XX New isolated Aspergillus ochraceus 11 alpha-hydroxylase or  
PT oxidoreductase, for bioconversion of steroid substances to their 11 alpha  
PT hydroxy counterparts in heterologous cells.  
XX  
PS Example 12; Page 178; 181pp; English.  
XX  
CC The present invention relates to novel cytochrome P450-like enzyme  
CC (Aspergillus ochraceus 11 alpha hydroxylase protein), oxidoreductases and  
CC polynucleotides encoding such proteins. Host cells comprising the  
CC sequences of the invention are useful for making one or more enzymes from  
CC the metabolic pathway for the synthesis of sitosterol to eplerenone. They  
CC are useful for selective oxidation of a compound to an hydroxylated  
CC product. Compositions of the invention are useful for producing spores  
CC from A. ochraceus, A. niger, A. nidulans, Rhizopus oryzae, R. stolonifer,  
CC R. arrhizus Trichothecium roseum, Fusarium oxysporum and M. olivaceum  
CC etc, preferably to produce spores from A. ochraceus. Sequences of the  
CC invention are useful in bioconversion of steroid substances to their 11  
CC alpha-hydroxy counterparts. They are also used in cell therapy. The  
CC present sequence is a primer used to sequence human cytochrome p450  
CC reductase DNA. This sequence is used in the exemplification of the  
CC invention  
XX  
SQ Sequence 22 BP; 4 A; 7 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 53.8%; Score 15.6; DB 1; Length 22;  
Best Local Similarity 81.8%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGACCTG 23  
| | | | | | | | | | | | | | | | | |  
Db 1 CATCGACCACCTGTGTGAGCTG 22

RESULT 3  
AAZ77065/C  
ID AAZ77065 standard; DNA; 21 BP.  
XX  
AC AAZ77065;  
XX  
DT 10-SEP-2001 (first entry)  
XX  
DE Human biallelic marker downstream amplification primer SEQ ID NO:11421.  
XX  
KW Human genome; biallelic marker; high density disequilibrium map;  
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;  
KW haplotyping; hybridisation; identification; characterisation;  
KW amplification; single nucleotide polymorphism; SNP; PCR primer;  
KW diagnosis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9954500-A2.  
XX  
PD 28-OCT-1999.  
XX  
PF 21-APR-1999; 99WO-IB0000822.  
XX  
PR 21-APR-1998; 98US-0082614P.  
PR 23-NOV-1998; 98US-0109732P.  
XX  
PA (GEST ) GENSET.  
XX  
PI Cohen D, Blumenfeld M, Chumakov I;

XX WPI; 2000-013267/01.  
DR  
XX  
XX Novel biallelic markers used to construct a high density disequilibrium  
PT map of the human genome.  
XX  
XX  
PS Claim 9; Page 2665; 2745pp; English.  
XX  
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present  
CC invention, which contain a polymorphic base at position 24 of their  
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification  
CC primers for the biallelic markers. The biallelic markers of the invention  
CC have a variety of uses: they can be used for high density mapping of the  
CC human genome, and in complex association studies and haplotyping studies  
CC which are useful in determining the genetic basis for disease states.  
CC Compositions and methods of the invention can also be useful for the  
CC identification of the targets for the development of pharmaceutical  
CC agents and diagnostic methods, as well as the characterisation of the  
CC differential efficacious responses to and side effects from  
CC pharmaceutical agents acting on a disease as well as other treatment.  
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and  
CC 3367, are not actually given a sequence in the Sequence Listing from the  
CC present invention  
XX  
SQ Sequence 21 BP; 7 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 52.4%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 18;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGTGACC 21  
| | | | | | | | | | | | | | | | | |  
Db 21 CATTGACTGTGTGTGACC 2

RESULT 4  
AAZ74984  
ID AAZ74984 standard; DNA; 20 BP.  
XX  
AC AAZ74984;  
XX  
DT 10-SEP-2001 (first entry)  
XX  
DE Human biallelic marker downstream amplification primer SEQ ID NO:9340.  
XX  
KW Human genome; biallelic marker; high density disequilibrium map;  
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;  
KW haplotyping; hybridisation; identification; characterisation;  
KW amplification; single nucleotide polymorphism; SNP; PCR primer;  
KW diagnosis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9954500-A2.  
XX  
PD 28-OCT-1999.  
XX  
PF 21-APR-1999; 99WO-IB0000822.  
XX  
PR 21-APR-1998; 98US-0082614P.  
PR 23-NOV-1998; 98US-0109732P.  
XX  
PA (GEST ) GENSET.  
XX  
PI Cohen D, Blumenfeld M, Chumakov I;  
XX  
XX WPI; 2000-013267/01.  
XX  
XX Novel biallelic markers used to construct a high density disequilibrium  
PT map of the human genome.  
XX  
XX  
PS Claim 8; Page 2222; 2745pp; English.  
XX



CC AAZ65654 to AAZ69578 represent human biallelic markers from the present  
CC invention, which contain a polymorphic base at position 24 of their  
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification  
CC primers for the biallelic markers. The biallelic markers of the invention  
CC have a variety of uses: they can be used for high density mapping of the  
CC human genome, and in complex association studies and haplotyping studies  
CC which are useful in determining the genetic basis for disease states.  
CC Compositions and methods of the invention can also be useful for the  
CC identification of the targets for the development of pharmaceutical  
CC agents and diagnostic methods, as well as the characterisation of the  
CC differential efficacious responses to and side effects from  
CC pharmaceutical agents acting on a disease as well as other treatment.  
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and  
CC 3367, are not actually given a sequence in the Sequence Listing from the  
CC present invention  
XX  
SQ Sequence 20 BP; 2 A; 7 C; 4 G; 7 T; 0 U; 0 Other;  
  
Query Match 51.0%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 21;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 4 TCCACCTGCTGTGACC 21  
Db | | | | | | | | | | | | | | | |  
3 TGCACCTGCTCTGACC 20  
  
RESULT 5  
ADY78981  
ID ADY78981 standard; DNA; 20 BP.  
XX  
AC ADY78981;  
XX  
DT 02-JUN-2005 (first entry)  
XX  
DE SARS coronavirus antisense primer SEQ ID NO 19539.  
KW Severe acute respiratory syndrome; SARS coronavirus infection;  
KW phosphorothioate; antisense; antisense oligonucleotide;  
KW antisense therapy; diagnostic; virucide; gene therapy; ss; primer.  
XX SARS coronavirus.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1. .5  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2-O-methoxyethyl (2-MOE) wing. Internucleoside  
FT linkages are phosphorothioate and all cytidine  
FT nucleotides are 5-methylcytidine."  
FT modified\_base 6. .15  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "2-O-methoxyethyl (2-MOE) wing. Internucleoside  
FT linkages are phosphorothioate and all cytidine  
FT nucleotides are 5-methylcytidine."  
FT modified\_base 16. .20  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate backbone. All cytidine  
FT nucleotides are 5methylcytidine"  
XX  
PN WO2005023083-A2.  
XX  
PD 17-MAR-2005.  
XX  
PF 27-APR-2004; 2004WO-US013050.  
XX  
PR 28-APR-2003; 2003US-0466426P.  
PR 30-APR-2003; 2003US-0467770P.  
PR 06-MAY-2003; 2003US-0468562P.  
PR 06-MAY-2003; 2003US-0468627P.

PR 10-JUN-2003; 2003US-0477637P.  
PR 27-JUN-2003; 2003US-0483579P.  
PR 26-APR-2004; 51US-00483579.  
XX (ISIS-) ISIS PHARM INC.  
XX  
PI Crooke ST, Ecker DJ, Sampath R, Freier SM, Massire C;  
PI Hofstadler SA, Lowery KS, Swayze EE, Baker BF, Bennett FC;  
XX  
DR WPI; 2005-223236/23.  
XX  
PT New oligomeric compound comprising 8-80 nucleobases targeted to a nucleic  
PT acid molecule encoding severe acute respiratory syndrome (SARS) virus,  
PT useful for treating a disease or condition associated with a SARS virus.  
XX  
PS Example 18; SEQ ID NO 19539; 130pp; English.  
XX  
CC This invention describes a novel oligomeric compound comprising 8-80  
CC nucleobases targeted to a nucleic acid molecule encoding severe acute  
CC respiratory syndrome (SARS) virus, where the compound hybridizes with the  
CC nucleic acid molecule encoding SARS virus and reduces the expression of  
CC SARS virus by at least 50%. The invention also describes 1) a method for  
CC reducing the expression of a SARS virus in cells or tissues; 2) a method  
CC of screening for a modulator of a SARS virus; 3) a diagnostic method for  
CC identifying a disease state; 4) a kit or assay device; 5) modulating the  
CC frameshift efficiency of a coronavirus; 6) screening for a modulator of a  
CC frameshift site; 7) a ribosomal frameshift reporting plasmid comprising a  
CC viral sequence containing a ribosomal frameshift site and a luciferase  
CC reporter gene and 8) characterization of a previously uncharacterized  
CC frameshift site in a coronavirus RNA. The compound is a 15-30 nucleobases  
CC antisense chimeric oligonucleotide. At least a portion of the compound  
CC hybridizes with RNA to form an oligonucleotide-RNA duplex. It has at  
CC least one modified internucleoside linkage, modified sugar moiety, or  
CC modified nucleobase, specifically, phosphorothioate internucleoside  
CC linkage, 2'-O-methoxyethyl sugar moiety, or 5-methylcytosine.  
CC Specifically, the compound is targeted to a frameshift site of viral RNA,  
CC where the compound specifically hybridizes with the frameshift site and  
CC modulates the process of ribosomal frameshift of the viral RNA. The  
CC modulator of SARS virus expression comprises an oligonucleotide, an  
CC antisense oligonucleotide, a DNA oligonucleotide, an RNA oligonucleotide,  
CC a chimeric oligonucleotide, or an RNA oligonucleotide having at least a  
CC portion that is hybridizable with RNA to form an oligonucleotide-RNA  
CC duplex. Characterizing a previously uncharacterized frameshift site in a  
CC coronavirus RNA comprises obtaining RNA sequences of known coronaviruses  
CC with known frameshift sites, obtaining an RNA sequence of a coronavirus  
CC with an uncharacterized frameshift site and performing covariance  
CC analysis on multiple sequence alignments of the RNA sequences of known  
CC coronaviruses and the RNA sequence of the coronavirus with an  
CC uncharacterized frameshift site. The compound is useful for treating an  
CC animal having a disease or condition associated with a SARS virus so that  
CC expression of SARS virus is reduced, where the disease or condition is a  
CC viral infection. The compound is also useful for treating an individual  
CC having a disease or condition associated with a coronavirus so that the  
CC propagation of the coronavirus is inhibited as a result of modulation of  
CC the frameshift site of the coronavirus. The compounds are useful for  
CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.  
CC Oligonucleotides were synthesized via solid phase P(III) phosphoramidite  
CC chemistry on an automated synthesizer. Phosphodiester internucleotide  
CC linkages were afforded by oxidation with aqueous iodine. Phosphorothioate  
CC internucleotide linkages were generated by sulfuration utilizing 3,H-  
CC 1,2-benzodithiole-3-one 1,1 dioxide in anhydrous acetonitrile. This  
CC sequence represents a chimeric phosphorothioate oligonucleotide targeted  
CC to SARS coronavirus.  
XX  
SQ Sequence 20 BP; 7 A; 4 C; 3 G; 6 T; 0 U; 0 Other;  
  
Query Match 51.0%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 21;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 12 CTGTGTGACCTGTTAAAT 29  
Db | | | | | | | | | | | | | | | |  
3 CTCTGTAACTCTGTTAAAT 20



```
RESULT 6
AAx85859
ID  AAX85859 standard; DNA; 20 BP.
XX
AC  AAX85859;
XX
DT  10-SEP-1999  (first entry)
XX
DE  Primer used to codon optimise KGF-2 delta33.
XX
KW  Human; keratinocyte growth factor-2; KGF-2; gut toxicity;
KW  epithelial cell proliferation; basal keratinocyte; wound healing;
KW  hair follicle production; dermal wound healing; cell differentiation;
KW  ischemia; diabetes; thrombocytopenia; hypofibrinogenemia;
KW  hypoalbuminemia; hypoglobulinemia; hemorrhagic cystitis; xerostomia;
KW  keratoconjunctivitis sicca; ss.
XX
OS  Synthetic.
OS  Homo sapiens.
XX
PN  WO9932135-A1.
XX
PD  01-JUL-1999.
XX
PF  22-DEC-1998; 98WO-US026085.
XX
PR  22-DEC-1997; 97US-0068493P.
XX
PA  (HUMA-) HUMAN GENOME SCI INC.
XX
PI  Gentz RL, Chopra A, Kaushal P, Spitznagel T, Unsworth E, Khan F;
XX
DR  WPI; 1999-418866/35.
XX
PT  New compositions containing keratinocyte growth factor-2.
XX
PS  Disclosure; Page 45; 86pp; English.
XX
CC  Oligonucleotides AAX85859-72 were used to codon optimise human
CC  keratinocyte growth factor-2 (KGF-2) deltion mutant KGF-2 delta33. The
CC  specification describes compositions containing KGF-2. The compositions
CC  can be used to stimulate epithelial cell proliferation and basal
CC  keratinocytes for the purpose of wound healing, and to stimulate hair
CC  follicle production and healing of dermal wounds. The compositions can
CC  also be used to stimulate differentiation of cells. They can be used to
CC  stimulate wound healing and burns resulting from heat exposure to extreme
CC  temperatures of heat or cold, or exposure to chemicals, in normal
CC  individuals and those subject to conditions which induce abnormal wound
CC  healing. The compositions are also useful for promoting the healing of
CC  wounds associated with ischemia and ischemia and ischemic injury. They
CC  may also be used to treat effects of gut toxicity that result from
CC  radiation, chemotherapy treatments or viral infections, to treat diseases
CC  and conditions of the liver, lung, kidney, breast, pancreas, stomach,
CC  small intestine, and large intestine, to treat inflammatory bowel
CC  diseases, diabetes, thrombocytopenia, hypofibrinogenemia,
CC  hypoalbuminemia, hypoglobulinemia, hemorrhagic cystitis, xerostomia,
CC  keratoconjunctivitis sicca, to stimulate the epithelial cells of the
CC  salivary glands, lacrimal glands and stimulating re-epithelialization of
CC  the sinuses and the growth of nasal mucosa
XX
SQ  Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;

Query Match          49.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 27;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2 CATCCACCTGCTGTGTGAC 20
    || ||||| |||||
Db  1 CAACCACCTGCAGGGTGAC 19
```

```
RESULT 7
AAZ111144
ID  AAZ111144 standard; DNA; 20 BP.
XX
AC  AAZ111144;
XX
DT  03-NOV-1999  (first entry)
XX
DE  PCR primer for E.coli optimised keratinocyte growth factor mutant.
XX
KW  Keratinocyte growth factor; KGF-2; human; platelet; fibrinogen; albumin;
KW  globulin; total serum protein; blood; hypofibrinogenaemia; cirrhosis;
KW  disseminated intravascular coagulation; thrombocytopenia; myelofibrosis;
KW  hypoalbuminaemia; posttransfusion purpura; metastatic tumour; anaemia;
KW  leukaemia; haemolytic syndrome; Zieve's syndrome; rheumatic disease;
KW  HELLP preecclampitic syndrome; congenital rubella syndrome; systemic lupus;
KW  Epstein-Barr infectious mononucleosis; thyrotoxicosis; uraemia; therapy;
KW  infection; tissue necrosis; vasculitis; ulcerative bowel disease;
KW  serositis; subacute bacterial endocarditis; liver disease; amyloidosis;
KW  congestive heart failure; constrictive pericarditis; nephrotic syndrome;
KW  cardiac valvular disease; hypoglobulinaemia; keratoconjunctivitis sicca;
KW  PCR primer; ss.
XX
OS  Synthetic.
OS  Homo sapiens.
OS  Escherichia coli.
XX
PN  WO9941282-A1.
XX
PD  19-AUG-1999.
XX
PF  12-FEB-1999; 99WO-US003018.
XX
PR  13-FEB-1998; 98US-0074585P.
PR  30-DEC-1998; 98US-0114387P.
XX
PA  (HUMA-) HUMAN GENOME SCI INC.
XX
PI  Jimenez P, Rampy MA, Mendrick D, Russell D, Louie A;
XX
WPI; 1999-527359/44.
XX
DR  Use of keratinocyte growth factor-2 to increase levels of platelets,
XX  fibrinogen, albumin, globulin and total serum protein.
PT
XX  Example 14; Page 129; 331pp; English.
PS
XX  This sequence is a PCR primer for DNA encoding a E. coli optimised human
CC  keratinocyte growth factor-2 (KGF-2) protein mutant. Fragments and
CC  mutants of KGF-2 are used in the methods of the invention, for increasing
CC  the level of platelets, fibrinogen, albumin, globulin, and total serum
CC  protein in the blood. KGF-2 can also be used to stimulate proliferation
CC  of salivary gland cells, lacrimal gland cells, sinus epithelium, and
CC  Goblet cells. The methods can also be used to treat hypofibrinogenaemia
CC  caused by a cirrhosis, and disseminated intravascular coagulation (DIC).
CC  The methods can be used to treat thrombocytopenia and to alleviate
CC  hypoalbuminaemia. The methods can also be used to treat
CC  hypoglobulinaemia, total protein loss, damage to the sinus epithelium,
CC  and can be used to increase proliferation of epithelial cells of the
CC  bladder or prostate, stimulate proliferation of the salivary gland cells
CC  and to increase Goblet cell proliferation for treating or preventing
CC  keratoconjunctivitis sicca
XX
SQ  Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;

Query Match          49.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 27;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2 CATCCACCTGCTGTGTGAC 20
    || ||||| |||||
Db  1 CAACCACCTGCAGGGTGAC 19
```

RESULT 8  
AAA71269  
ID AAA71269 standard; DNA; 20 BP.  
XX  
AC AAA71269;  
XX  
DT 20-NOV-2000 (first entry)  
XX  
DE Human KGF-2 mutant KGF2delta33 codon optimised primer SEQ ID NO: 97.  
XX  
KW Human; keratinocyte growth factor; KGF-2; antiulcer; antidiabetic;  
KW antiinflammatory; cytoprotective; dermatological; gastrointestinal;  
KW hepatic; respiratory; renal; cerebroprotective; mucositis; treatment;  
KW epithelial cell proliferation; inflammatory bowel disease; lung damage;  
KW liver disorder; diabetes; oral injury; gastrointestinal injury;  
KW gut toxicity; gastric; duodenal; epidermolysis bullosa; skin graft;  
KW skin disorder; renal failure; brain injury; intestinal fibrosis;  
KW proctitis; female reproductive tract disorder; pulmonary fibrosis;  
KW pneumonitis; pleural retraction; hemopoietic syndrome; myelotoxicity;  
KW mutant; primer; ss.  
XX  
OS Homo sapiens.  
XX  
OS  
XX  
PN US6077692-A.  
XX  
XX  
PD 20-JUN-2000.  
XX  
XX  
PF 13-FEB-1998; 98US-00023082.  
XX  
PR 14-FEB-1995; 95WO-US001790.  
PR 05-JUN-1995; 95US-00461195.  
PR 13-AUG-1996; 96US-0023852P.  
PR 28-FEB-1997; 97US-0039045P.  
PR 23-MAY-1997; 97US-00862432.  
PR 13-AUG-1997; 97US-0055561P.  
PR 13-AUG-1997; 97US-00910875.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX  
PI Mendrick D, Duan DR, Ni J, Jimenez P, Coleman TA, Gruber JR;  
PI Dillon PJ, Gentz RL, Ruben SM, Zhang J, Moore PA, Rampy MA;  
XX  
XX WPI; 2000-441307/38.  
XX  
PT Novel keratinocyte growth factor useful for promoting and accelerating  
PT wound healing, comprising at least 10 contiguous amino acids from a  
PT specific amino acid sequence.  
XX  
XX Example 16; Col 187-188; 190pp; English.  
XX  
CC This invention describes a novel human keratinocyte growth factor, KGF-2  
CC (I), which has antiulcer, antidiabetic, antiinflammatory, cytoprotective,  
CC dermatological, gastrointestinal, hepatic, respiratory, renal and  
CC cerebroprotective activity. (I) is useful for stimulating epithelial cell  
CC proliferation in patients suffering from wound, mucositis, ulcer such as  
CC venous stasis ulcer, diabetic ulcer and cubitus ulcer. (I) is also useful  
CC for treating inflammatory bowel disease, liver disorder, lung damage,  
CC diabetes, oral injury, gastrointestinal injury, gut toxicity, gastric  
CC ulcer, duodenal ulcer, epidermolysis bullosa, skin graft, skin disorder,  
CC renal failure, brain injury, breast tissue injury, urothelial damage,  
CC female reproductive tract disorder, intestinal fibrosis, proctitis,  
CC pulmonary fibrosis, pneumonitis, pleural retraction, hemopoietic syndrome  
CC and myelotoxicity. (I) is also useful for increasing the adherence of  
CC skin grafts to wound beds and to stimulate re-epithelialization from the  
CC wound bed, to produce changes in hepatocyte proliferation, to reduce the  
CC side effects of gut toxicity, to regenerate skin in full and partial  
CC thickness skin defects, and to prevent and heal damage to lungs. KGF-2  
CC shows enhanced activity, increased stability, higher yield and better  
CC solubility. This sequence represents a human KGF-2 mutant protein primer  
CC described in the method of the invention  
XX  
SQ Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 49.0%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 27;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 CATCCACCTGCTGTGTGAC 20  
Db ||||||| |||||  
1 CAACCACCTGCAGGGTGAC 19  
RESULT 9  
AAF31967  
ID AAF31967 standard; DNA; 20 BP.  
XX  
AC AAF31967;  
XX  
DT 10-APR-2001 (first entry)  
XX  
DE PCR primer #10 for mutant KGF-2 construct.  
XX  
KW Keratinocyte growth factor; KGF-2; epithelial cell proliferation; wound;  
KW mucositis; ulcer; inflammatory bowel disease; liver disorder;  
KW lung damage; diabetes; oral injury; gastrointestinal injury;  
KW epidermolysis bullosa; renal failure; brain injury; proctitis;  
KW pulmonary fibrosis; haemopoietic syndrome; ovary injury; infertility;  
KW liver fibrosis; PCR primer; ss.  
XX  
OS Unidentified.  
XX  
XX WO200102433-A1.  
PN  
XX  
PD 11-JAN-2001.  
XX  
XX  
PF 03-JUL-2000; 2000WO-US018328.  
XX  
PR 02-JUL-1999; 99US-0142343P.  
PR 14-JUL-1999; 99US-0143648P.  
PR 15-JUL-1999; 99US-0144024P.  
PR 12-AUG-1999; 99US-0148628P.  
PR 19-AUG-1999; 99US-0149935P.  
PR 03-NOV-1999; 99US-0163375P.  
PR 22-DEC-1999; 99US-0171677P.  
PR 19-APR-2000; 2000US-0198322P.  
PR 19-MAY-2000; 2000US-0205417P.  
PR 30-JUN-2000; 2000US-00142343.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX  
PI Ruben SM, Jimenez P, Duan DR, Rampy MA, Mendrick D, Zhang J;  
PI Ni J, Moore PA, Coleman TA, Gruber JR, Dillon PJ, Gentz RL;  
XX  
DR WPI; 2001-071578/08.  
XX  
PT A polynucleotide encoding the human keratinocyte growth factor useful for  
PT stimulating epithelial cell proliferation in a patients that has e.g a  
PT wound.  
XX  
XX Example 16; Page 337; 591pp; English.  
PS  
XX  
CC The present invention relates to human keratinocyte growth factor (KGF-2;  
CC see AAF31901 and AAB61657). The present sequence is a PCR primer for KGF-  
CC 2. KGF-2 can be used to stimulate epithelial cell proliferation in a  
CC patient, where the patient has a wound, mucositis, an ulcer, inflammatory  
CC bowel disease, liver disorder, lung damage, diabetes, oral injury,  
CC gastrointestinal injury, gut toxicity, epidermolysis bullosa, skin graft,  
CC skin disorder, renal failure, brain injury, breast tissue injury,  
CC urothelial damage, female reproductive tract disorder, intestinal  
CC fibrosis, proctitis, pulmonary fibrosis, pneumonitis, plural  
CC retraction, haemopoietic syndrome, and myelotoxicity. In addition, KGF-2  
CC can be used in the treatment or prevention of ovary injury, infertility,  
CC or fibrosis of the liver. KGF-2 also promotes internal healing, donor  
CC site healing, internal surgical wound healing or healing of incisional  
CC wounds made during cosmetic surgery in a patient

XX SQ Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;  
Query Match 49.0%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 27;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 CATCCACCTGCTGTGTGAC 20  
Db 1 CAACCACCTGCAGGGTGAC 19  
RESULT 10  
AAC92946  
ID AAC92946 standard; DNA; 20 BP.  
XX AAC92946;  
XX  
DT 27-MAR-2001 (first entry)  
XX  
DE Codon-optimised KGF-2 delta-33 PCR primer PM05, SEQ ID NO:18.  
XX  
KW Human; keratinocyte growth factor-2; KGF-2; wound healing; vulnery;  
KW epithelial cell proliferation; epidermal keratinocyte proliferation;  
KW soft tissue growth; ischaemic injury; skin disorder;  
KW skin graft adherence; deletion mutant; Escherichia coli;  
KW codon optimisation; PCR primer; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX WO200072872-A1.  
XX  
XX 07-DEC-2000.  
XX  
XX 02-JUN-2000; 2000WO-US015186.  
XX  
XX 02-JUN-1999; 99US-0137448P.  
PR 22-OCT-1999; 99US-0160913P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (GENT/) GENTZ R L.  
PA (CHOP/) CHOPRA A.  
PA (KAUS/) KAUSHAL P.  
PA (SPIT/) SPITZNAGEL T.  
PA (UNSW/) UNSWORTH E.  
PA (KHAN/) KHAN F.  
XX  
PI Gentz RL, Chopra A, Kaushal P, Spitznagel T, Unsworth E, Khan F;  
XX  
DR WPI; 2001-041105/05.  
XX  
PT Pharmaceutical composition useful for stimulating epithelial cell  
PT proliferation and basal keratinocytes for wound healing comprises  
PT keratinocyte growth factor-2, in liquid or lyophilized forms.  
XX  
PS Disclosure; Page 54; 101pp; English.  
XX  
CC The invention relates to a pharmaceutical composition comprising 0.02-40  
CC mg/ml (w/v) keratinocyte growth factor-2 (KGF-2) protein; a buffer having  
CC buffering capacity of pH 5-8 at 5-50 mM; a diluent to bring the  
CC composition to a designated volume; and a preservative such as m-cresol,  
CC chlorobutanol, or a mixture of methyl paraben and propyl paraben or their  
CC reaction products. The KGF-2 used in the composition of the invention is  
CC preferably a novel mutant selected from the KGF-2 deletion mutants  
CC AAB60202 and AAB60204-B60214, and particularly the deletion mutant KGF-2  
CC delta-33 (AAB60202). KGF-2 stimulates the proliferation of epithelial  
CC cells and epidermal keratinocytes but not mesenchymal cells such as  
CC fibroblasts. The compositions of the invention may therefore be used for  
CC promoting or accelerating soft tissue growth or wound healing, or for  
CC treating mucocytis or inflammatory bowel disease. The compositions may be  
CC used to promote the healing of both superficial and deep wounds,  
CC including those which involve damage of the dermis, and is effective both

CC in individuals with normal wound healing capacity, and in those in whom  
CC healing is impaired (e.g., those with conditions such as diabetes,  
CC infection, immunosuppression, malnutrition, and ischaemic blockage or  
CC injury). The compositions may also be used to stimulate the healing of  
CC eye tissue wounds, dental tissue wounds, oral cavity wounds, vascular and  
CC dermal ulcers, burns, wounds associated with ischaemic injury, and skin  
CC disorders such as psoriasis and epidermolysis bullosa. The KGF-2  
CC compositions may additionally be used to increase the adherence of skin  
CC grafts to a wound bed, to stimulate re-epithelialisation from the wound  
CC bed, and to reduce the side effects of gut toxicity that result from  
CC radiation, chemotherapy treatments or viral infections. The compositions  
CC of the invention are stable over prolonged periods of storage, have  
CC increased KGF-2 pharmacological activity and/or facilitate the  
CC application or administration of KGF-2 in therapeutic regimens. The  
CC present sequence represents a PCR primer used in the generation of  
CC Escherichia coli codon-optimised DNA encoding the KGF-2 deletion mutant,  
CC KGF-2 delta-33  
XX  
SQ Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;  
Query Match 49.0%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 27;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 CATCCACCTGCTGTGTGAC 20  
Db 1 CAACCACCTGCAGGGTGAC 19  
RESULT 11  
ABQ83060  
ID ABQ83060 standard; DNA; 20 BP.  
XX  
AC ABQ83060;  
XX  
DT 16-JAN-2003 (first entry)  
XX  
DE KGF-2 delta-33s codon optimised PCR primer SEQ ID NO:97.  
XX  
KW Keratinocyte growth factor 2; KGF-2; fibroblast growth factor 12; FGF-12;  
KW KGF-2 Delta28; inflammation; vulnery; dermatological;  
KW pulmonary epithelial cell; mucositis; epidermolysis bullosa;  
KW wound healing; PCR primer; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200277155-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 04-JAN-2002; 2002WO-US000101.  
XX  
PR 08-JAN-2001; 2001US-0259853P.  
PR 26-APR-2001; 2001US-0286368P.  
PR 09-NOV-2001; 2001US-0331168P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ruben SM, Jimenez P, Duan DR, Rampy MA, Mendrick D, Zhang J;  
PI Ni J, Moore PA, Coleman TA, Gruber JR, Dillon PJ, Gentz RL;  
XX  
DR WPI; 2003-018897/01.  
XX  
PT Treating inflammation comprises administering Keratinocyte Growth Factor  
PT -2Delta28 to a patient.  
XX  
PS Example 16; Page 356; 583pp; English.  
XX  
CC The present invention describes a method for treating inflammation. The  
CC method comprises administering keratinocyte growth factor 2 (KGF-2)  
CC Delta28 to a patient. Also described: (1) a method for stimulating the  
CC growth of pulmonary epithelial cells; or (2) a method of preventing

CC mucositis. KGF-2 Delta28 has vulnerary and dermatological activities, and  
CC can be used in gene therapy. KGF-2 Delta28 is useful for treating  
CC inflammation, stimulating the growth of pulmonary epithelial cells or  
CC preventing mucositis. It can also be used for treating epidermolysis  
CC bullosa and for promoting wound healing. ABQ82994 to ABQ83130 and  
CC ABP54273 to ABP54311 represent sequences used in the exemplification of  
CC the present invention  
XX  
SQ Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;  
  
Query Match 49.0%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 27;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 CATCCACCTGCTGTGTGAC 20  
Db 1 CAACCACCTGCAGGGTGAC 19  
  
RESULT 12  
ADA95533  
ID ADA95533 standard; DNA; 20 BP.  
XX  
AC ADA95533;  
XX  
DT 20-NOV-2003 (first entry)  
DE E. coli keratinocyte growth factor 2 (KGF-2) mutant PCR primer #6.  
XX  
KW PCR; primer; ss; keratinocyte growth factor 2; KGF-2; epidermal cell;  
KW keratinocyte; wrinkle; aged skin; skin strength; epidermal thickening;  
KW scarring reduction; cosmetic surgery; epithelial cell; liver; pancreas;  
KW kidney; prostate; bladder; lung; oesophagus; wound healing; diabetes;  
KW ischaemic blockage; ischaemic injury; steroid; uraemia; malnutrition;  
KW vitamin deficiency; obesity; immunosuppression; radiation therapy;  
KW chemotherapy; anastomosis; ulcer; burn; mucositis;  
KW inflammatory bowel disease; inflammation; radiation-induced condition;  
KW viral hepatitis; liver failure; pancreatitis; lung damaging condition;  
KW renal failure.  
XX  
OS Escherichia coli.  
XX  
PN US2003077695-A1.  
XX  
PD 24-APR-2003.  
XX  
PF 01-JUL-1999; 99US-00345373.  
XX  
PR 14-FEB-1995; 95WO-US001790.  
PR 13-AUG-1996; 96US-0023852P.  
PR 28-FEB-1997; 97US-0039405P.  
PR 23-MAY-1997; 97US-00862432.  
PR 13-AUG-1997; 97US-0055561P.  
PR 13-AUG-1997; 97US-00910875.  
PR 13-FEB-1998; 98US-00023082.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ruben SM, Jimenez P, Duan DR, Rampy MA, Mendrick D, Zhang J;  
PI Ni J, Moore PA, Coleman TA, Gruber JR, Dillon PJ, Gentz RL;  
XX  
DR WPI; 2003-596836/56.  
XX  
PT New Keratinocyte Growth Factor (KGF-2) polypeptides and polynucleotides,  
PT useful for treating or preventing mucositis or Crohn's disease, reducing  
PT scarring, or improving wound healing or skin strength.  
XX  
PS Example 16; Page 44; 195pp; English.  
XX  
CC The invention relates to Keratinocyte Growth Factor 2 (KGF-2)  
CC polypeptides and the polynucleotides encoding them. The KGF-2  
CC polypeptides are useful for stimulating the proliferation of epidermal  
CC cells (e.g. keratinocytes) to prevent or improve the appearance of

CC wrinkles or aged skin, improve skin strength, promote epidermal  
CC thickening, reduce scarring or improve healing after cosmetic surgery.  
CC The KGF-2 polypeptide is also useful for stimulating epithelial cells  
CC (e.g. epithelial cells of the liver, pancreas, kidney, prostate, bladder,  
CC lung or oesophagus) or promoting wound healing in a wound healing  
CC impaired individual (due to diabetes, ischaemic blockage or injury,  
CC steroids, non-steroid compounds, uraemia, malnutrition, vitamin  
CC deficiencies, obesity, infection, immunosuppression, radiation therapy or  
CC chemotherapy). The wound may be caused by surgery (e.g. colonic or  
CC gastrointestinal surgical procedures such as anastomosis), ulcers, burns,  
CC etc. The KGF-2 polypeptide is also useful for treating or preventing  
CC mucositis (e.g. oral, oesophageal, gastric or rectal), inflammatory bowel  
CC disease (e.g. ulcerative colitis or Crohn's disease), inflammation (e.g.  
CC psoriasis, eczema, dermatitis or arthritis), a radiation-induced  
CC condition (e.g. oral injury, pulmonary fibrosis, myelotoxicity), viral  
CC hepatitis, liver failure (caused by e.g. hepatitis, cirrhosis),  
CC pancreatitis, lung damaging conditions (e.g. emphysema, lung cancer,  
CC pancreatitis, or renal failure. The polypeptide is further useful for  
CC promoting hair growth, treating tissue exposed to radiation (e.g.  
CC radiation for treating malignancy) or protecting tissue to be exposed to  
CC radiation, or promoting tissue growth or repair. This sequence represents  
CC a PCR primer used to amplify DNA encoding a KGF-2 polypeptide of the  
CC invention.  
XX  
SQ Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;  
  
Query Match 49.0%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 27;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 CATCCACCTGCTGTGTGAC 20  
Db 1 CAACCACCTGCAGGGTGAC 19  
  
RESULT 13  
ADD66206  
ID ADD66206 standard; DNA; 20 BP.  
XX  
AC ADD66206;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Codon optimised KGF-2delta33 PCR primer #1.  
XX  
KW Human; keratinocyte growth factor-2; KGF-2; ss; PCR;  
KW epidermal cell proliferation; epithelial cell proliferation;  
KW wound healing; colonic surgery; gastrointestinal surgery; mucositis;  
KW inflammatory bowel disease; inflammation; hair growth; radiation damage;  
KW tissue growth; female genital tract repair; urothelial healing;  
KW viral hepatitis; liver failure; pancreatitis; lung damaging condition;  
KW renal failure; primer; codon optimisation.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN US2003129687-A1.  
XX  
PD 10-JUL-2003.  
XX  
PF 15-FEB-2002; 2002US-00075446.  
XX  
PR 14-FEB-1995; 95WO-US001790.  
PR 05-JUN-1995; 95US-00461195.  
PR 13-AUG-1996; 96US-0023852P.  
PR 28-FEB-1997; 97US-0039045P.  
PR 13-AUG-1997; 97US-0055561P.  
PR 13-AUG-1997; 97US-00910875.  
PR 13-FEB-1998; 98US-00023082.  
PR 01-JUL-1999; 99US-00345373.  
XX  
PA (RUBE/) RUBEN S M.  
PA (JIME/) JIMENEZ P.







|           |                                                                          |           |                                                                           |
|-----------|--------------------------------------------------------------------------|-----------|---------------------------------------------------------------------------|
| PA        | (HUMA-) HUMAN GENOME SCI INC.                                            | DR        | WPI; 2004-441082/41.                                                      |
| XX        |                                                                          | XX        |                                                                           |
| PI        | Rampy M, Jimenez P, Louie A, Russell D, Mendrick D;                      | PT        | Identifying a subject at risk of breast cancer by detecting the presence  |
| XX        |                                                                          | PT        | or absence of one or more nucleotide polymorphic variations, useful for   |
| DR        | WPI; 2004-662619/65.                                                     | PT        | diagnosing, preventing and/or treating breast cancer.                     |
| XX        |                                                                          | XX        |                                                                           |
| PT        | Stimulating (M1) proliferation of lung epithelial cells, or inducing     | PS        | Example 5; Page 102; 286pp; English.                                      |
| PT        | hyperkeratosis of the buccal mucosa, tongue and esophagus, by            | XX        |                                                                           |
| PT        | administering to individual polypeptide having specific amino acid       | CC        | The invention relates to a novel method for identifying a subject at risk |
| PT        | residues of keratinocyte growth factor.                                  | CC        | of breast cancer which comprises detecting the presence or absence of one |
| XX        |                                                                          | CC        | or more polymorphic variations associated with breast cancer in a nucleic |
| PS        | Example 14; SEQ ID NO 97; 330pp; English.                                | CC        | acid sample from a subject. The method of the invention has cytostatic    |
| XX        |                                                                          | CC        | applications and may be useful for identifying a risk of breast cancer,   |
| CC        | This invention relates to a novel method of stimulating proliferation of | CC        | as well as therapeutic and prophylactic treatments that specifically      |
| CC        | lung epithelial cells, or inducing hyperkeratosis of the buccal mucosa,  | CC        | target breast cancer, such as gene therapy. The current sequence is that  |
| CC        | tongue and esophagus. The method involves administering to an individual | CC        | of an Extend primer of the invention which was used to genotype single    |
| CC        | a polypeptide comprising an amino acid sequence having amino acid        | CC        | nucleotide polymorphisms within human chromogranin B (CHGB;secretogranin  |
| CC        | residues Arg(80)-Ser-(208), Val(77)-Ser(208), Cys(37)-Ser(208), Thr(36)- | CC        | 1;SCG1) DNA which is located at chromosomal position 20pter-p12.          |
| CC        | Ser(208) or Met(1)-Ser(208) of fully defined sequence of keratinocyte    | XX        |                                                                           |
| CC        | growth factor (KGF-2) having 208 amino acids as given in specification.  | SQ        | Sequence 17 BP; 3 A; 5 C; 5 G; 4 T; 0 U; 0 Other;                         |
| CC        | The invention may be useful for the production of compounds with a       |           |                                                                           |
| CC        | keratolytic or respiratory-Gen activity. The method is useful for        |           | Query Match 47.6%; Score 13.8; DB 1; Length 17;                           |
| CC        | stimulating proliferation of lung epithelial cells, or inducing          |           | Best Local Similarity 88.2%; Pred. No. 27;                                |
| CC        | hyperkeratosis of the buccal mucosa, tongue and esophagus, where the     |           | Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;               |
| CC        | polypeptide is administered to treat or prevent lung diseases or lung    |           |                                                                           |
| CC        | damage. The lung disease is acute or chronic lung disease, emphysema,    | QY        | 2 CATCCACCTGCTGTGTG 18                                                    |
| CC        | inhalation injuries, hyaline membrane disease, infant respiratory        |           |                                                                           |
| CC        | distress syndrome or bronchiopulmonary dysplasia. The lung damage is     | Db        | 1 CATGCACACAGCTGTGTG 17                                                   |
| CC        | caused by lung fibrosis. The method enables stimulation of proliferation |           |                                                                           |
| CC        | of lung epithelial cells, or induction of hyperkeratosis of the buccal   |           |                                                                           |
| CC        | mucosa, tongue and esophagus. The present sequence is that of an         | RESULT 17 |                                                                           |
| CC        | oligonucleotide which was used in the exemplification of the invention.  | ADZ20529  |                                                                           |
| XX        |                                                                          | ID        | ADZ20529 standard; DNA; 18 BP.                                            |
| SQ        | Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;                        | XX        |                                                                           |
|           |                                                                          | AC        | ADZ20529;                                                                 |
|           | Query Match 49.0%; Score 14.2; DB 1; Length 20;                          | XX        |                                                                           |
|           | Best Local Similarity 84.2%; Pred. No. 27;                               | DT        | 30-JUN-2005 (first entry)                                                 |
|           | Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;              | XX        |                                                                           |
|           |                                                                          | DE        | Mouse G alpha-15 tail oligonucleotide SEQ ID NO:3.                        |
| QY        | 2 CATCCACCTGCTGTGTGAC 20                                                 | XX        |                                                                           |
|           |                                                                          | KW        | guanine nucleotide binding protein alpha 15; G alpha-15 protein;          |
| Db        | 1 CAACACACCTGCAGGGTGAC 19                                                | KW        | G protein coupled receptor modulator; ss.                                 |
|           |                                                                          | XX        |                                                                           |
|           |                                                                          | OS        | Mus musculus.                                                             |
| RESULT 16 |                                                                          | XX        |                                                                           |
| ADP09253  |                                                                          | PN        | US2005085625-A1.                                                          |
| ID        | ADP09253 standard; DNA; 17 BP.                                           | XX        |                                                                           |
| XX        |                                                                          | PD        | 21-APR-2005.                                                              |
| AC        | ADP09253;                                                                | XX        |                                                                           |
| DT        | 26-AUG-2004 (first entry)                                                | PF        | 16-DEC-2002; 2002US-00319821.                                             |
| XX        |                                                                          | XX        |                                                                           |
| DE        | Extend primer 48 used to genotype human chromogranin B polymorphism.     | PR        | 30-OCT-2000; 2000US-0243770P.                                             |
| XX        |                                                                          | PR        | 29-OCT-2001; 2001US-00984292.                                             |
| KW        | breast cancer; cytostatic; gene therapy; human; chromogranin B; CHGB;    | PR        | 21-NOV-2001; 2001US-00989497.                                             |
| KW        | secretogranin 1; SCG1; chromosome 20pter-p12; ss; PCR; primer; SNP;      | PR        | 14-DEC-2001; 2001US-0339466P.                                             |
| KW        | single nucleotide polymorphism.                                          | XX        |                                                                           |
| XX        |                                                                          | PA        | (SENO-) SENOMYX INC.                                                      |
| OS        | Homo sapiens.                                                            | XX        |                                                                           |
| XX        |                                                                          | PI        | Li X, Xu H, Staszewski L, Adler JE;                                       |
| XX        |                                                                          | XX        |                                                                           |
| PN        | WO2004047767-A2.                                                         | DR        | WPI; 2005-305201/31.                                                      |
| XX        |                                                                          | XX        |                                                                           |
| PD        | 10-JUN-2004.                                                             | PT        | New isolated chimeric G alpha 15 variant protein, useful for analyzing    |
| XX        |                                                                          | PT        | and discovering modulators of G-protein coupled receptors.                |
| PF        | 25-NOV-2003; 2003WO-US037966.                                            | XX        |                                                                           |
| XX        |                                                                          | PS        | Example 1; SEQ ID NO 3; 15pp; English.                                    |
| XX        |                                                                          | XX        |                                                                           |
| PR        | 25-NOV-2002; 2002US-0429136P.                                            | CC        | The invention relates to an isolated variant of a guanine nucleotide      |
| PR        | 24-JUL-2003; 2003US-0490234P.                                            | CC        | binding protein alpha 15 (G alpha-15) protein (I) that exhibits increased |
| XX        |                                                                          | CC        | coupling to a given G-protein coupled receptor (GPCR) relative to the     |
| XX        |                                                                          | CC        | native G alpha-15 protein and/or which couples to a particular GPCR not   |
| PA        | (SEQU-) SEQUENOM INC.                                                    | CC        | normally coupled by the native G alpha-15 protein. Specifically claimed   |
| XX        |                                                                          | CC        | is an isolated G alpha-15 variant protein (I) that has greater than 95 %  |
| PI        | Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;                    |           |                                                                           |
| XX        |                                                                          |           |                                                                           |

CC amino acid sequence identity to the 374 amino acid sequence of ADZ20528,  
CC where the 5 carboxy-terminal codons are identical to the 5 carboxy-  
CC terminal codons of another G protein, e.g. G alpha-11 , G alpha-q , G  
CC alpha-s , G alpha-13 , G alpha-z , G alpha-o , G alpha-13 , or G alpha-  
CC 14. Also described: (1) an isolated nucleic acid sequence encoding (1)  
CC including a nucleic acid encoding a polypeptide with greater than 80%,  
CC 90%, or 95% amino acid sequence identity to ADZ20528, where the last six  
CC codons are contained in any of ADZ20530-ADZ20538; (2) an antibody that  
CC selectively binds to (1), but not to the native G alpha-15 alpha protein;  
CC (3) an expression vector encoding (1), the vector including the nucleic  
CC acid sequence of (1) operably linked to a promoter that functions in  
CC mammalian cells or Xenopus oocytes; (4) a method for identifying a  
CC compound that modulates GPCR signaling; and (5) a method for producing a  
CC functional umami taste receptor or sweet taste receptor including  
CC producing a cell expressing (1) and T1R1/T1R3. The variants and methods  
CC are useful for analyzing and discovering modulators of G-protein coupled  
CC receptors. The present sequence represents the wild type mouse G alpha-15  
CC tail nucleotide sequence, which is given in an example from the present  
CC invention for the construction of G 15 chimeras.  
XX  
SQ Sequence 18 BP; 5 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 46.2%; Score 13.4; DB 1; Length 18;  
Best Local Similarity 93.3%; Pred. No. 34;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTG 16  
||| |||||  
Db 3 CATCAACCTGCTGTG 17

RESULT 18  
AAZ72126/c  
ID AAZ72126 standard; DNA; 19 BP.  
XX  
AC AAZ72126;  
XX  
DT 10-SEP-2001 (first entry)  
XX  
DE Human biallelic marker upstream amplification primer SEQ ID NO:6482.  
XX

KW Human genome; biallelic marker; high density disequilibrium map;  
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;  
KW haplotyping; hybridisation; identification; characterisation;  
KW amplification; single nucleotide polymorphism; SNP; PCR primer;  
KW diagnosis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9954500-A2.  
XX  
PD 28-OCT-1999.  
XX  
PF 21-APR-1999; 99WO-IB000822.  
XX  
PR 21-APR-1998; 98US-0082614P.  
PR 23-NOV-1998; 98US-0109732P.  
XX  
XX (GEST ) GENSET.  
XX  
PI Cohen D, Blumenfeld M, Chumakov I;  
XX  
DR WPI; 2000-013267/01.  
XX  
PT Novel biallelic markers used to construct a high density disequilibrium  
PT map of the human genome.  
XX  
XX Claim 9; Page 1613; 2745pp; English.  
XX  
XX AAZ65654 to AAZ69578 represent human biallelic markers from the present  
CC invention, which contain a polymorphic base at position 24 of their  
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification  
CC primers for the biallelic markers. The biallelic markers of the invention

CC have a variety of uses: they can be used for high density mapping of the  
CC human genome, and in complex association studies and haplotyping studies  
CC which are useful in determining the genetic basis for disease states.  
CC Compositions and methods of the invention can also be useful for the  
CC identification of the targets for the development of pharmaceutical  
CC agents and diagnostic methods, as well as the characterisation of the  
CC differential efficacious responses to and side effects from  
CC pharmaceutical agents acting on a disease as well as other treatment.  
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and  
CC 3367, are not actually given a sequence in the Sequence Listing from the  
CC present invention  
XX  
SQ Sequence 19 BP; 4 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 46.2%; Score 13.4; DB 1; Length 19;  
Best Local Similarity 93.3%; Pred. No. 37;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTGA 19  
||| |||||  
Db 19 CCGCTGCTGTGTGA 5

RESULT 19  
ADV60526  
ID ADV60526 standard; DNA; 19 BP.  
XX  
AC ADV60526;

XX  
DT 24-FEB-2005 (first entry)  
XX

DE siRNA-9 used to inhibit human BAMBI expression Seq 5.

XX  
KW ss; antibody engineering;  
KW bone morphogenetic protein and activin brave bound inhibitor; BAMBI;  
KW colon cancer; liver cancer; antisense therapy; cytostatic; siRNA;  
KW RNA interference; small interfering RNA.

XX Synthetic.

XX WO2004106515-A1.

XX 09-DEC-2004.

XX 27-MAY-2004; 2004WO-JP007677.

XX 28-MAY-2003; 2003JP-00151302.

XX (SCIM-) SCIMEDIA LTD.

XX (AKIY/) AKIYAMA T.

PI Akiyama T, Sekiya T, Ohwada S;

XX WPI; 2005-021288/02.

XX  
PT Novel anti-bone morphogenetic protein and activin brave bound inhibitor  
PT antibody, useful as colon cancer or liver cancer diagnostic agent and  
PT therapeutic agent.

XX Claim 12; SEQ ID NO 5; 52pp; Japanese.

XX  
CC This invention relates to a novel antibody, namely the anti-bone  
CC morphogenetic protein and activin brave bound inhibitor (BAMBI) antibody.  
CC Specifically, it refers to a preparation of a monoclonal antibody that  
CC can be used as a colon cancer or liver cancer diagnostic agent. The  
CC present invention describes a diagnostic containing a primer or a probe  
CC that can detect the BAMBI gene. Furthermore, it provides a remedy for  
CC colon or liver cancer that comprises transformation with a vector in  
CC order to introduce nucleic acids that can be used in antisense therapy  
CC and the formation of BAMBI dsRNA. As such, these compositions exhibit  
CC cytostatic activity. This oligonucleotide sequence is an siRNA sequence  
CC used to inhibit BAMBI expression, given in an exemplification of the  
CC invention.

```
XX
SQ   Sequence 19 BP; 2 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

    Query Match          46.2%;   Score 13.4;  DB 1;   Length 19;
    Best Local Similarity 93.3%;   Pred. No. 37;
    Matches 14;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY   9 CTGCTGTGTGACCTG 23
    ||||| |||||
Db   1 CTGCTGTCTGACCTG 15

RESULT 20
AAZ44771/c
ID   AAZ44771 standard; DNA; 18 BP.
XX
AC   AAZ44771;
XX
DT   19-APR-2000 (first entry)
XX
DE   Human FADD primer ISIS #23871.
XX
KW   FADD; human; antisense; inhibitor; Fas-associated death domain; primer;
    probe; ss.
XX
OS   Homo sapiens.
XX
PN   US6015712-A.
XX
PD   18-JAN-2000.
XX
PF   19-JUL-1999; 99US-00357072.
XX
PR   19-JUL-1999; 99US-00357072.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP, Cowsert LM, Baker BF, Zhang H;
XX
DR   WPI; 2000-126316/11.
XX
PT   Antisense oligonucleotides, useful for inhibiting human Fas-associated
    death domain (FADD) expression are targeted to the 3' untranslated region
    of the FADD gene.
XX
PS   Example 16; Col 53-54; 37pp; English.
XX
CC   This invention describes novel antisense oligonucleotides (OGNs) (I) 8-20
    nucleotides in length that specifically hybridize with and inhibit
    nucleic acids encoding human Fas-associated death domain (FADD), targeted
    to the 3' untranslated region (3'UTR). (I) can be used to treat animals,
    especially humans, suspected of having or being prone to a disease or
    condition associated with FADD expression. AAZ44746-244831 represent
    primers and probes used in the method of the invention
XX
SQ   Sequence 18 BP; 5 A; 7 C; 4 G; 2 T; 0 U; 0 Other;

    Query Match          45.5%;   Score 13.2;  DB 1;   Length 18;
    Best Local Similarity 83.3%;   Pred. No. 38;
    Matches 15;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

QY   9 CTGCTGTGTGACCTGGTA 26
    ||| || ||||| |||||
Db   18 CTGGTGGCTGACCTGGTA 1

RESULT 21
AAS99971
ID   AAS99971 standard; DNA; 15 BP.
XX
AC   AAS99971;
XX
DT   12-MAR-2002 (first entry)
```

```
XX
DE   Human NPR1 gene allele-specific oligonucleotide probe #13.
XX
KW   Human; natriuretic peptide receptor A/guanylate cyclase A; NPR1; ss;
    atrionatriuretic peptide receptor A; haplotyping; cytostatic; genotyping;
    haplotype pair; single nucleotide polymorphism; gene therapy; PCR primer;
    drug screening; hypertension; hypotensive; sequencing primer; probe.
XX
OS   Homo sapiens.
XX
PN   WO200179231-A2.
XX
PD   25-OCT-2001.
XX
PF   16-APR-2001; 2001WO-US012300.
XX
PR   14-APR-2000; 2000US-0197330P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Bentivegna SC, Choi JY, Kliem SE, Nandabalan K;
XX
DR   WPI; 2002-066340/09.
XX
PT   Genotyping human natriuretic peptide receptor A/guanylate cyclase gene of
    an individual, involves determining identity of nucleotide pair at
    specific polymorphic sites for two copies of the gene.
XX
PS   Claim 15; Page 14; 96pp; English.
XX
CC   The invention relates to single nucleotide polymorphisms in the gene
    encoding the human natriuretic peptide receptor A/guanylate cyclase A
    (atrionatriuretic peptide receptor A) or NPR1 polypeptide. A method for
    haplotyping the NPR1 gene in an individual comprises identifying the
    nucleotide at one or more polymorphic sites and determining whether one
    of the copies of the gene is defined by one of the NPR1 haplotypes given
    in the specification or whether both copies are defined by a haplotype
    pair. This method is useful in genotyping, whereby all possible haplotype
    pairs can be assigned to specific genotypes. An association between a
    trait and a haplotype or haplotype pair of the NPR1 gene can be
    identified by comparing the frequency of the haplotype or haplotype pair
    in a population exhibiting the trait with the frequency of the haplotype
    or haplotype pair in a reference population, where a higher haplotype
    frequency in the trait population indicates the trait is associated with
    the haplotype or haplotype pair. NPR1 and its corresponding DNA are used
    for studying the expression and function of NPR1, for use in screening
    for candidate drugs to treat diseases related to NPR1 activity, such as
    hypertension. The sequences are also useful for studying the effect of
    variation on the biological activity of NPR1 as well as on the binding
    affinity of candidate drugs targeting NPR1. Sequences AAS99959-AAS99990
    and ABK09390-ABK09462 represent probes, sequencing primers and PCR
    primers used to detect NPR1 gene polymorphisms
XX
SQ   Sequence 15 BP; 2 A; 4 C; 3 G; 5 T; 0 U; 1 Other;

    Query Match          44.8%;   Score 13;   DB 1;   Length 15;
    Best Local Similarity 86.7%;   Pred. No. 34;
    Matches 13;   Conservative 1;   Mismatches 1;   Indels 0;   Gaps 0;

QY   7 ACCTGCTGTGTGACC 21
    |||||:|||||
Db   1 ACTTGCTRTGTGACC 15

RESULT 22
AAT80089/c
ID   AAT80089 standard; cDNA; 17 BP.
XX
AC   AAT80089;
XX
DT   21-NOV-1997 (first entry)
XX
DE   Primer #1 for 4-coumaric acid coenzyme A ligase gene.
```

XX 4-coumaric acid coenzyme A ligase; 4CL gene; tobacco; Nicotiana tabacum;  
KW lignin; polymerase chain reaction; primer; amplify; PCR; ss.  
XX  
OS Synthetic.  
XX JP09173069-A.  
PN  
XX  
PD 08-JUL-1997.  
XX  
PF 22-DEC-1995; 95JP-00334834.  
XX  
PR 22-DEC-1995; 95JP-00334834.  
XX  
PA (MITY ) MITSUBISHI PAPER MILLS LTD.  
XX  
DR WPI; 1997-397027/37.  
XX  
PT 4-coumaric acid:coenzyme A ligase gene - used to reduce the lignin  
PT content of plants.  
XX  
PS Example 3; Page 4; 10pp; Japanese.  
XX  
CC AAT80089 and AAT80090 represent amplification primers for the 4-coumaric  
CC acid coenzyme A ligase gene (4CL gene) of Nicotiana tabacum strain SR1.  
CC The amplified sequence (see AAT80088), or the 4CL gene fragments shown in  
CC AAT80086 and AAT80087, are introduced into a plant in the method of the  
CC invention. The method of the invention is for the reduction of lignin in  
CC a plant  
XX  
SQ Sequence 17 BP; 3 A; 3 C; 5 G; 1 T; 0 U; 5 Other;  
SQ  
Query Match 44.1%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 68.8%; Pred. No. 42;  
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CCATCCACCTGCTGTG 16  
Db ||:||:||:||:||  
17 CCRTCNACYTGYTGNG 2  
RESULT 23  
ABV90926  
ID ABV90926 standard; DNA; 17 BP.  
XX  
AC ABV90926;  
XX  
DT 23-DEC-2002 (first entry)  
XX  
DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1639.  
XX  
KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;  
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;  
KW gene therapy; transgenic; ss.  
XX  
OS Homo sapiens.  
XX EP1239051-A2.  
XX  
PN 11-SEP-2002.  
XX  
PD  
XX  
PF 28-JAN-2002; 2002EP-00001165.  
XX  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 23-MAY-2001; 2001US-00864761.  
PR 10-OCT-2001; 2001US-0328205P.

XX (AEOM-) AEOMICA INC.  
PA Shannon M;  
XX  
XX WPI; 2002-684061/74.  
DR  
XX  
PT Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL  
PT -1, useful for treating disorders associated with decreased expression or  
PT activity of human POSHL1.  
XX  
PS Example 2; SEQ ID NO 1639; 60pp + Sequence Listing; English.  
XX  
CC The invention relates to an isolated SH3 domain (POSH)-like signalling  
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino  
CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),  
CC (S1) having 95% deviations, especially conservative substitutions or a  
CC fragment of the sequences comprising at least 8 contiguous amino acids.  
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an  
CC adaptor protein that interacts with Rho family small GTPases as well as  
CC downstream components of the signal transduction pathway. (I) is useful  
CC for identifying a specific binding partner. (I) and nucleic acids (II)  
CC encoding (I) are useful for diagnosing, monitoring disease and treating  
CC caused by altered expression of human POSHL1 including diagnosing and  
CC treating cancer, they useful in the development of vaccines and (II) is  
CC useful in gene therapy. (II) is useful for constructing microarrays which  
CC are useful for measuring and for surveying gene expression and creating  
CC transgenic non-human animals capable of producing the proteins. The  
CC present sequence is that of a scanning oligonucleotide useful in examples  
CC of the invention. Note: The present sequence did not form part of the  
CC printed specification, but is based on sequence information supplied to  
CC Derwent by the European Patent Office  
XX  
SQ Sequence 17 BP; 2 A; 7 C; 2 G; 6 T; 0 U; 0 Other;  
SQ  
Query Match 44.1%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 42;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3 ATCCACCTGCTGTGTG 18  
Db ||:||:||:||||  
1 ATCCACCTCCTCTGTG 16  
RESULT 24  
ABV90925  
ID ABV90925 standard; DNA; 17 BP.  
XX  
AC ABV90925;  
XX  
DT 23-DEC-2002 (first entry)  
XX  
DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1638.  
XX  
KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;  
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;  
KW gene therapy; transgenic; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP1239051-A2.  
XX  
PD 11-SEP-2002.  
XX  
PF 28-JAN-2002; 2002EP-00001165.  
XX  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 30-JAN-2001; 2001WO-US000671.  
PR 30-JAN-2001; 2001WO-US000672.



```
PR 30-JAN-2001; 2001WO-US0000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M;
XX
XX WPI; 2002-684061/74.
XX
XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX
XX Example 2; SEQ ID NO 1638; 60pp + Sequence Listing; English.
XX
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC (S1) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX
XX Sequence 17 BP; 2 A; 7 C; 2 G; 6 T; 0 U; 0 Other;
SQ
Query Match 44.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 42;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 ATCCACCTGCTGTGTG 18
Db ||||||| |||||
2 ATCCACCTCCTCTGTG 17
RESULT 25
AAT96932/c
ID AAT96932 standard; DNA; 18 BP.
XX
AC AAT96932;
XX
DT 27-APR-1998 (first entry)
XX
DE Human pRb2/p130 tumour suppressor gene intron 17/exon 18 boundary.
XX
KW Retinoblastoma susceptibility gene; pRb2; p130; pRb2/p130 gene;
KW cell cycle; tumour suppressor gene; cancer; molecular marker; diagnosis;
KW prognosis; predisposition; endometrial carcinoma; ovary cancer;
KW lung squamous cell carcinoma; lung adenocarcinoma; human; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT intron 1..9
FT /*tag= a
FT /note= "3' end of 1079 bp intron 17"
FT 10..18
FT /*tag= b
FT /note= "5' end of 72 bp exon 18"
XX
PN WO9738125-A1.
```

```
XX 16-OCT-1997.
PD
XX 03-APR-1997; 97WO-US005598.
PF
XX 05-APR-1996; 96US-0014943P.
PR 05-JUN-1996; 96US-0019372P.
PR 21-JUN-1996; 96US-0020196P.
PR 03-MAR-1997; 97US-0039532P.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
PA
XX Giordano A, Baldi A;
PI
XX WPI; 1997-512731/47.
DR
XX Tumour suppressor pRb2/p130 gene intron and promoter sequences - used for
PT the diagnosis and prognosis of cancer and predicting pre-disposition to
PT cancer.
XX Example 5; Page 64; 169pp; English.
PS
XX This DNA sequence comprises the boundary region between intron 17 and
CC exon 18 of the human pRb2/p130 tumour suppressor gene. The gene was
CC isolated from a human P1 genomic library by PCR amplification (see
CC AAT96897-98). It contains 22 exons and 21 introns. Exon/intron boundaries
CC (see AAT96899-940) were identified by comparison of the genomic DNA
CC sequence with a previously isolated cDNA sequence. The level of pRb2/p130
CC expression correlates with the presence of cancer, tumour grade, and
CC patient prognosis. Methods are provided for the diagnosis and prognosis
CC of cancer and for prediction of predisposition to cancer, particularly
CC endometrial carcinoma, ovarian cancer, a squamous cell carcinoma of the
CC lung, or adenocarcinoma of the lung (see AAT96831-96)
XX
XX Sequence 18 BP; 6 A; 4 C; 4 G; 4 T; 0 U; 0 Other;
SQ
Query Match 44.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 45;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 13 TGTGTGACCTGGTAAA 28
Db ||||||| |||||
17 TTTGTGACCTGGCAAA 2
RESULT 26
AAX63330
ID AAX63330 standard; RNA; 18 BP.
XX
AC AAX63330;
XX
DT 16-JUL-1999 (first entry)
XX
DE Delta-9 desaturase hairpin ribozyme substrate SEQ ID NO:1205.
XX
KW Maize; corn; Zea mays; delta-9 desaturase; GBSS; target; substrate;
KW granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme;
KW modulation; gene expression; transgenic plant; cleavage; canola plant;
KW caffeine synthesis; coffee plant; nicotine production; tobacco;
KW fruit ripening; flower pigmentation; lignin production; ss.
XX
OS Zea mays.
XX
XX WO9710328-A2.
PN
XX 20-MAR-1997.
PD
XX 12-JUL-1996; 96WO-US011689.
PF
XX 13-JUL-1995; 95US-0001135P.
PR
XX (RIBO-) RIBOZYME PHARM INC.
PA (DOWC ) DOWELANCO.
```



XX Zwick MG, Edington BE, Mcswiggen JA, Merlo PAO, Guo L, Skokut TA;  
PI Young SA, Folkerts O, Merlo DJ;  
XX WPI; 1997-202224/18.  
DR Ribozyme which modulates plant gene expression - preferably modulates  
XX expression of DELTA-9 desaturase or granule bound starch synthase in  
PT maize or canola.  
PT Claim 40; Page 94; 155pp; English.  
XX The present invention describes an enzymatic nucleic acid molecule (I)  
CC with RNA cleaving activity, which modulates the expression of a plant  
CC gene. Also described is a gene comprising a cDNA sequence encoding maize  
CC Delta-9 desaturase. (I) can be used to modulate expression of a gene,  
CC preferably Delta-9 desaturase or a granule bound starch synthase (GBSS)  
CC gene, in a plant (preferably a maize or canola plant). (I) can be used to  
CC modulate caffeine synthesis in a coffee plant, nicotine production in a  
CC tobacco plant, fruit ripening processes in an apple, tomato, pear, plum  
CC or peach plant, flower pigmentation in a rose, petunia, chrysanthemum or  
CC marigold plant or lignin production in a tobacco, aspen, poplar or pine  
CC plant  
XX  
SQ Sequence 18 BP; 3 A; 6 C; 4 G; 0 T; 5 U; 0 Other;  
Query Match 44.1%; Score 12.8; DB 1; Length 18;  
Best Local Similarity 62.5%; Pred. No. 45;  
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
QY 5 CCACCTGCTGTGTGAC 20  
Db |||||:|:|:|  
2 CCACCUGAUGUUGAC 17  
RESULT 27  
ADW64053  
ID ADW64053 standard; DNA; 15 BP.  
XX  
AC ADW64053;  
XX  
DT 07-APR-2005 (first entry)  
XX  
DE Human superoxide dismutase 1 gene antisense oligo #130.  
XX  
KW antimicrobial; antiinflammatory; cytostatic; antisense therapy;  
KW superoxide dismutase; superoxide dismutase modulator; infection;  
KW inflammation; tumor; ss; gene expression; 2'-MOE; 2'-MOE wings;  
KW 2'-methoxyethyl; phosphorothioate.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..15  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "all internucleotide linkages are phosphorothioate  
FT linkages. All C bases are 5-methylcytidine bases"  
XX  
PN US2005019915-A1.  
XX  
PD 27-JAN-2005.  
XX  
PF 26-SEP-2003; 2003US-00672866.  
XX  
PR 21-JUN-2001; 2001US-00888360.  
PR 04-AUG-2003; 2003US-00633843.  
XX  
PA (BENN/) BENNETT C F.  
PA (DOBI/) DOBIE K W.  
XX  
PI Bennett CF, Dobie KW;

XX WPI; 2005-100832/11.  
DR  
XX New antisense compound which specifically hybridizes with and inhibits  
PT the expression of human superoxide dismutase 1, soluble, useful for  
PT treating diseases associated with expression of superoxide dismutase 1,  
PT soluble.  
XX Example 15; SEQ ID NO 142; 116pp; English.  
PS The invention relates to an antisense compound 8-50 nucleobases in length  
XX targeted to nucleobases 96-523 of a coding region of a nucleic acid  
CC molecule encoding human superoxide dismutase 1, soluble comprising 874 bp  
CC fully defined in the specification, where the compound specifically  
CC hybridizes with and inhibits the expression of human superoxide dismutase  
CC 1, soluble. The compound is useful for modulating of superoxide dismutase  
CC 1, soluble expression or for treating diseases associated with expression  
CC of superoxide dismutase 1, soluble. It can also be used to prevent or  
CC delay infection, inflammation, or tumor formation. This sequence  
CC corresponds to an antisense oligonucleotide targeted to the human  
CC superoxide dismutase 1 gene for inhibition of gene expression.  
XX  
SQ Sequence 15 BP; 3 A; 7 C; 2 G; 3 T; 0 U; 0 Other;  
Query Match 42.8%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 44;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 CATCCACCTGCTGT 15  
Db |||||  
1 CACCCACCTGCTGT 14  
RESULT 28  
ABN02182  
ID ABN02182 standard; DNA; 17 BP.  
XX  
AC ABN02182;  
XX  
DT 29-MAY-2002 (first entry)  
XX  
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2174.  
XX  
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.  
XX  
OS Homo sapiens.  
XX WO200192524-A2.  
PN  
XX  
PD 06-DEC-2001.  
XX  
PF 25-MAY-2001; 2001WO-US016981.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 05-FEB-2001; 2001US-0266860P.  
XX  
PA (AEOM-) AEOMICA INC.  
XX

PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX WPI; 2002-179446/23.  
DR  
XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.  
XX  
PS Disclosure; SEQ ID NO 2174; 214pp; English.  
XX  
XX The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1  
CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMLP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX  
SQ Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;  
  
Query Match 42.8%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 92.9%; Pred. No. 50;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 CCACCTGCTGTGTG 18  
Db 1 CCACCTGCTGTGAG 14  
  
RESULT 29  
ABN02180  
ID ABN02180 standard; DNA; 17 BP.  
XX  
XX  
AC ABN02180;  
XX  
DT 29-MAY-2002 (first entry)  
XX  
DE Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2172.  
XX  
KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200192524-A2.  
XX  
PD 06-DEC-2001.  
XX  
PF 25-MAY-2001; 2001WO-US016981.  
XX  
XX 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
XX  
XX (AEOM-) AEOMICA INC.  
PA  
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
PI WPI; 2002-179446/23.  
XX  
XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.  
XX  
PS Disclosure; SEQ ID NO 2172; 214pp; English.  
XX  
XX The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1  
CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMLP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX  
SQ Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;  
  
Query Match 42.8%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 92.9%; Pred. No. 50;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 CCACCTGCTGTGTG 18  
Db 3 CCACCTGCTGTGAG 16  
  
RESULT 30  
ABN02179  
ID ABN02179 standard; DNA; 17 BP.  
XX  
XX AC ABN02179;  
XX  
DT 29-MAY-2002 (first entry)  
XX  
DE Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2171.  
XX  
KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200192524-A2.  
XX



|                       |                                                                           |                 |                |                                 |
|-----------------------|---------------------------------------------------------------------------|-----------------|----------------|---------------------------------|
| Db                    |                                                                           | 2               | CCACCTGCTGTGAG | 15                              |
| RESULT 32             |                                                                           |                 |                |                                 |
| ABT39421              |                                                                           |                 |                |                                 |
| ID                    | ABT39421                                                                  | standard;       | DNA;           | 17 BP.                          |
| XX                    |                                                                           |                 |                |                                 |
| AC                    | ABT39421;                                                                 |                 |                |                                 |
| XX                    |                                                                           |                 |                |                                 |
| DT                    | 12-JUN-2003                                                               | (first entry)   |                |                                 |
| XX                    |                                                                           |                 |                |                                 |
| DE                    | Tumour suppression related human fukutin oligo                            | SEQ ID No 5058. |                |                                 |
| XX                    |                                                                           |                 |                |                                 |
| KW                    | Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip; |                 |                |                                 |
| KW                    | antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease; |                 |                |                                 |
| KW                    | schizophrenia; protein chip; gene therapy; tumour suppression;            |                 |                |                                 |
| KW                    | human fukutin; ds.                                                        |                 |                |                                 |
| XX                    |                                                                           |                 |                |                                 |
| OS                    | Homo sapiens.                                                             |                 |                |                                 |
| XX                    |                                                                           |                 |                |                                 |
| PN                    | WO2003025175-A2.                                                          |                 |                |                                 |
| XX                    |                                                                           |                 |                |                                 |
| PD                    | 27-MAR-2003.                                                              |                 |                |                                 |
| XX                    |                                                                           |                 |                |                                 |
| PF                    | 17-SEP-2002; 2002WO-IB004208.                                             |                 |                |                                 |
| XX                    |                                                                           |                 |                |                                 |
| PR                    | 17-SEP-2001; 2001FR-00011978.                                             |                 |                |                                 |
| XX                    |                                                                           |                 |                |                                 |
| PA                    | (MOLE-) MOLECULAR ENGINES LAB.                                            |                 |                |                                 |
| XX                    |                                                                           |                 |                |                                 |
| PI                    | Telerman A, Amson R, Tuijnder M;                                          |                 |                |                                 |
| XX                    |                                                                           |                 |                |                                 |
| DR                    | WPI; 2003-313353/30.                                                      |                 |                |                                 |
| XX                    |                                                                           |                 |                |                                 |
| PT                    | New isolated nucleic acid, useful for treating viral diseases associated  |                 |                |                                 |
| PT                    | with tumors and cell degeneration, also related polypeptides, antibodies  |                 |                |                                 |
| PT                    | and transfected cells.                                                    |                 |                |                                 |
| XX                    |                                                                           |                 |                |                                 |
| PS                    | Disclosure; Page 625; 720pp; French.                                      |                 |                |                                 |
| XX                    |                                                                           |                 |                |                                 |
| CC                    | The invention relates to a novel isolated 17 mer nucleic acid sequence,   |                 |                |                                 |
| CC                    | given in the specification, a sequence containing at least 15 consecutive |                 |                |                                 |
| CC                    | nucleotides from the 17 mer sequence, a sequence with, after optimal      |                 |                |                                 |
| CC                    | alignment, at least 80 % identity to the 17 mer sequence, a sequence that |                 |                |                                 |
| CC                    | hybridizes to them under highly stringent conditions, or the complement   |                 |                |                                 |
| CC                    | of any of them, or the corresponding RNA. The novel isolated nucleic      |                 |                |                                 |
| CC                    | acids of the invention are useful as probes and primers for detecting,    |                 |                |                                 |
| CC                    | identifying, quantifying and/or amplifying a nucleic acid, e.g. as one    |                 |                |                                 |
| CC                    | component of a gene chip, in vitro as (anti)sense reagents, and for       |                 |                |                                 |
| CC                    | production of recombinant polypeptides. Any of the nucleic acids,         |                 |                |                                 |
| CC                    | polypeptides, vectors containing the nucleic acids, cells containing the  |                 |                |                                 |
| CC                    | vector or antibodies directed against the polypeptides are useful for     |                 |                |                                 |
| CC                    | preparation of pharmaceuticals for prevention and/or treatment of viral   |                 |                |                                 |
| CC                    | diseases that are characterised by development of tumours or cell         |                 |                |                                 |
| CC                    | degeneration, specifically cancer but also Alzheimer's disease and        |                 |                |                                 |
| CC                    | schizophrenia. Analysis of the expression of the 17 mer nucleic acids in  |                 |                |                                 |
| CC                    | patient samples is useful for diagnosis and/or prognosis of these         |                 |                |                                 |
| CC                    | diseases. The polypeptides can also be used to generate antibodies, and   |                 |                |                                 |
| CC                    | both the polypeptide and antibodies are useful as components of protein   |                 |                |                                 |
| CC                    | chips. The nucleic acid sequences of the invention can be used in gene    |                 |                |                                 |
| CC                    | therapy. This polynucleotide sequence represents a tumour suppression     |                 |                |                                 |
| CC                    | related human fukutin oligonucleotide of the invention                    |                 |                |                                 |
| XX                    |                                                                           |                 |                |                                 |
| SQ                    | Sequence 17 BP; 2 A; 6 C; 3 G; 6 T; 0 U; 0 Other;                         |                 |                |                                 |
| Query Match           | 42.8%;                                                                    | Score 12.4;     | DB 1;          | Length 17;                      |
| Best Local Similarity | 92.9%;                                                                    | Pred. No. 50;   |                |                                 |
| Matches               | 13;                                                                       | Conservative    | 0;             | Mismatches 1; Indels 0; Gaps 0; |
| QY                    | 2                                                                         | CATCCACCTGCTGT  | 15             |                                 |
| Db                    |                                                                           |                 |                |                                 |
|                       | 4                                                                         | CATCCTCCTGCTGT  | 17             |                                 |

|                       |        |                |       |                                 |
|-----------------------|--------|----------------|-------|---------------------------------|
| Query Match           | 42.8%; | Score 12.4;    | DB 1; | Length 17;                      |
| Best Local Similarity | 92.9%; | Pred. No. 50;  |       |                                 |
| Matches               | 13;    | Conservative   | 0;    | Mismatches 1; Indels 0; Gaps 0; |
| QY                    | 3      | ATCCACCTGCTGTG | 16    |                                 |
| Db                    |        |                |       |                                 |
|                       | 2      | ATCCACCTGCTTTG | 15    |                                 |

|                       |        |                |       |                                 |
|-----------------------|--------|----------------|-------|---------------------------------|
| Query Match           | 42.8%; | Score 12.4;    | DB 1; | Length 17;                      |
| Best Local Similarity | 92.9%; | Pred. No. 50;  |       |                                 |
| Matches               | 13;    | Conservative   | 0;    | Mismatches 1; Indels 0; Gaps 0; |
| QY                    | 3      | ATCCACCTGCTGTG | 16    |                                 |
| Db                    |        |                |       |                                 |
|                       | 2      | ATCCACCTGCTTTG | 15    |                                 |



RESULT 34  
ADIS1118  
ID ADIS1118 standard; DNA; 17 BP.  
XX  
AC ADIS1118;  
XX  
DT 15-APR-2004 (first entry)  
XX  
DE Human tumour suppression/reversion-related DNA sequence SeqID3621.  
XX  
KW tumour suppression; tumour reversion; apoptosis; virus resistance;  
KW cytostatic; virucide; neuroprotective; neuroleptic; probe;  
KW primer; PCR; gene chip; antisense; viral disease; tumour;  
KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2003025177-A2.  
XX  
PD 27-MAR-2003.  
XX  
PF 17-SEP-2002; 2002WO-IB004523.  
XX  
PR 17-SEP-2001; 2001FR-00011980.  
XX  
PA (MOLE-) MOLECULAR ENGINES LAB.  
XX  
PI Telerman A, Amson R, Tuijndèr M;  
XX  
DR WPI; 2003-313354/30.  
XX  
PT New isolated nucleic acid, useful for treating viral diseases associated  
PT with tumors and cell degeneration, also related polypeptides, antibodies  
PT and transfected cells.  
XX  
PS Disclosure; SEQ ID NO 3621; 30pp; French.  
XX  
CC This invention relates to novel isolated nucleic acid sequences involved  
CC in the phenomena of tumour suppression, tumour reversion, apoptosis  
CC and/or resistance to viruses. The invention may be useful for the  
CC development of compounds with a cytostatic, virucide, neuroprotective,  
CC neuroleptic or neuroleptic activity. The DNA sequences may be useful as  
CC probes and primers for detecting, identifying, quantifying and/or  
CC amplifying nucleic acid, for example as one component of a gene chip, in  
CC vitro as antisense reagents and for production of recombinant  
CC polypeptides. The invention may therefore be useful for preparation of  
CC pharmaceuticals for prevention and/or treatment of viral diseases that  
CC are characterised by development of tumours or cell degeneration,  
CC specifically cancer but also Alzheimer's disease and schizophrenia. The  
CC present sequence is that of a nucleic acid sequence of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/publishedpct\_sequences  
XX  
SQ Sequence 17 BP; 3 A; 4 C; 5 G; 5 T; 0 U; 0 Other;  
  
Query Match 42.8%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 92.9%; Pred. No. 50;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 ATCCACCTGCTGTG 16  
|||||  
Db 2 ATCCACCTGCTGTG 15  
  
RESULT 35  
ACN65269  
ID ACN65269 standard; DNA; 17 BP.  
XX  
AC ACN65269;  
XX  
DT 02-DEC-2004 (first entry)  
XX

DE Human GDMLP-1 probe SEQ ID NO:2171.  
XX  
KW Human; ss; probe; myosin-like protein-1; hGDMLP-1;  
KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;  
KW skeletal muscle function.  
XX  
OS Homo sapiens.  
XX  
PN US2004137589-A1.  
XX  
PD 15-JUL-2004.  
PF 26-NOV-2003; 2003US-00723361.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
PR 25-MAY-2001; 2001US-00866108.  
XX  
PA (GUY/) GU Y.  
PA (JIY/) JI Y.  
PA (PENN/) PENN S G.  
PA (Hanz/) HANZEL D K.  
PA (RANK/) RANK D.  
PA (CHEN/) CHEN W.  
PA (SHAN/) SHANNON M E.  
XX  
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
XX  
DR WPI; 2004-533378/51.  
XX  
PT Novel myosin-like protein-1, useful for treating or preventing disorder  
PT associated with decreased expression or activity of human genome-derived  
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
PT function.  
XX  
PS Disclosure; SEQ ID NO 2171; Opp; English.  
XX  
CC The invention relates to a novel polypeptide (I) comprising a sequence  
CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully  
CC defined in the specification, a fragment of at least 8 amino acids of  
CC (S1), 95% deviation from (S1) which are conservative substitutions, and  
CC 65% identity to (S1). A polypeptide of the invention acts as a agonist or  
CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A  
CC pharmaceutical composition of the invention is useful for treating or  
CC preventing a disorder associated with decreased expression or activity of  
CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.  
CC The present sequence represents a 17-mer nucleotide, used in the  
CC invention for scanning the sequence represented in ACN63102  
XX  
SQ Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;  
  
Query Match 42.8%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 92.9%; Pred. No. 50;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 CCACCTGCTGTG 18  
|||||  
Db 4 CCACCTGCTGTG 17



RESULT 36  
ACN65270  
ID ACN65270 standard; DNA; 17 BP.  
XX  
AC ACN65270;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Human GDMLP-1 probe SEQ ID NO:2172.  
XX  
KW Human; ss; probe; myosin-like protein-1; hGDMLP-1;  
KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;  
KW skeletal muscle function.  
XX  
OS Homo sapiens.  
XX  
PN US2004137589-A1.  
XX  
PD 15-JUL-2004.  
XX  
PF 26-NOV-2003; 2003US-00723361.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
PR 25-MAY-2001; 2001US-00866108.  
XX  
PA (GUY/) GU Y.  
PA (JIY/) JI Y.  
PA (PENN/) PENN S G.  
PA (HANZ/) HANZEL D K.  
PA (RANK/) RANK D.  
PA (CHEN/) CHEN W.  
PA (SHAN/) SHANNON M E.  
XX  
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
XX  
DR WPI; 2004-533378/51.  
XX  
PT Novel myosin-like protein-1, useful for treating or preventing disorder  
PT associated with decreased expression or activity of human genome-derived  
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
PT function.  
XX  
PS Disclosure; SEQ ID NO 2172; Opp; English.  
XX  
CC The invention relates to a novel polypeptide (I) comprising a sequence  
CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully  
CC defined in the specification, a fragment of at least 8 amino acids of  
CC (S1), 95% deviation from (S1) which are conservative substitutions, and  
CC 65% identity to (S1). A polypeptide of the invention acts as a agonist or  
CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A  
CC pharmaceutical composition of the invention is useful for treating or  
CC preventing a disorder associated with decreased expression or activity of  
CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.  
CC The present sequence represents a 17-mer nucleotide, used in the  
CC invention for scanning the sequence represented in ACN63102  
XX  
SQ Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 42.8%; Score 12.4; DB 1; Length 17;

Best Local Similarity 92.9%; Pred. No. 50;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 CCACCTGCTGTGTG 18  
| | | | | | | | | |  
Db 3 CCACCTGCTGTGAG 16  
  
RESULT 37  
ACN65272  
ID ACN65272 standard; DNA; 17 BP.  
XX  
AC ACN65272;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Human GDMLP-1 probe SEQ ID NO:2174.  
XX  
KW Human; ss; probe; myosin-like protein-1; hGDMLP-1;  
KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;  
KW skeletal muscle function.  
XX  
OS Homo sapiens.  
XX  
PN US2004137589-A1.  
XX  
PD 15-JUL-2004.  
XX  
PF 26-NOV-2003; 2003US-00723361.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
PR 25-MAY-2001; 2001US-00866108.  
XX  
PA (GUY/) GU Y.  
PA (JIY/) JI Y.  
PA (PENN/) PENN S G.  
PA (HANZ/) HANZEL D K.  
PA (RANK/) RANK D.  
PA (CHEN/) CHEN W.  
PA (SHAN/) SHANNON M E.  
XX  
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
XX  
DR WPI; 2004-533378/51.  
XX  
PT Novel myosin-like protein-1, useful for treating or preventing disorder  
PT associated with decreased expression or activity of human genome-derived  
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
PT function.  
XX  
PS Disclosure; SEQ ID NO 2174; Opp; English.  
XX  
CC The invention relates to a novel polypeptide (I) comprising a sequence  
CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully  
CC defined in the specification, a fragment of at least 8 amino acids of  
CC (S1), 95% deviation from (S1) which are conservative substitutions, and  
CC 65% identity to (S1). A polypeptide of the invention acts as a agonist or  
CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A  
CC pharmaceutical composition of the invention is useful for treating or

CC preventing a disorder associated with decreased expression or activity of  
CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.  
CC The present sequence represents a 17-mer nucleotide, used in the  
CC invention for scanning the sequence represented in ACN63102  
XX  
SQ Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;  
  
Query Match 42.8%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 92.9%; Pred. No. 50;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 CCACCTGCTGTGTG 18  
| | | | | | | | | | | | | | | |  
Db 1 CCACCTGCTGTGAG 14  
  
RESULT 38  
ACN65271  
ID ACN65271 standard; DNA; 17 BP.  
XX  
AC ACN65271;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Human GDMLP-1 probe SEQ ID NO:2173.  
XX  
KW Human; ss; probe; myosin-like protein-1; hGDMLP-1;  
KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;  
KW skeletal muscle function.  
XX  
OS Homo sapiens.  
XX  
PN US2004137589-A1.  
XX  
PD 15-JUL-2004.  
XX  
PF 26-NOV-2003; 2003US-00723361.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
PR 25-MAY-2001; 2001US-00866108.  
XX  
PA (GUYV/) GU Y.  
PA (JIYY/) JI Y.  
PA (PENN/) PENN S G.  
PA (HANZ/) HANZEL D K.  
PA (RANK/) RANK D.  
PA (CHEN/) CHEN W.  
PA (SHAN/) SHANNON M E.  
XX  
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
XX WPI; 2004-533378/51.  
DR  
XX  
PT Novel myosin-like protein-1, useful for treating or preventing disorder  
PT associated with decreased expression or activity of human genome-derived  
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
PT function.  
XX  
PS Disclosure; SEQ ID NO 2173; 0pp; English.

XX The invention relates to a novel polypeptide (I) comprising a sequence  
CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully  
CC defined in the specification, a fragment of at least 8 amino acids of  
CC (S1), 95% deviation from (S1) which are conservative substitutions, and  
CC 65% identity to (S1). A polypeptide of the invention acts as a agonist or  
CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A  
CC pharmaceutical composition of the invention is useful for treating or  
CC preventing a disorder associated with decreased expression or activity of  
CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.  
CC The present sequence represents a 17-mer nucleotide, used in the  
CC invention for scanning the sequence represented in ACN63102  
XX  
SQ Sequence 17 BP; 4 A; 6 C; 4 G; 3 T; 0 U; 0 Other;  
  
Query Match 42.8%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 92.9%; Pred. No. 50;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 CCACCTGCTGTGTG 18  
| | | | | | | | | | | | | | | |  
Db 2 CCACCTGCTGTGAG 15  
  
RESULT 39  
ABV90927  
ID ABV90927 standard; DNA; 17 BP.  
XX  
AC ABV90927;  
XX  
DT 23-DEC-2002 (first entry)  
XX  
DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1640.  
XX  
KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;  
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;  
KW gene therapy; transgenic; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP1239051-A2.  
XX  
PD 11-SEP-2002.  
XX  
PF 28-JAN-2002; 2002EP-00001165.  
XX  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 23-MAY-2001; 2001US-00864761.  
PR 10-OCT-2001; 2001US-0328205P.  
XX  
PA (AEOM-) AEOMICA INC.  
XX  
PI Shannon M;  
XX  
DR WPI; 2002-684061/74.  
XX  
PT Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL  
PT -1, useful for treating disorders associated with decreased expression or  
PT activity of human POSHL1.  
XX  
PS Example 2; SEQ ID NO 1640; 60pp + Sequence Listing; English.  
XX  
CC The invention relates to an isolated SH3 domain (POSH)-like signalling  
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino  
CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),  
CC (S1) having 95% deviations, especially conservative substitutions or a

CC fragment of the sequences comprising at least 8 contiguous amino acids.  
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an  
CC adaptor protein that interacts with Rho family small GTPases as well as  
CC downstream components of the signal transduction pathway. (I) is useful  
CC for identifying a specific binding partner. (I) and nucleic acids (II)  
CC encoding (I) are useful for diagnosing, monitoring disease and treating  
CC caused by altered expression of human POSHL1 including diagnosing and  
CC treating cancer, they useful in the development of vaccines and (II) is  
CC useful in gene therapy. (II) is useful for constructing microarrays which  
CC are useful for measuring and for surveying gene expression and creating  
CC transgenic non-human animals capable of producing the proteins. The  
CC present sequence is that of a scanning oligonucleotide useful in examples  
CC of the invention. Note: The present sequence did not form part of the  
CC printed specification, but is based on sequence information supplied to  
CC Derwent by the European Patent Office  
XX  
SQ Sequence 17 BP; 1 A; 8 C; 2 G; 6 T; 0 U; 0 Other;  
  
Query Match 42.1%; Score 12.2; DB 1; Length 17;  
Best Local Similarity 82.4%; Pred. No. 55;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 4 TCCACCTGCTGTGTGAC 20  
Db 1 TCCACCTCCTCTGTGTC 17  
  
RESULT 40  
ABV90929  
ID ABV90929 standard; DNA; 17 BP.  
XX  
AC ABV90929;  
XX  
DT 23-DEC-2002 (first entry)  
XX Human POSHL1 scanning oligonucleotide SEQ ID NO 1642.  
DE Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;  
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;  
KW gene therapy; transgenic; ss.  
XX Homo sapiens.  
OS EP1239051-A2.  
PN 11-SEP-2002.  
XX  
PF 28-JAN-2002; 2002EP-00001165.  
XX  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 23-MAY-2001; 2001US-00864761.  
PR 10-OCT-2001; 2001US-0328205P.  
XX  
PA (AEOM-) AEOMICA INC.  
XX  
PI Shannon M;  
DR WPI; 2002-684061/74.  
XX  
XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL  
PT -1, useful for treating disorders associated with decreased expression or  
PT activity of human POSHL1.  
XX  
PS Example 2; SEQ ID NO 1642; 60pp + Sequence Listing; English.  
XX  
CC The invention relates to an isolated SH3 domain (POSH)-like signalling

CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino  
CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),  
CC (S1) having 95% deviations, especially conservative substitutions or a  
CC fragment of the sequences comprising at least 8 contiguous amino acids.  
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an  
CC adaptor protein that interacts with Rho family small GTPases as well as  
CC downstream components of the signal transduction pathway. (I) is useful  
CC for identifying a specific binding partner. (I) and nucleic acids (II)  
CC encoding (I) are useful for diagnosing, monitoring disease and treating  
CC caused by altered expression of human POSHL1 including diagnosing and  
CC treating cancer, they useful in the development of vaccines and (II) is  
CC useful in gene therapy. (II) is useful for constructing microarrays which  
CC are useful for measuring and for surveying gene expression and creating  
CC transgenic non-human animals capable of producing the proteins. The  
CC present sequence is that of a scanning oligonucleotide useful in examples  
CC of the invention. Note: The present sequence did not form part of the  
CC printed specification, but is based on sequence information supplied to  
CC Derwent by the European Patent Office  
XX  
SQ Sequence 17 BP; 1 A; 8 C; 2 G; 6 T; 0 U; 0 Other;  
  
Query Match 42.1%; Score 12.2; DB 1; Length 17;  
Best Local Similarity 82.4%; Pred. No. 55;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 6 CACCTGCTGTGTGACCT 22  
Db 1 CACCTCCTCTGTGTCT 17  
  
RESULT 41  
ABV90928  
ID ABV90928 standard; DNA; 17 BP.  
XX  
AC ABV90928;  
XX  
DT 23-DEC-2002 (first entry)  
XX Human POSHL1 scanning oligonucleotide SEQ ID NO 1641.  
DE Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;  
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;  
KW gene therapy; transgenic; ss.  
XX Homo sapiens.  
OS EP1239051-A2.  
PN 11-SEP-2002.  
XX  
PD 28-JAN-2002; 2002EP-00001165.  
XX  
PF 30-JAN-2001; 2001WO-US000663.  
XX 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 23-MAY-2001; 2001US-00864761.  
PR 10-OCT-2001; 2001US-0328205P.  
XX  
PA (AEOM-) AEOMICA INC.  
XX  
PI Shannon M;  
XX WPI; 2002-684061/74.  
DR  
XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL  
PT -1, useful for treating disorders associated with decreased expression or  
PT activity of human POSHL1.  
XX

PS Example 2; SEQ ID NO 1641; 60pp + Sequence Listing; English.  
XX  
CC The invention relates to an isolated SH3 domain (POSH)-like signalling  
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino  
CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),  
CC (S1) having 95% deviations, especially conservative substitutions or a  
CC fragment of the sequences comprising at least 8 contiguous amino acids.  
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an  
CC adaptor protein that interacts with Rho family small GTPases as well as  
CC downstream components of the signal transduction pathway. (I) is useful  
CC for identifying a specific binding partner. (I) and nucleic acids (II)  
CC encoding (I) are useful for diagnosing, monitoring disease and treating  
CC caused by altered expression of human POSHL1 including diagnosing and  
CC treating cancer, they useful in the development of vaccines and (II) is  
CC useful in gene therapy. (II) is useful for constructing microarrays which  
CC are useful for measuring and for surveying gene expression and creating  
CC transgenic non-human animals capable of producing the proteins. The  
CC present sequence is that of a scanning oligonucleotide useful in examples  
CC of the invention. Note: The present sequence did not form part of the  
CC printed specification, but is based on sequence information supplied to  
CC Derwent by the European Patent Office  
XX  
SQ Sequence 17 BP; 1 A; 9 C; 2 G; 5 T; 0 U; 0 Other;  
  
Query Match 42.1%; Score 12.2; DB 1; Length 17;  
Best Local Similarity 82.4%; Pred. No. 55;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 5 CCACCTGCTGTGACC 21  
Db 1 CCACCTCCTCTGTGTC 17  
  
RESULT 42  
ACN03462  
ID ACN03462 standard; RNA; 17 BP.  
XX  
AC ACN03462;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE WNV Zinzyme substrate SEQ ID NO 3465.  
XX  
KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
KW Amberzyme; Zinzyme; ss.  
XX  
OS West Nile Virus.  
XX  
PN WO200268637-A2.  
XX  
PD 06-SEP-2002.  
XX  
PF 19-OCT-2001; 2001WO-US048350.  
XX  
PR 20-OCT-2000; 2000US-0242411P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MCSW/) MCSWIGGEN J A.  
XX  
PI Blatt L, Mcswiggen JA;  
XX  
DR WPI; 2002-706994/76.  
XX  
PT New nucleic acid molecule that modulates replication of West Nile Virus  
PT (WNV), useful for treating a condition related to WNV infection e.g.  
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
XX  
PS Claim 23; SEQ ID NO 3465; 495pp; English.  
XX

CC The invention relates to nucleic acid molecules that modulate replication  
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
CC treating a condition related to WNV infection e.g. pancreatitis,  
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
CC molecule is selected from the group of ribozymes consisting of  
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The  
CC nucleic acid molecules further comprise at least five ribose residues, at  
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
CC least three of the 5' terminal nucleotides and a 3' end modification of a  
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
CC in the specification. The present sequence is that of a nucleic acid  
CC molecule of the invention  
XX  
SQ Sequence 17 BP; 5 A; 3 C; 5 G; 0 T; 4 U; 0 Other;  
  
Query Match 42.1%; Score 12.2; DB 1; Length 17;  
Best Local Similarity 58.8%; Pred. No. 55;  
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
  
QY 12 CTGTGTGACCTGGTAAA 28  
Db 1 CUGUGUGAGCUGACAAA 17  
  
RESULT 43  
ACA07683  
ID ACA07683 standard; RNA; 17 BP.  
XX  
AC ACA07683;  
XX  
DT 03-JUN-2003 (first entry)  
XX  
DE NFKB sub-unit modulating zinzyme substrate #82.  
XX  
KW Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;  
KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;  
KW lung cancer; prostate cancer; colorectal cancer; brain cancer;  
KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;  
KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;  
KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;  
KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;  
KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;  
KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;  
KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;  
KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;  
KW transplant/graft rejection; reperfusion injury; glomerulonephritis;  
KW allergic airway inflammation; inflammatory bowel disease; infection; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2002177568-A1.  
XX  
PD 28-NOV-2002.  
XX  
PF 23-MAY-2001; 2001US-00864785.  
XX  
PR 07-DEC-1992; 92US-00987132.  
PR 18-MAY-1994; 94US-00245466.  
PR 15-AUG-1994; 94US-00291932.  
PR 23-DEC-1996; 96US-00777916.  
XX  
PA (STIN/) STINCHCOMB D T.  
PA (MCSW/) MCSWIGGEN J.  
PA (DRAP/) DRAPER K G.  
XX  
PI Stinchcomb DT, Mcswiggen J, Draper KG;  
XX  
DR WPI; 2003-340953/32.  
XX  
PT Novel enzymatic nucleic acid molecules which down regulates expression of  
PT a sequence encoding a subunit of nuclear factor kappa B useful for



PT treating cancer, inflammatory disorders and autoimmune diseases.

XX

PS Claim 4; Page 38; 72pp; English.

XX

CC The invention describes an enzymatic nucleic acid molecule (I) which down

CC regulates expression of a sequence encoding a subunit of nuclear factor

CC kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme

CC configuration. The enzymatic nucleic acid molecule is adapted to treat

CC cancer and is useful for down-regulating REL-A activity in a cell, for

CC treating a patient having a condition associated with the level of REL-A.

CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in

CC the presence of a divalent cation, especially Mg<sup>2+</sup>. The enzymatic and

CC antisense nucleic acid molecules are useful for treating breast, lung,

CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,

CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or

CC multidrug resistant cancer. The method involves use of other drug

CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or

CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,

CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,

CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic

CC acid molecules are also useful for treating inflammatory disease such as

CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,

CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft

CC rejection, gene therapy applications, ischaemia/reperfusion injury

CC (central nervous system (CNS) and myocardial), glomerulonephritis,

CC sepsis, allergic airway inflammation, inflammatory bowel disease or

CC infection. This sequence represents the substrate of a novel enzymatic

CC nucleic acid molecule

XX

SQ Sequence 17 BP; 4 A; 4 C; 5 G; 0 T; 4 U; 0 Other;

Query Match 42.1%; Score 12.2; DB 1; Length 17;

Best Local Similarity 58.8%; Pred. No. 55;

Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 8 CCTGCTGTGTGACCTGG 24  
||:|:|:|:|:|

Db 1 CCUACUGUGGACAAGG 17

RESULT 44

ACA08233

ID ACA08233 standard; DNA; 17 BP.

XX

AC ACA08233;

XX

XX 03-JUN-2003 (first entry)

XX

DE Necrosis factor kappa B (NFKB) sub-unit modulating DNazyme #2.

XX

KW Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;

KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; lung cancer;

KW prostate cancer; colorectal cancer; brain cancer; oesophageal cancer;

KW stomach cancer; bladder cancer; pancreatic cancer; cervical cancer;

KW head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma;

KW multidrug resistant cancer; REL-A-specific inhibitor; chemotherapy;

KW paclitaxel; docetaxel; cisplatin; methotrexate; cyclophosphamide;

KW doxorubin; fluorouracil carboplatin; edatrexate; gemcitabine;

KW radiation therapy; inflammatory disease; asthma; diabetes;

KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;

KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;

KW transplant/graft rejection; reperfusion injury; glomerulonephritis;

KW allergic airway inflammation; inflammatory bowel disease; infection; ss.

XX

OS Synthetic.

XX

PN US2002177568-A1.

XX

PD 28-NOV-2002.

XX

PF 23-MAY-2001; 2001US-00864785.

XX

PR 07-DEC-1992; 92US-00987132.

PR 18-MAY-1994; 94US-00245466.

PR 15-AUG-1994; 94US-00291932.

PR 23-DEC-1996; 96US-00777916.

XX

PA (STIN/) STINCHOMB D T.

PA (MCSW/) MCSWIGGEN J.

PA (DRAP/) DRAPER K G.

XX

PI Stinchcomb DT, Mcswiggen J, Draper KG;

XX

DR WPI; 2003-340953/32.

XX

PT Novel enzymatic nucleic acid molecules which down regulates expression of

PT a sequence encoding a subunit of nuclear factor kappa B useful for

PT treating cancer, inflammatory disorders and autoimmune diseases.

XX

PS Claim 3; Page 44; 72pp; English.

XX

CC The invention describes an enzymatic nucleic acid molecule (I) which down

CC regulates expression of a sequence encoding a subunit of nuclear factor

CC kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme

CC configuration. The enzymatic nucleic acid molecule is adapted to treat

CC cancer and is useful for down-regulating REL-A activity in a cell, for

CC treating a patient having a condition associated with the level of REL-A.

CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in

CC the presence of a divalent cation, especially Mg<sup>2+</sup>. The enzymatic and

CC antisense nucleic acid molecules are useful for treating breast, lung,

CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,

CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or

CC multidrug resistant cancer. The method involves use of other drug

CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or

CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,

CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,

CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic

CC acid molecules are also useful for treating inflammatory disease such as

CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,

CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft

CC rejection, gene therapy applications, ischaemia/reperfusion injury

CC (central nervous system (CNS) and myocardial), glomerulonephritis,

CC sepsis, allergic airway inflammation, inflammatory bowel disease or

CC infection. This sequence represents an enzymatic nucleic acid used to

CC modulate the function of a necrosis factor kappa B sub-unit

XX

SQ Sequence 17 BP; 3 A; 4 C; 3 G; 0 T; 7 U; 0 Other;

Query Match 42.1%; Score 12.2; DB 1; Length 17;

Best Local Similarity 52.9%; Pred. No. 55;

Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 ATCCACCTGCTGTGTGA 19  
|:|:|:|:|:|:|

Db 1 AUCUCCUACUGUGUGA 17

RESULT 45

ABN02177

ID ABN02177 standard; DNA; 17 BP.

XX

AC ABN02177;

XX

XX 29-MAY-2002 (first entry)

DT

XX

DE Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2169.

XX

KW Human; genome-derived myosin-like protein 1; GDMLP-1; heart;

KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;

KW skeletal muscle disorder; amplicon; screening; ss.

XX

OS Homo sapiens.

XX

PN WO200192524-A2.

XX

PD 06-DEC-2001.



XX PF 25-MAY-2001; 2001WO-US016981.  
XX PR 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
XX PA (AEOM-) AEOMICA INC.  
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX WPI; 2002-179446/23.  
DR XX  
XX PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.  
XX PS  
PS Disclosure; SEQ ID NO 2169; 214pp; English.  
XX CC  
CC The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1  
CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMLP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX SQ  
SQ Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;  
Query Match 41.4%; Score 12; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 CCACCTGCTGTG 16  
Db 6 CCACCTGCTGTG 17  
RESULT 46  
ABN02178  
ID ABN02178 standard; DNA; 17 BP.  
XX AC ABN02178;  
XX DT 29-MAY-2002 (first entry)  
XX

DE XX Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2170.  
XX KW Human; genome-derived myosin-like protein 1; GDMLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
XX skeletal muscle disorder; amplicon; screening; ss.  
OS Homo sapiens.  
XX WO200192524-A2.  
XX PD 06-DEC-2001.  
XX PF 25-MAY-2001; 2001WO-US016981.  
XX PR 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
XX PA (AEOM-) AEOMICA INC.  
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX WPI; 2002-179446/23.  
XX DR  
XX PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.  
XX PS  
PS Disclosure; SEQ ID NO 2170; 214pp; English.  
XX CC  
CC The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1  
CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMLP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX SQ  
SQ Sequence 17 BP; 5 A; 5 C; 4 G; 3 T; 0 U; 0 Other;  
Query Match 41.4%; Score 12; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 CCACCTGCTGTG 16  
|||  
DB 6 CCACCTGCTGTG 17  
|||  
RESULT 46  
ABN02178  
ID ABN02178 standard; DNA; 17 BP.  
XX AC ABN02178;  
XX DT 29-MAY-2002 (first entry)  
XX

Db 5 CCACCTGCTGTG 16

RESULT 47

ADB41885

ID ADB41885 standard; DNA; 17 BP.

XX

AC ADB41885;

XX

DT 18-DEC-2003 (revised)

DT 04-DEC-2003 (first entry)

XX

DE Tumour suppression/reversion associated nucleotide #2208.

XX

KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;

KW primer; probe; tumour suppression; tumour reversion; apoptosis;

KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;

KW diagnosis.

XX

OS Homo sapiens.

XX

PN WO2003040369-A2.

XX

PD 15-MAY-2003.

XX

PF 17-SEP-2002; 2002WO-IB004219.

XX

PR 17-SEP-2001; 2001FR-00011981.

XX

PA (MOLE-) MOLECULAR ENGINES LAB.

XX

PI Telerman A, Amson R, Tuijnder M;

XX

DR WPI; 2003-441574/41.

XX

PT New nucleic acid encoding human prostate membrane-specific antigen,

PT useful e.g. for treatment of tumors and viral infection, also related

PT polypeptide and antibodies.

XX

PS Disclosure; Page 290; 771pp; French.

XX

CC The invention relates to the isolation of 6327 nucleotide sequences,

CC fragments of at least 15 consecutive nucleotides of these nucleotides, a

CC sequence having at least 80% identity, after optimal alignment, with the

CC nucleotides, a sequence that hybridizes under stringing conditions with

CC the nucleotides, or the complement, or corresponding RNA, of the

CC nucleotides. The nucleotides are used as probes or primers for detecting,

CC identifying, quantifying and/or amplifying nucleic acids, as in vitro

CC sense and antisense sequences, of nucleotides involved in tumour

CC suppression or reversion, apoptosis and or viral resistance, to produce

CC recombinant polypeptides, and to prepare transgenic animals, as

CC experimental models. The nucleotides (also vectors containing them and

CC cells containing the vectors), the encoded polypeptides and antibodies

CC (Ab) against the polypeptide are useful for prevention and/or treatment

CC of viral infections or diseases characterized by development of tumours

CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).

CC Analysis of the expression of the nucleotides can be used for diagnosis

CC and/or prognosis of these diseases. The nucleotides and polypeptides can

CC also be used to screen for their specific interactive molecules,

CC potentially useful for treating diseases associated with abnormal

CC expression of the nucleotides.

XX

SQ Sequence 17 BP; 3 A; 8 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 41.4%; Score 12; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 60;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCCACCTGC 12

Db 4 CCATCCACCTGC 15

RESULT 48

ACC51536

ID ACC51536 standard; DNA; 17 BP.

XX

AC ACC51536;

XX

DT 27-JUN-2003 (first entry)

XX

DE Human tumour suppressor sequence #303.

XX

KW ss; tumour suppressor; antitumour; cytostatic; tumour suppression;

KW tumour regression; apoptosis; virus resistance; diagnosis;

KW cellular degeneration.

XX

OS Homo sapiens.

XX

PN FR2826373-A1.

XX

PD 27-DEC-2002.

XX

PF 20-JUN-2001; 2001FR-00008139.

XX

PR 20-JUN-2001; 2001FR-00008139.

XX

PA (MOLE-) MOLECULAR ENGINES LAB SA.

XX

PI Tuijnder M, Telerman A, Amson R;

XX

DR WPI; 2003-250498/25.

XX

PT New nucleic acid sequences associated with tumor suppression, regression,

PT apoptosis or virus resistance are useful to diagnose and treat viral

PT disease, development of tumor cells and cell degeneration.

XX

PS Claim 1; Page 110; 798pp; French.

XX

CC This sequence represents an isolated nucleic acid sequence associated

CC with tumour suppression or regression, apoptosis or virus resistance. The

CC invention relates to these sequences or sequences having at least 80%

CC identity to them, and polypeptides encoded by the sequences or

CC polypeptides having 80% identity to the polypeptide sequences. The

CC invention is used to diagnose or treat viral disease or disease

CC characterized by development of tumour cells or cellular degeneration

XX

SQ Sequence 17 BP; 4 A; 8 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 41.4%; Score 12; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 60;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCCACCTGC 12

Db 6 CCATCCACCTGC 17

RESULT 49

ACN65268

ID ACN65268 standard; DNA; 17 BP.

XX

AC ACN65268;

XX

DT 02-DEC-2004 (first entry)

XX

DE Human GDMLP-1 probe SEQ ID NO:2170.

XX

KW Human; ss; probe; myosin-like protein-1; hGDMLP-1;

KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;

KW skeletal muscle function.

XX

OS Homo sapiens.

XX

PN US2004137589-A1.

XX

|                                                             |                                                                           |
|-------------------------------------------------------------|---------------------------------------------------------------------------|
| KW                                                          | Human; ss; probe; myosin-like protein-1; hGDMLP-1;                        |
| KW                                                          | hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;     |
| KW                                                          | skeletal muscle function.                                                 |
| XX                                                          |                                                                           |
| OS                                                          | Homo sapiens.                                                             |
| XX                                                          |                                                                           |
| PN                                                          | US2004137589-A1.                                                          |
| XX                                                          |                                                                           |
| PD                                                          | 15-JUL-2004.                                                              |
| XX                                                          |                                                                           |
| PF                                                          | 26-NOV-2003; 2003US-00723361.                                             |
| XX                                                          |                                                                           |
| PR                                                          | 26-MAY-2000; 2000US-0207456P.                                             |
| PR                                                          | 21-SEP-2000; 2000US-0234687P.                                             |
| PR                                                          | 27-SEP-2000; 2000US-0236359P.                                             |
| PR                                                          | 04-OCT-2000; 2000GB-00024263.                                             |
| PR                                                          | 30-JAN-2001; 2001WO-US000661.                                             |
| PR                                                          | 30-JAN-2001; 2001WO-US000662.                                             |
| PR                                                          | 30-JAN-2001; 2001WO-US000663.                                             |
| PR                                                          | 30-JAN-2001; 2001WO-US000664.                                             |
| PR                                                          | 30-JAN-2001; 2001WO-US000665.                                             |
| PR                                                          | 30-JAN-2001; 2001WO-US000666.                                             |
| PR                                                          | 30-JAN-2001; 2001WO-US000667.                                             |
| PR                                                          | 30-JAN-2001; 2001WO-US000668.                                             |
| PR                                                          | 30-JAN-2001; 2001WO-US000669.                                             |
| PR                                                          | 30-JAN-2001; 2001WO-US000670.                                             |
| PR                                                          | 05-FEB-2001; 2001US-0266860P.                                             |
| PR                                                          | 25-MAY-2001; 2001US-00866108.                                             |
| XX                                                          |                                                                           |
| PA                                                          | (GUYV/) GU Y.                                                             |
| PA                                                          | (JIYY/) JI Y.                                                             |
| PA                                                          | (PENN/) PENN S G.                                                         |
| PA                                                          | (HANZ/) HANZEL D K.                                                       |
| PA                                                          | (RANK/) RANK D.                                                           |
| PA                                                          | (CHEN/) CHEN W.                                                           |
| PA                                                          | (SHAN/) SHANNON M E.                                                      |
| XX                                                          |                                                                           |
| PI                                                          | Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;               |
| XX                                                          |                                                                           |
| DR                                                          | WPI; 2004-533378/51.                                                      |
| XX                                                          |                                                                           |
| PT                                                          | Novel myosin-like protein-1, useful for treating or preventing disorder   |
| PT                                                          | associated with decreased expression or activity of human genome-derived  |
| PT                                                          | myosin-like protein-1 such as disorder of heart and/or skeletal muscle    |
| PT                                                          | function.                                                                 |
| XX                                                          |                                                                           |
| PS                                                          | Disclosure; SEQ ID NO 2169; Opp; English.                                 |
| XX                                                          |                                                                           |
| CC                                                          | The invention relates to a novel polypeptide (I) comprising a sequence    |
| CC                                                          | (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully    |
| CC                                                          | defined in the specification, a fragment of at least 8 amino acids of     |
| CC                                                          | (S1), 95% deviation from (S1) which are conservative substitutions, and   |
| CC                                                          | 65% identity to (S1). A polypeptide of the invention acts as a agonist or |
| CC                                                          | antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A        |
| CC                                                          | pharmaceutical composition of the invention is useful for treating or     |
| CC                                                          | preventing a disorder associated with decreased expression or activity of |
| CC                                                          | hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.    |
| CC                                                          | The present sequence represents a 17-mer nucleotide, used in the          |
| CC                                                          | invention for scanning the sequence represented in ACN63102               |
| XX                                                          |                                                                           |
| SQ                                                          | Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;                         |
| Query Match 41.4%; Score 12; DB 1; Length 17;               |                                                                           |
| Best Local Similarity 100.0%; Pred. No. 60;                 |                                                                           |
| Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                                                                           |
| QY                                                          | 5 CCACCTGCTGTG 16                                                         |
| Db                                                          |                                                                           |
| 5 CCACCTGCTGTG 16                                           |                                                                           |
| RESULT 50                                                   |                                                                           |
| ACN65267                                                    |                                                                           |
| ID                                                          | ACN65267 standard; DNA; 17 BP.                                            |
| XX                                                          |                                                                           |
| AC                                                          | ACN65267;                                                                 |
| XX                                                          |                                                                           |
| DT                                                          | 02-DEC-2004 (first entry)                                                 |
| XX                                                          |                                                                           |
| DE                                                          | Human GDMLP-1 probe SEQ ID NO:2169.                                       |
| XX                                                          |                                                                           |

ID ADV35523 standard; RNA; 15 BP.  
XX  
AC ADV35523;  
XX  
DT 10-FEB-2005 (first entry)  
XX  
DE Human anti-HER2 NCH ribozyme substrate sequence #154.  
XX  
KW Enzymatic nucleic acid molecule; gene expression; down regulation;  
KW protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase;  
KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;  
KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;  
KW amberzyme; zinzyme; DNzyme; cancer; breast cancer; Alzheimer's disease;  
KW diabetes; obesity; cardiac disease; heart disease; age-related disease;  
KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;  
ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200116312-A2.  
XX  
PD 08-MAR-2001.  
XX  
PF 30-AUG-2000; 2000WO-US023998.  
XX  
PR 31-AUG-1999; 99US-0151713P.  
PR 27-SEP-1999; 99US-00406643.  
PR 27-SEP-1999; 99US-0156236P.  
PR 27-SEP-1999; 99US-0156467P.  
PR 08-NOV-1999; 99US-00436430.  
PR 06-DEC-1999; 99US-0169100P.  
PR 29-DEC-1999; 99US-00474432.  
PR 29-DEC-1999; 99US-0173612P.  
PR 30-DEC-1999; 99US-00476387.  
PR 04-FEB-2000; 2000US-00498824.  
PR 20-MAR-2000; 2000US-00531025.  
PR 14-APR-2000; 2000US-0197769P.  
PR 23-MAY-2000; 2000US-00578223.  
PR 09-AUG-2000; 2000US-00636385.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Mcswiggen J, Usman N, Blatt L, Beigelman L, Burgin A;  
PI Karpeisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;  
PI Stinchcomb D, Beaudry A, Zinnen S, Lugwig J, Sproat BS;  
XX  
DR WPI; 2001-244406/25.  
XX  
PT Enzymatic nucleic acid molecules able to cleave separate RNA molecules  
PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,  
PT obesity and heart disease.  
XX  
PS Example 7; Page 474; 717pp; English.  
XX  
CC The present invention relates to the use of enzymatic nucleic acid  
CC molecules (e.g. ribozymes) to modulate gene expression. The invention  
CC also methods for their use to down regulate or inhibit the expression of  
CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine  
CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C  
CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor  
CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),  
CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic  
CC nucleic acid molecules used to inhibit the expression of the said genes  
CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,  
CC zinzyme, and/or DNzyme motifs. The methods of the invention are useful  
CC for treating cancer, in particular breast cancer, Alzheimer's disease,  
CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related  
CC diseases, hepatitis B infections, and hepatitis and hepatocellular  
CC carcinoma. The enzymatic nucleic acid molecules can also be used as  
CC diagnostic tools to examine genetic drift and mutations within diseased  
CC cells and to detect the presence of specific RNA in a cell. The present

CC sequence represents a substrate/target sequence for an anti-HER2 NCH  
CC ribozyme used in the examples of the present invention. Note: Some SEQ ID  
CC Nos are repeated more than once in the specification, but these have  
CC different sequences associated with them.  
XX  
SQ Sequence 15 BP; 3 A; 6 C; 4 G; 0 T; 2 U; 0 Other;  
  
Query Match 40.7%; Score 11.8; DB 1; Length 15;  
Best Local Similarity 86.7%; Pred. No. 57;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 9 CTGCTGTGTGACCTG 23  
||| ||| ||| ||| |||  
Db 15 CTGCAGTGGGACCTG 1  
  
RESULT 52  
ADV35886  
ID ADV35886 standard; RNA; 15 BP.  
XX  
AC ADV35886;  
XX  
DT 10-FEB-2005 (first entry)  
XX  
DE Human anti-HER2 NCH ribozyme substrate sequence #329.  
XX  
KW Enzymatic nucleic acid molecule; gene expression; down regulation;  
KW protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase;  
KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;  
KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;  
KW amberzyme; zinzyme; DNzyme; cancer; breast cancer; Alzheimer's disease;  
KW diabetes; obesity; cardiac disease; heart disease; age-related disease;  
KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;  
ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200116312-A2.  
XX  
PD 08-MAR-2001.  
XX  
PF 30-AUG-2000; 2000WO-US023998.  
XX  
PR 31-AUG-1999; 99US-0151713P.  
PR 27-SEP-1999; 99US-00406643.  
PR 27-SEP-1999; 99US-0156236P.  
PR 27-SEP-1999; 99US-0156467P.  
PR 08-NOV-1999; 99US-00436430.  
PR 06-DEC-1999; 99US-0169100P.  
PR 29-DEC-1999; 99US-00474432.  
PR 29-DEC-1999; 99US-0173612P.  
PR 30-DEC-1999; 99US-00476387.  
PR 04-FEB-2000; 2000US-00498824.  
PR 20-MAR-2000; 2000US-00531025.  
PR 14-APR-2000; 2000US-0197769P.  
PR 23-MAY-2000; 2000US-00578223.  
PR 09-AUG-2000; 2000US-00636385.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Mcswiggen J, Usman N, Blatt L, Beigelman L, Burgin A;  
PI Karpeisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;  
PI Stinchcomb D, Beaudry A, Zinnen S, Lugwig J, Sproat BS;  
XX  
DR WPI; 2001-244406/25.  
XX  
PT Enzymatic nucleic acid molecules able to cleave separate RNA molecules  
PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,  
PT obesity and heart disease.  
XX  
PS Example 7; Page 478; 717pp; English.



XX The present invention relates to the use of enzymatic nucleic acid  
CC molecules (e.g. ribozymes) to modulate gene expression. The invention  
CC also methods for their use to down regulate or inhibit the expression of  
CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine  
CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C  
CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor  
CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),  
CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic  
CC nucleic acid molecules used to inhibit the expression of the said genes  
CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,  
CC zinzyme, and/or DNAzyme motifs. The methods of the invention are useful  
CC for treating cancer, in particular breast cancer, Alzheimer's disease,  
CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related  
CC diseases, hepatitis B infections, and hepatitis and hepatocellular  
CC carcinoma. The enzymatic nucleic acid molecules can also be used as  
CC diagnostic tools to examine genetic drift and mutations within diseased  
CC cells and to detect the presence of specific RNA in a cell. The present  
CC sequence represents a substrate/target sequence for an anti-HER2 NCH  
CC ribozyme used in the examples of the present invention. Note: Some SEQ ID  
CC Nos are repeated more than once in the specification, but these have  
CC different sequences associated with them.  
XX  
SQ Sequence 15 BP; 2 A; 5 C; 5 G; 0 T; 3 U; 0 Other;

Query Match 40.7%; Score 11.8; DB 1; Length 15;  
Best Local Similarity 66.7%; Pred. No. 57;  
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 CACCTGCTGTGTGAC 20  
Db 1 CGCCAGCUGUGGAC 15

RESULT 53  
ABF45364/c  
ID ABF45364 standard; DNA; 13 BP.  
XX  
AC ABF45364;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 145361 for detecting SNP TSC0036590.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 145361; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 3 A; 0 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 39.3%; Score 11.4; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCT 13  
Db 13 CCATCCACCTACT 1

RESULT 54  
ABF45365  
ID ABF45365 standard; DNA; 13 BP.  
XX  
AC ABF45365;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 145362 for detecting SNP TSC0036590.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 145362; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 3 A; 7 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 39.3%; Score 11.4; DB 1; Length 13;



|                                            |                                                                           |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
|--------------------------------------------|---------------------------------------------------------------------------|---------------|--------------|----|------------|----|--------|----|------|----|------------|----|--------|----|------|
| Best Local Similarity 92.3%; Pred. No. 58; |                                                                           |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| Matches                                    |                                                                           | 12;           | Conservative | 0; | Mismatches | 1; | Indels | 0; | Gaps | 0; |            |    |        |    |      |
| QY                                         | 1                                                                         | CCATCCACCTGCT | 13           |    |            |    |        |    |      |    |            |    |        |    |      |
| Db                                         | 1                                                                         | CCATCCACCTACT | 13           |    |            |    |        |    |      |    |            |    |        |    |      |
| RESULT 55                                  |                                                                           |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| ABA02592/c                                 |                                                                           |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| ID                                         | ABA02592 standard; DNA; 15 BP.                                            |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| XX                                         | ABA02592;                                                                 |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| AC                                         | 05-FEB-2002 (first entry)                                                 |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| DT                                         | HBV targeted ribozyme flanking sequence m1Rz-247.                         |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| XX                                         | Infection; antisense RNA; ribozyme; DNzyme; antiviral; gene therapy;      |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| KW                                         | papilloma virus; hepatitis B virus; cytotoxic; cytostatic; wart;          |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| KW                                         | cervical dysplasia; cervical carcinoma; carcinoma; laryngeal papilloma;   |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| KW                                         | ss.                                                                       |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| XX                                         | Unidentified.                                                             |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| OS                                         | WO200179524-A2.                                                           |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| XX                                         | 25-OCT-2001.                                                              |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| PN                                         | 13-APR-2001; 2001WO-US012130.                                             |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| XX                                         | 13-APR-2000; 2000US-00548449.                                             |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| PR                                         | 07-DEC-2000; 2000US-0251810P.                                             |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| XX                                         | (UYSC-) UNIV SOUTH CAROLINA.                                              |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| PA                                         | (PENN-) PENN STATE RES FOUND.                                             |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| XX                                         | Norris JS, Clawson GA, Westwater C, Schofield D, Schmidt MG;              |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| PI                                         | Hoel B, Dolan J, Pan W;                                                   |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| PI                                         | WPI; 2001-607700/69.                                                      |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| DR                                         | Novel nucleic acid for the treatment of papilloma or hepatitis virus      |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| XX                                         | induced conditions comprises a catalytic region which produces a          |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| PT                                         | cytotoxic or cytostatic effect in the infected cell.                      |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| PT                                         | Example; Page 97; 143pp; English.                                         |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| XX                                         | The invention relates to the discovery, identification and                |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| CC                                         | characterisation of toxic agents lethal to pathogens and methods for      |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| CC                                         | targeting such toxic agents to a pathogen or pathogen infected cells in   |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| CC                                         | order to treat and/or eradicate the infection. In particular the          |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| CC                                         | invention relates to at least one nucleic acid molecule, which            |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| CC                                         | specifically hybridises to mRNA encoding at least one vital protein       |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| CC                                         | associated with the transformation or plasmid copy number control, which  |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| CC                                         | hybridises to a viral polyadenylation signal or a core, pre core or       |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| CC                                         | polymerase encoding sequence. Specifically, the invention relates to the  |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| CC                                         | delivery of one or more toxic gene products, antisense RNAs, ribozymes,   |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| CC                                         | DNazymes or a combination thereof. The nucleic acids have antiviral       |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| CC                                         | activity and can be used in gene therapy. They are useful for the         |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| CC                                         | treatment of papilloma or hepatitis virus induced conditions and can      |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| CC                                         | produce a cytotoxic or cytostatic effect in papillomavirus or hepatitis B |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| CC                                         | infected cells. The papilloma virus induced condition is selected from    |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| CC                                         | warts, cervical dysplasia, cervical carcinoma, carcinoma in situ and      |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| CC                                         | laryngeal papilloma. ABA02588-ABA02610 comprise ribozyme flanking         |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| CC                                         | sequences and ABA02612-ABA02660 comprise DNzyme target sequences, useful  |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| CC                                         | to the invention                                                          |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| XX                                         | Sequence 15 BP; 3 A; 4 C; 7 G; 1 T; 0 U; 0 Other;                         |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| SQL                                        | Query Match 39.3%; Score 11.4; DB 1; Length 15;                           |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| Best Local Similarity 92.3%; Pred. No. 68; |                                                                           |               |              |    |            |    |        |    |      |    |            |    |        |    |      |
| Matches                                    |                                                                           | 12;           | Conservative |    |            |    |        |    |      | 0; | Mismatches | 1; | Indels | 0; | Gaps |

|                                            |                                                                           |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
|--------------------------------------------|---------------------------------------------------------------------------|---------------|--------------|----|------------|----|--------|----|------|----|--|--|--|--|--|
| Best Local Similarity 92.3%; Pred. No. 58; |                                                                           |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| Matches                                    |                                                                           | 12;           | Conservative | 0; | Mismatches | 1; | Indels | 0; | Gaps | 0; |  |  |  |  |  |
| QY                                         | 4                                                                         | TCCACCTGCTGTG | 16           |    |            |    |        |    |      |    |  |  |  |  |  |
| Db                                         | 13                                                                        | TCCACCTGCTGCG | 1            |    |            |    |        |    |      |    |  |  |  |  |  |
| RESULT 56                                  |                                                                           |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| ABS64208                                   |                                                                           |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| ID                                         | ABS64208 standard; DNA; 15 BP.                                            |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| XX                                         | ABS64208;                                                                 |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| AC                                         | 15-NOV-2002 (first entry)                                                 |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| XX                                         | Tachykinin receptor gene TACR2, allele-specific primer #18.               |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| DT                                         | Human; single nucleotide polymorphism; SNP; TACR2; primer; probe; ss;     |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| XX                                         | tachykinin receptor.                                                      |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| KW                                         | Homo sapiens.                                                             |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| XX                                         | WO200263046-A1.                                                           |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| PN                                         | 15-AUG-2002.                                                              |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| XX                                         | 09-NOV-2001; 2001WO-US047394.                                             |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| PD                                         | 09-NOV-2000; 2000US-0247649P.                                             |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| XX                                         | (GENA-) GENAISSANCE PHARM INC.                                            |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| XX                                         | Cappola G, Chew A, Gilson CR, Koshy B;                                    |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| PI                                         | WPI; 2002-636600/68.                                                      |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| XX                                         | New genetic variants having polymorphisms in the Tachykinin receptor      |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| PT                                         | (TACR2) protein, useful for studying the function of TACR2, and for       |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| PT                                         | treating disorders associated with abnormal expression or function of     |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| PT                                         | TACR2 isogene.                                                            |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| XX                                         | Claim 14; Page 14; 139pp; English.                                        |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| PS                                         | The invention relates to an isolated polypeptide comprising a polymeric   |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| XX                                         | variant of a reference sequence for the Tachykinin receptor (TACR2)       |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| CC                                         | protein. Also described is a method for: (1) haplotyping or genotyping    |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| CC                                         | the TACR2 gene of an individual; (2) predicting a haplotype pair for the  |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| CC                                         | TACR2 gene of an individual; (3) identifying an association between a     |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| CC                                         | trait and at least one haplotype or haplotype pair of the TACR2 gene; and |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| CC                                         | (4) isolated oligonucleotide for detecting a single nucleotide            |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| CC                                         | polymorphism in the TACR2 gene. Polymorphic variants of the TACR2 gene    |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| CC                                         | are useful in studying the expression and biological function of TACR2,   |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| CC                                         | and in identifying drugs targeting TACR2 protein for treating disorders   |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| CC                                         | associated with abnormal expression or function of TACR2, e.g. asthma or  |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| CC                                         | breast cancer. Polynucleotides comprising a polymorphic gene variant or   |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| CC                                         | fragment may be used for therapeutic purposes, where a patient could      |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| CC                                         | benefit from expression or increased expression of a particular TACR2     |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| CC                                         | protein isoform, or an expression vector encoding the isoform may be      |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| CC                                         | administered to the patient. Haplotype information is useful in improving |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| CC                                         | the efficiency and output of several steps in drug discovery and          |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| CC                                         | development process, including target validation, identifying lead        |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| CC                                         | compounds, and early phase clinical trials. Information on polymorphisms  |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| CC                                         | may be applied in studying biological functions of TACR2 as well as in    |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| CC                                         | identifying drugs targeting this protein for the treatment of disorders   |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| CC                                         | related to its abnormal expression or function. ABS64163-ABS64302         |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| CC                                         | represent human TACR2 gene allele-specific oligonucleotide probes and     |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| CC                                         | primers used to detect haplotypes of the TACR2 gene of the invention      |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| XX                                         | Sequence 15 BP; 3 A; 3 C; 3 G; 5 T; 0 U; 1 Other;                         |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| SQL                                        | Query Match 39.3%; Score 11.4; DB 1; Length 15;                           |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| Best Local Similarity 80.0%; Pred. No. 68; |                                                                           |               |              |    |            |    |        |    |      |    |  |  |  |  |  |
| Matches                                    |                                                                           | 12;           | Conservative | 1; | Mismatches | 2; | Indels | 0; | Gaps | 0; |  |  |  |  |  |

QY 7 ACCTGCTGTGTGACC 21  
Db 1 ACTTGCTGTGTAAYC 15

RESULT 57  
AAX27264/c  
ID AAX27264 standard; DNA; 16 BP.  
XX  
AC AAX27264;  
XX  
DT 02-JUN-1999 (first entry)  
XX  
DE PCR primer for prostate-tumour derived antigen polynucleotide.  
XX  
KW Prostate-tumour derived polynucleotide; prostate tumour antigen;  
KW tumour cell; prostate carcinoma; therapy; PCR primer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9909166-A2.  
XX  
PD 25-FEB-1999.  
XX  
PF 18-AUG-1998; 98WO-US017058.  
XX  
PR 20-AUG-1997; 97US-0056110P.  
PR 09-JUL-1998; 98US-00112096.  
XX  
PA (DEND-) DENDREON CORP.  
XX  
PI Laus R, Shapero MH, Tsavaler L;  
XX  
DR WPI; 1999-181036/15.  
XX  
PT Novel human prostate tumour antigens and coding sequences - useful to  
PT detect and treat especially prostate carcinoma.  
XX  
PS Disclosure; Page 40; 85pp; English.  
XX  
CC This sequence represents a PCR primer for DNA encoding a prostate tumour  
CC antigen of the invention. The polynucleotides and polypeptides can be  
CC used to detect and treat tumour cells, especially prostate carcinoma  
XX  
SQ Sequence 16 BP; 7 A; 5 C; 1 G; 3 T; 0 U; 0 Other;  
  
Query Match 38.6%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 80;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 10 TGCTGTGTGACCTGGT 25  
Db 16 TGCTGTGTGAAATTGT 1

RESULT 58  
AAD27231/c  
ID AAD27231 standard; DNA; 16 BP.  
XX  
AC AAD27231;  
XX  
DT 09-APR-2002 (first entry)  
XX  
DE M13 universal reverse primer used in FDD.  
XX  
KW Human; congestive heart failure; dilative cardiomyopathy; sudden death;  
KW hypertrophic cardiomyopathy; ischaemic cardiomyopathy; rhythm disorder;  
KW heart muscle disease; conduction disorder; coronary heart disease;  
KW systemic arterial hypertension; pulmonary hypertension; endocarditis;  
KW pulmonary heart disease; valvular heart disease; pericardial disease;  
KW congenital heart disease; gene therapy; syncope; transgenic animal;  
KW primer; ss.

XX Unidentified.  
OS  
XX WO200192567-A2.  
PN  
XX  
PD 06-DEC-2001.  
XX  
PF 30-MAY-2001; 2001WO-EP006165.  
XX  
PR 30-MAY-2000; 2000US-0207400P.  
XX  
PA (MEDI-) MEDIGENE AG.  
XX  
PI Bunk D, Reuner B, Beck J, Henkel T;  
XX  
DR WPI; 2002-122073/16.  
XX  
PT Identifying a subject at risk for a heart disease e.g. congestive heart  
PT failure, dilative cardiomyopathy, heart muscle disease, by quantifying  
PT the polypeptide expressed by genes abnormally expressed in heart tissue.  
XX  
PS Disclosure; Page 53; 154pp; English.  
XX  
CC The patent discloses novel target genes abnormally expressed in heart  
CC tissues and their corresponding proteins. The invention also relates to  
CC methods for assessing the expression level of these genes. The method is  
CC used for testing the predisposition of mammals and preferably humans for  
CC a heart disease or for an acute state of such a disease. It is also  
CC useful to treat diseases of the heart such as congestive heart failure,  
CC dilative cardiomyopathy, hypertrophic cardiomyopathy, ischaemic cardio-  
CC myopathy, specific heart muscle disease, rhythm and conduction disorders,  
CC syncope and sudden death, coronary heart disease, systemic arterial  
CC hypertension, pulmonary hypertension, pulmonary heart disease, valvular  
CC heart disease, congenital heart disease, pericardial disease and  
CC endocarditis. Sequences of the invention are also used in gene therapy. A  
CC transgenic non-human mammal comprising the sequences of the invention are  
CC useful for the development for medicaments for the treatments of heart  
CC diseases. The present DNA sequence is M13 universal reverse priming  
CC sequence which is incorporated in M13r-ARPX10 arbitrary primer for  
CC amplifying cDNAs of the invention. This sequence used in the fluorescence  
CC differential display (FDD) method in the exemplification of the invention  
XX  
SQ Sequence 16 BP; 7 A; 5 C; 1 G; 3 T; 0 U; 0 Other;  
  
Query Match 38.6%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 80;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 10 TGCTGTGTGACCTGGT 25  
Db 16 TGCTGTGTGAAATTGT 1

RESULT 59  
ABZ75913/c  
ID ABZ75913 standard; DNA; 16 BP.  
XX  
AC ABZ75913;  
XX  
DT 15-MAY-2003 (first entry)  
XX  
DE M13 universal reverse primer.  
XX  
KW Cardiant; hypotension; antiarrhythmic; gene therapy; heart disease;  
KW transgenic; PCR; primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO2003006687-A2.  
XX  
PD 23-JAN-2003.  
XX  
PF 10-JUL-2002; 2002WO-EP007704.

XX 10-JUL-2001; 2001US-0304385P.  
XX (MEDI-) MEDIGENE AG.  
XX Reuner B, Bunk D, Henkel T;  
XX WPI; 2003-229493/22.  
DR Identifying a subject at risk for a disease of the heart, comprises  
XX quantitating the amount of at least one RNA or a polypeptide in the heart  
PT tissue or serum of the blood of the subject.  
XX Example 1; Page 56; 197pp; English.  
PS  
XX The invention relates to identifying a subject at risk for a disease of  
CC the heart and involves quantitating the amount of at least one RNA or a  
CC polypeptide in the heart tissue or serum of the blood of the subject. The  
CC DNA, polypeptides, compounds identified by the methods above, the refined  
CC or modified compounds, and the monoclonal antibodies are useful for  
CC manufacturing a pharmaceutical composition for preventing or treating  
CC heart diseases, e.g. congestive heart failure, dilative cardiomyopathy,  
CC hypertrophic cardiomyopathy, ischaemic cardiomyopathy, specific heart  
CC muscle disease, rhythm and conduction disorders, syncope and sudden  
CC death, coronary heart disease, systemic arterial hypertension, pulmonary  
CC hypertension and pulmonary heart disease, valvular heart disease,  
CC congenital heart disease, pericardial disease or endocarditis. Transgenic  
CC animals are useful for developing medicaments for treating heart  
CC diseases. The methods are useful for identifying a subject at risk for a  
CC heart disease, or for identifying compounds for treating heart disease.  
CC The present sequence represents a M13 universal reverse primer  
XX  
SQ Sequence 16 BP; 7 A; 5 C; 1 G; 3 T; 0 U; 0 Other;  
  
Query Match 38.6%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 80;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 10 TGCTGTGTGACCTGGT 25  
Db ||||| |||  
16 TGCTGTGTGAAATTGT 1  
  
RESULT 60  
ID ADR70024/c  
XX ADR70024 standard; DNA; 16 BP.  
AC ADR70024;  
XX  
DT 04-NOV-2004 (first entry)  
DE Human survivin gene modulatory oligonucleotide #92.  
XX ss; antiangiogenic; cytostatic; antiarteriosclerotic; antipsoriatic;  
KW antidiabetic; ophthalmologic; antiarthritic; antirheumatic;  
KW antiasthmatic; antiallergic; antiinflammatory; dermatological; anti-HIV;  
KW virucide; survivin antagonist; apoptosis inhibitor;  
KW cellular proliferation inhibitor; survivin; gene expression;  
KW abnormal angiogenesis; chemotherapeutic agent; busulfan; myleran;  
KW carboplatin; paraplatin; Taxol; doxorubicin; adriamycin; atherosclerosis;  
KW psoriasis; diabetic retinopathy; rheumatoid arthritis; asthma; warts;  
KW allergic dermatitis; cancer; tumour; sarcoma; glioma; carcinoma;  
KW melanoma; osteosarcoma; Ewing's sarcoma; chondrosarcoma;  
KW malignant fibrous histiocyoma; fibrosarcoma; Kaposi's sarcoma;  
KW Paclitaxel; Docetaxel.  
XX Homo sapiens.  
OS Synthetic.  
OS  
XX Key Location/Qualifiers  
FH modified\_base 1. .16  
FT /\*tag= b  
FT /mod\_base= OTHER

FT /note= "OTHER = phosphorothioate internucleotide  
FT linkages, all locked nucleic acid (LNA) residues are 5'-  
FT methyl cytosine residues"  
FT 1. .4  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER = beta-D-oxy-locked nucleic acid but  
FT optionally DNA nucleotides, optionally phosphate  
FT internucleotide linkages"  
FT 13. .16  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "OTHER = beta-D-oxy-locked nucleic acid but  
FT optionally DNA nucleotides, optionally phosphate  
FT internucleotide linkages"  
XX  
PN WO2004069991-A2.  
XX 19-AUG-2004.  
XX 10-FEB-2004; 2004WO-DK000096.  
XX 10-FEB-2003; 2003DK-00000183.  
PR 18-NOV-2003; 2003DK-00001708.  
XX (SANT-) SANTARIS PHARMA AS.  
XX Hansen B, Thru CA, Petersen KD, Westergaard M, Wissenbach M;  
PI WPI; 2004-625494/60.  
XX  
PT New locked nucleic acid containing oligomeric compound capable of  
PT modulating survivin expression, useful for treating cancer such as breast  
PT carcinoma, lung carcinoma, etc.  
XX  
PS Claim 1; SEQ ID NO 93; 122pp; English.  
PS  
XX The invention relates to an oligomeric compound (I) capable of modulating  
CC survivin expression, having 8-50 nucleotides and/or nucleotide analogues,  
CC where the compound comprises a subsequence of at least 8 nucleotides or  
CC nucleotide analogues, where the subsequence is located within a sequence  
CC chosen from one of 143 sequences given in the specification. (I) is  
CC useful for treating a mammal suffering from or susceptible from a disease  
CC caused by abnormal angiogenesis, by administering (I) containing one or  
CC more LNA units that are targeted to survivin. (I) is useful as a  
CC medicament and for the manufacture of a medicament for the treatment of  
CC cancer, in combination with chemotherapeutic agent such as busulfan  
CC (myleran), carboplatin (paraplatin), Taxol, doxorubicin (adriamycin),  
CC etc. (I) or a conjugate (II) containing (I) is useful in the preparation  
CC of a medicament for the treatment of atherosclerosis, psoriasis, diabetic  
CC retinopathy, rheumatoid arthritis, asthma, warts and allergic dermatitis.  
CC (I), (II) or a pharmaceutical (III) containing (I) is useful for treating  
CC cancer in the form of a solid tumour, sarcoma, glioma or carcinoma chosen  
CC from malignant melanoma, basal cell carcinoma, ovarian carcinoma, breast  
CC carcinoma, non-small cell lung cancer, renal cell carcinoma, bladder  
CC carcinoma, recurrent superficial bladder cancer, stomach carcinoma,  
CC prostatic carcinoma, pancreatic carcinoma, lung carcinoma, cervical  
CC carcinoma, cervical dysplasia, laryngeal papillomatosis, colon carcinoma,  
CC colorectal carcinoma and carcinoma tumours. The malignant melanoma is  
CC chosen from superficial spreading melanoma, nodular melanoma, lentigo  
CC maligna melanoma, acral melanoma, amelanotic melanoma, and desmoplastic  
CC melanoma. The sarcoma is chosen from osteosarcoma, Ewing's sarcoma,  
CC chondrosarcoma, malignant fibrous histiocyoma, fibrosarcoma and Kaposi's  
CC sarcoma. The treatment further involves administration of a  
CC chemotherapeutic agent such as taxanes, preferably Taxol, Paclitaxel or  
CC Docetaxel. (I), (II) or (III) is also useful for preventing or limiting  
CC apoptosis or for preventing cellular proliferation. This sequence  
CC corresponds to an antisense oligonucleotide targeted to the human  
CC survivin gene.  
XX  
SQ Sequence 16 BP; 5 A; 5 C; 4 G; 2 T; 0 U; 0 Other;  
  
Query Match 38.6%; Score 11.2; DB 1; Length 16;

```
Best Local Similarity 81.2%; Pred. No. 80;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      4 TCCACCTGCTGTGTGA 19
      | | |||||
Db      16 TGCCACTGCTGTGTGA 1

RESULT 61
ADW09956/c
ID      ADW09956 standard; DNA; 16 BP.
XX
AC      ADW09956;
XX
DT      07-APR-2005 (first entry)
XX
DE      Human survivin antisense oligonucleotide 93C, SEQ ID NO:514.
XX
KW      Antisense therapy; apoptosis stimulation; neoplasm; carcinoma; melanoma;
KW      basal cell carcinoma; ovary tumor; breast tumor;
KW      non-small-cell lung cancer; renal cell carcinoma; bladder tumor;
KW      stomach tumor; prostatic cancer; pancreas tumor; lung tumor;
KW      uterine cervix tumor; cervical dysplasia; colon tumor; colorectal tumor;
KW      sarcoma; osteosarcoma; Kaposi sarcoma; anti-HIV; glioma; cytostatic;
KW      endocrine disease; gynecology and obstetrics; genitourinary disease;
KW      respiratory disease; musculoskeletal disease; dermatological disease;
KW      proliferative disorder; atherosclerosis; arteriosclerosis;
KW      cardiovascular disease; metabolic disorder; psoriasis; antipsoriatic;
KW      immune disorder; diabetic retinopathy; antidiabetic; ophthalmological;
KW      cardiovascular disease; ocular disease; rheumatoid arthritis;
KW      antiarthritic; antiallergic; antiinflammatory; dermatological;
KW      skin allergy; antiasthmatic; inflammation; asthma; antiasthmatic;
KW      verruca vulgaris; virucide; cell proliferation; apoptosis modulation;
KW      angiogenesis disorder; survivin; phosphorothioate; cytosine methylation;
KW      antisense oligonucleotide; ss.
XX
OS      Homo sapiens.
XX
FH      Key Location/Qualifiers
FT      misc_binding 1..16 /*tag= b
FT      /bound moiety= "Bases 1248-1233 of human survivin cDNA
FT      (SEQ ID NO:1)"
FT      modified_base 1..4 /*tag= a
FT      /mod_base= OTHER
FT      /note= "Beta-D-oxy-LNAs (locked nucleic acid). All beta-D
FT      -oxy-LNA cytosines are 5-methylcytosine"
FT      modified_base 5..13 /*tag= c
FT      /mod_base= OTHER
FT      /note= "Phosphorothioate linkages"
FT      modified_base 13..16 /*tag= d
FT      /mod_base= OTHER
FT      /note= "Beta-D-oxy-LNAs. All beta-D-oxy-LNA cytosines are
FT      5-methylcytosine"
XX
PN      US2005014712-A1.
XX
XX
PD      20-JAN-2005.
XX
XX      10-FEB-2004; 2004US-00776934.
XX
PR      10-FEB-2003; 2003US-0446372P.
PR      19-NOV-2003; 2003US-0523591P.
XX
PA      (HANS/) HANSEN B.
PA      (THRU/) THRU C A.
PA      (WEST/) WESTERGAARD M.
PA      (PETE/) PETERSEN K D.
PA      (WISS/) WISSENBACH M.
XX
```

```
PI      Hansen B, Thru CA, Westergaard M, Petersen KD, Wissenbach M;
XX      WPI; 2005-100663/11.
DR
XX      New oligomeric compound for the modulation of survivin, useful for
PT      treating e.g. cancers, atherosclerosis, psoriasis, diabetic retinopathy,
PT      rheumatoid arthritis, asthma, warts, or allergic dermatitis.
XX
PS      Example 10; SEQ ID NO 514; 264pp; English.
XX
CC      The invention relates to antisense oligonucleotides consisting of 8-50
CC      nucleotides and/or nucleotide analogs which inhibit expression of human
CC      survivin, an inhibitor of apoptosis which is also essential for cell
CC      division and angiogenesis. The antisense oligonucleotides comprise a
CC      subsequence of 8 or more nucleotides or nucleotide analogs, wherein the
CC      subsequence is located within a sequence selected from ADW09444-ADW09586.
CC      The oligonucleotides preferably contain one or more (preferably 6-10)
CC      nucleotide analogs, especially a locked nucleic acid (LNA), and also
CC      preferably contain a linkage group selected from a phosphate group, a
CC      phosphorothioate group or a boranophosphate group. The invention also
CC      relates to a conjugate comprising a survivin antisense oligonucleotide of
CC      the invention and one or more non-nucleotide or non-polynucleotide
CC      moieties covalently attached to the oligonucleotide; and a pharmaceutical
CC      composition comprising a survivin antisense oligonucleotide or conjugate
CC      of the invention, optionally further comprising a chemotherapeutic agent.
CC      The survivin antisense oligonucleotides, and conjugates and compositions
CC      containing them, are useful in the treatment of cancers such as
CC      carcinomas (e.g., malignant melanoma, basal cell carcinoma, ovarian
CC      carcinoma, breast carcinoma, non-small cell lung cancer, renal cell
CC      carcinoma, bladder carcinoma, recurrent pancreatic bladder cancer,
CC      stomach carcinoma, prostatic carcinoma, pancreatic carcinoma, lung
CC      carcinoma, cervical carcinoma, cervical dysplasia, laryngeal
CC      papillomatosis, colon carcinoma, colorectal carcinoma and carcinoid
CC      tumors); sarcomas (e.g., osteosarcoma, Ewing's sarcoma, chondrosarcoma,
CC      malignant fibrous histiocytoma, fibrosarcoma, and Kaposi's sarcoma); or
CC      gliomas. The survivin antisense oligonucleotides are also useful in the
CC      treatment of conditions such as atherosclerosis, psoriasis, diabetic
CC      retinopathy, rheumatoid arthritis, asthma, warts, and allergic
CC      dermatitis. They may additionally be used for inhibiting cellular
CC      proliferation, for modulating apoptosis and for treating a disease
CC      related to abnormal angiogenesis. The survivin antisense oligonucleotides
CC      of the invention are shorter than prior art survivin antisense
CC      oligonucleotides (16-mers compared to 20-25-mers), therefore having
CC      increased specificity and affinity for survivin mRNA, and also have
CC      higher biostability and cell permeability. The present sequence
CC      represents an antisense oligonucleotide targeted to the human survivin
CC      cDNA target sequence shown in ADW09443 used in an example of the
CC      invention.
XX
SQ      Sequence 16 BP; 5 A; 5 C; 4 G; 2 T; 0 U; 0 Other;

      Query Match 38.6%; Score 11.2; DB 1; Length 16;
      Best Local Similarity 81.2%; Pred. No. 80;
      Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      4 TCCACCTGCTGTGTGA 19
      | | |||||
Db      16 TGCCACTGCTGTGTGA 1

RESULT 62
ADW09954/c
ID      ADW09954 standard; DNA; 16 BP.
XX
AC      ADW09954;
XX
DT      07-APR-2005 (first entry)
XX
DE      Human survivin antisense oligonucleotide 93A, SEQ ID NO:512.
XX
KW      Antisense therapy; apoptosis stimulation; neoplasm; carcinoma; melanoma;
KW      basal cell carcinoma; ovary tumor; breast tumor;
KW      non-small-cell lung cancer; renal cell carcinoma; bladder tumor;
```



KW stomach tumor; prostatic cancer; pancreas tumor; lung tumor;  
KW uterine cervix tumor; cervical dysplasia; colon tumor; colorectal tumor;  
KW sarcoma; osteosarcoma; Kaposi sarcoma; anti-HIV; glioma; cytostatic;  
KW endocrine disease; gynecology and obstetrics; genitourinary disease;  
KW respiratory disease; musculoskeletal disease; dermatological disease;  
KW proliferative disorder; atherosclerosis; antiarteriosclerotic;  
KW cardiovascular disease; metabolic disorder; psoriasis; antipsoriatic;  
KW immune disorder; diabetic retinopathy; antidiabetic; ophthalmological;  
KW cardiovascular disease; ocular disease; rheumatoid arthritis;  
KW antiarthritic; antirheumatic; inflammation; asthma; antiasthmatic;  
KW skin allergy; antiallergic; antiinflammatory; dermatological;  
KW verruca vulgaris; virucide; cell proliferation; apoptosis modulation;  
KW angiogenesis disorder; survivin; phosphorothioate; cytosine methylation;  
KW antisense oligonucleotide; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT misc\_binding 1. .16  
FT /\*tag= b  
FT /bound\_moiety= "Bases 1248-1233 of human survivin cDNA  
FT (SEQ ID NO:1)"  
FT 1. .16  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate linkages"  
FT modified\_base 1. .4  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "Beta-D-oxy-LNAs (locked nucleic acid). All beta-D  
FT -oxy-LNA cytosines are 5-methylcytosine"  
FT modified\_base 13. .16  
FT /\*tag= d  
FT /mod\_base= OTHER  
FT /note= "Beta-D-oxy-LNAs. All beta-D-oxy-LNA cytosines are  
FT 5-methylcytosine"  
XX  
PN US2005014712-A1.  
XX  
XX 20-JAN-2005.  
XX  
XX 10-FEB-2004; 2004US-00776934.  
XX  
XX 10-FEB-2003; 2003US-0446372P.  
PR 19-NOV-2003; 2003US-0523591P.  
XX  
XX (HANS/) HANSEN B.  
PA (THRU/) THRU C A.  
PA (WEST/) WESTERGAARD M.  
PA (PETE/) PETERSEN K D.  
PA (WISS/) WISSENBACH M.  
XX  
XX Hansen B, Thru CA, Westergaard M, Petersen KD, Wissenbach M;  
PI WPI; 2005-100663/11.  
XX  
XX New oligomeric compound for the modulation of survivin, useful for  
PT treating e.g. cancers, atherosclerosis, psoriasis, diabetic retinopathy,  
PT rheumatoid arthritis, asthma, warts, or allergic dermatitis.  
XX  
PS Example 10; SEQ ID NO 512; 264pp; English.  
XX  
CC The invention relates to antisense oligonucleotides consisting of 8-50  
CC nucleotides and/or nucleotide analogs which inhibit expression of human  
CC survivin, an inhibitor of apoptosis which is also essential for cell  
CC division and angiogenesis. The antisense oligonucleotides comprise a  
CC subsequence of 8 or more nucleotides or nucleotide analogs, wherein the  
CC subsequence is located within a sequence selected from ADW09444-ADW09586.  
CC The oligonucleotides preferably contain one or more (preferably 6-10)  
CC nucleotide analogs, especially a locked nucleic acid (LNA), and also  
CC preferably contain a linkage group selected from a phosphate group, a  
CC phosphorothioate group or a boranophosphate group. The invention also  
CC relates to a conjugate comprising a survivin antisense oligonucleotide of

CC the invention and one or more non-nucleotide or non-polynucleotide  
CC moieties covalently attached to the oligonucleotide; and a pharmaceutical  
CC composition comprising a survivin antisense oligonucleotide or conjugate  
CC of the invention, optionally further comprising a chemotherapeutic agent.  
CC The survivin antisense oligonucleotides, and conjugates and compositions  
CC containing them, are useful in the treatment of cancers such as  
CC carcinomas (e.g., malignant melanoma, basal cell carcinoma, ovarian  
CC carcinoma, breast carcinoma, non-small cell lung cancer, renal cell  
CC carcinoma, bladder carcinoma, recurrent superficial bladder cancer,  
CC stomach carcinoma, prostatic carcinoma, pancreatic carcinoma, lung  
CC carcinoma, cervical carcinoma, cervical dysplasia, laryngeal  
CC papillomatosis, colon carcinoma, colorectal carcinoma and carcinoma  
CC tumors); sarcomas (e.g., osteosarcoma, Ewing's sarcoma, Chondrosarcoma,  
CC malignant fibrous histiocytoma, fibrosarcoma, and Kaposi's sarcoma); or  
CC gliomas. The survivin antisense oligonucleotides are also useful in the  
CC treatment of conditions such as atherosclerosis, psoriasis, diabetic  
CC retinopathy, rheumatoid arthritis, asthma, warts, and allergic  
CC dermatitis. They may additionally be used for inhibiting cellular  
CC proliferation, for modulating apoptosis and for treating a disease  
CC related to abnormal angiogenesis. The survivin antisense oligonucleotides  
CC of the invention are shorter than prior art survivin antisense  
CC oligonucleotides (16-mers compared to 20-25-mers), therefore having  
CC increased specificity and affinity for survivin mRNA, and also have  
CC higher biostability and cell permeability. The present sequence  
CC represents an antisense oligonucleotide targeted to the human survivin  
CC cDNA target sequence shown in ADW09443 used in an example of the  
CC invention.  
XX  
SQ Sequence 16 BP; 5 A; 5 C; 4 G; 2 T; 0 U; 0 Other;  
Query Match 38.6%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 80;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 4 TCCACCTGCTGTGTGA 19  
Db | | |||||  
16 TGCCACTGCTGTGTGA 1  
RESULT 63  
ADW09955/c  
ID ADW09955 standard; DNA; 16 BP.  
XX  
AC ADW09955;  
XX  
XX 07-APR-2005 (first entry)  
XX  
DE Human survivin antisense oligonucleotide 93B, SEQ ID NO:513.  
XX  
KW Antisense therapy; apoptosis stimulation; neoplasm; carcinoma; melanoma;  
KW basal cell carcinoma; ovary tumor; breast tumor;  
KW non-small-cell lung cancer; renal cell carcinoma; bladder tumor;  
KW stomach tumor; prostatic cancer; pancreas tumor; lung tumor;  
KW uterine cervix tumor; cervical dysplasia; colon tumor; colorectal tumor;  
KW sarcoma; osteosarcoma; Kaposi sarcoma; anti-HIV; glioma; cytostatic;  
KW endocrine disease; gynecology and obstetrics; genitourinary disease;  
KW respiratory disease; musculoskeletal disease; dermatological disease;  
KW proliferative disorder; atherosclerosis; antiarteriosclerotic;  
KW cardiovascular disease; metabolic disorder; psoriasis; antipsoriatic;  
KW immune disorder; diabetic retinopathy; antidiabetic; ophthalmological;  
KW immune disorder; diabetic retinopathy; antidiabetic; ophthalmological;  
KW cardiovascular disease; ocular disease; rheumatoid arthritis;  
KW antiarthritic; antirheumatic; inflammation; asthma; antiasthmatic;  
KW skin allergy; antiallergic; antiinflammatory; dermatological;  
KW verruca vulgaris; virucide; cell proliferation; apoptosis modulation;  
KW angiogenesis disorder; survivin; phosphorothioate; cytosine methylation;  
KW antisense oligonucleotide; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT misc\_binding 1. .16  
FT /\*tag= b  
FT /bound\_moiety= "Bases 1248-1233 of human survivin cDNA



FT modified\_base (SEQ ID NO:1)"  
FT 1. .16 /tag= c  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate linkages"  
FT 1. .4  
FT /tag= a  
FT /mod\_base= OTHER  
FT /note= "Beta-D-oxy-LNAs (locked nucleic acid). All beta-D  
FT -oxy-LNA cytosines are 5-methylcytosine"  
FT 13. .15  
FT /tag= d  
FT /mod\_base= OTHER  
FT /note= "Beta-D-oxy-LNAs. All beta-D-oxy-LNA cytosines are  
FT 5-methylcytosine"  
PN US2005014712-A1.  
XX  
XX  
PD 20-JAN-2005.  
XX  
PF 10-FEB-2004; 2004US-00776934.  
XX  
PR 10-FEB-2003; 2003US-0446372P.  
PR 19-NOV-2003; 2003US-0523591P.  
XX  
XX (HANS/) HANSEN B.  
PA (THRU/) THRU C A.  
PA (WEST/) WESTERGAARD M.  
PA (PETE/) PETERSEN K D.  
PA (WISS/) WISSENBACH M.  
XX  
PI Hansen B, Thru CA, Westergaard M, Petersen KD, Wissenbach M;  
XX WPI; 2005-100663/11.  
DR  
XX  
PT New oligomeric compound for the modulation of survivin, useful for  
PT treating e.g. cancers, atherosclerosis, psoriasis, diabetic retinopathy,  
PT rheumatoid arthritis, asthma, warts, or allergic dermatitis.  
XX  
PS Example 10; SEQ ID NO 513; 264pp; English.  
XX  
CC The invention relates to antisense oligonucleotides consisting of 8-50  
CC nucleotides and/or nucleotide analogs which inhibit expression of human  
CC survivin, an inhibitor of apoptosis which is also essential for cell  
CC division and angiogenesis. The antisense oligonucleotides comprise a  
CC subsequence of 8 or more nucleotides or nucleotide analogs, wherein the  
CC subsequence is located within a sequence selected from ADW09444-ADW09586.  
CC The oligonucleotides preferably contain one or more (preferably 6-10)  
CC nucleotide analogs, especially a locked nucleic acid (LNA), and also  
CC preferably contain a linkage group selected from a phosphate group, a  
CC phosphorothioate group or a boranophosphate group. The invention also  
CC relates to a conjugate comprising a survivin antisense oligonucleotide of  
CC the invention and one or more non-nucleotide or non-polynucleotide  
CC moieties covalently attached to the oligonucleotide; and a pharmaceutical  
CC composition comprising a survivin antisense oligonucleotide or conjugate  
CC of the invention, optionally further comprising a chemotherapeutic agent.  
CC The survivin antisense oligonucleotides, and conjugates and compositions  
CC containing them, are useful in the treatment of cancers such as  
CC carcinomas (e.g., malignant melanoma, basal cell carcinoma, ovarian  
CC carcinoma, breast carcinoma, non-small cell lung cancer, renal cell  
CC carcinoma, bladder carcinoma, recurrent superficial bladder cancer,  
CC stomach carcinoma, prostatic carcinoma, pancreatic carcinoma, lung  
CC carcinoma, cervical carcinoma, cervical dysplasia, laryngeal  
CC papillomatosis, colon carcinoma, colorectal carcinoma and carcinoma  
CC tumors); sarcomas (e.g., osteosarcoma, Ewing's sarcoma, chondrosarcoma,  
CC malignant fibrous histiocytoma, fibrosarcoma, and Kaposi's sarcoma); or  
CC gliomas. The survivin antisense oligonucleotides are also useful in the  
CC treatment of conditions such as atherosclerosis, psoriasis, diabetic  
CC retinopathy, rheumatoid arthritis, asthma, warts, and allergic  
CC dermatitis. They may additionally be used for inhibiting cellular  
CC proliferation, for modulating apoptosis and for treating a disease  
CC related to abnormal angiogenesis. The survivin antisense oligonucleotides  
CC of the invention are shorter than prior art survivin antisense

CC oligonucleotides (16-mers compared to 20-25-mers), therefore having  
CC increased specificity and affinity for survivin mRNA, and also have  
CC higher biostability and cell permeability. The present sequence  
CC represents an antisense oligonucleotide targeted to the human survivin  
CC cDNA target sequence shown in ADW09443 used in an example of the  
CC invention.  
XX  
SQ Sequence 16 BP; 5 A; 5 C; 4 G; 2 T; 0 U; 0 Other;  
Query Match 38.6%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred.No. 80;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 4 TCCACCTGCTGTGTGA 19  
Db 16 TGCCACTGCTGTGTGA 1  
RESULT 64  
ADW09535/C  
ID ADW09535 standard; DNA; 16 BP.  
XX  
AC ADW09535;  
XX  
DT 07-APR-2005 (first entry)  
XX Human survivin antisense oligonucleotide, SEQ ID NO:93.  
DE  
XX Antisense therapy; apoptosis stimulation; neoplasm; carcinoma; melanoma;  
KW basal cell carcinoma; ovary tumor; breast tumor;  
KW non-small-cell lung cancer; renal cell carcinoma; bladder tumor;  
KW stomach tumor; prostatic cancer; pancreas tumor; lung tumor;  
KW uterine cervix tumor; cervical dysplasia; colon tumor; colorectal tumor;  
KW sarcoma; osteosarcoma; Kaposi sarcoma; anti-HIV; glioma; cytostatic;  
KW endocrine disease; gynecology and obstetrics; genitourinary disease;  
KW respiratory disease; musculoskeletal disease; dermatological disease;  
KW proliferative disorder; atherosclerosis; antiarteriosclerotic;  
KW cardiovascular disease; metabolic disorder; psoriasis; antipsoriatic;  
KW immune disorder; diabetic retinopathy; antidiabetic; ophthalmological;  
KW cardiovascular disease; ocular disease; rheumatoid arthritis;  
KW antiarthritic; antirheumatic; inflammation; asthma; antiasthmatic;  
KW skin allergy; antiallergic; antiinflammatory; dermatological;  
KW verruca vulgaris; virucide; cell proliferation; apoptosis modulation;  
KW angiogenesis disorder; survivin; phosphorothioate; cytosine methylation;  
KW antisense oligonucleotide; ss.  
XX Homo sapiens.  
OS  
XX  
FH Key Location/Qualifiers  
FT misc\_binding 1. .16  
FT /tag= c  
FT /bound moiety= "Bases 1248-1233 of human survivin cDNA  
FT (SEQ ID NO:1)"  
FT modified\_base 1. .5  
FT /tag= b  
FT /mod\_base= OTHER  
FT /note= "Optionally phosphorothioate linkages when  
FT nucleotides 1-4 are beta-D-oxy-LNAs. When nucleotides 1-4  
FT are unmodified, the internucleotide linkages are  
FT phosphorothioate"  
FT modified\_base 1. .4  
FT /tag= a  
FT /mod\_base= OTHER  
FT /note= "Optionally beta-D-oxy-LNAs (locked nucleic acid).  
FT All beta-D-oxy-LNA cytosines are 5-methylcytosine"  
FT modified\_base 5. .13  
FT /tag= d  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate linkages"  
FT modified\_base 13. .15  
FT /tag= e  
FT /mod\_base= OTHER  
FT /note= "Optionally beta-D-oxy-LNAs. All beta-D-oxy-LNA

FT cytosines are 5-methylcytosine. Optionally

FT phosphorothioate linkages when bases 13-15 are beta-D-oxy

FT -LNAs. When nucleotides 13-15 are unmodified, the

FT internucleotide linkages are phosphorothioate"

FT 15. .16

FT /\*tag= f

FT /mod\_base= OTHER

FT /note= "Optionally phosphorothioate linkage when

FT nucleotide 16 is beta-D-oxy-LNA. This linkage is

FT phosphorothioate when nucleotide 16 is unmodified"

FT 16

FT /\*tag= g

FT /mod\_base= OTHER

FT /note= "Optionally beta-D-oxy-LNA. When this nucleotide

FT is unmodified, the linkage between nucleotides 15 and 16

FT is phosphorothioate"

XX

PN US2005014712-A1.

XX

PD 20-JAN-2005.

XX

PF 10-FEB-2004; 2004US-00776934.

XX

PR 10-FEB-2003; 2003US-0446372P.

PR 19-NOV-2003; 2003US-0523591P.

XX

PA (HANS/) HANSEN B.

PA (THRU/) THRU C A.

PA (WEST/) WESTERGAARD M.

PA (PETE/) PETERSEN K D.

PA (WISS/) WISSENBACH M.

XX

PI Hansen B, Thru CA, Westergaard M, Petersen KD, Wissenbach M;

XX WPI; 2005-100663/11.

DR

XX

PT New oligomeric compound for the modulation of survivin, useful for

PT treating e.g. cancers, atherosclerosis, psoriasis, diabetic retinopathy,

PT rheumatoid arthritis, asthma, warts, or allergic dermatitis.

XX

PS Claim 1; SEQ ID NO 93; 264pp; English.

XX

CC The invention relates to antisense oligonucleotides consisting of 8-50

CC nucleotides and/or nucleotide analogs which inhibit expression of human

CC survivin, an inhibitor of apoptosis which is also essential for cell

CC division and angiogenesis. The antisense oligonucleotides comprise a

CC subsequence of 8 or more nucleotides or nucleotide analogs, wherein the

CC subsequence is located within a sequence selected from ADW09444-ADW09586.

CC The oligonucleotides preferably contain one or more (preferably 6-10)

CC nucleotide analogs, especially a locked nucleic acid (LNA), and also

CC preferably contain a linkage group selected from a phosphate group, a

CC phosphorothioate group or a boranophosphate group. The invention also

CC relates to a conjugate comprising a survivin antisense oligonucleotide of

CC the invention and one or more non-nucleotide or non-polynucleotide

CC moieties covalently attached to the oligonucleotide; and a pharmaceutical

CC composition comprising a survivin antisense oligonucleotide or conjugate

CC of the invention, optionally further comprising a chemotherapeutic agent.

CC The survivin antisense oligonucleotides, and conjugates and compositions

CC containing them, are useful in the treatment of cancers such as

CC carcinomas (e.g., malignant melanoma, basal cell carcinoma, ovarian

CC carcinoma, breast carcinoma, non-small cell lung cancer, renal cell

CC carcinoma, bladder carcinoma, recurrent superficial bladder cancer,

CC stomach carcinoma, prostatic carcinoma, pancreatic carcinoma, lung

CC papillomatosis, colon carcinoma, colorectal carcinoma and carcinoid

CC tumors); sarcomas (e.g., osteosarcoma, Ewing's sarcoma, chondrosarcoma,

CC malignant fibrous histiocytoma, fibrosarcoma, and Kaposi's sarcoma); or

CC gliomas. The survivin antisense oligonucleotides are also useful in the

CC treatment of conditions such as atherosclerosis, psoriasis, diabetic

CC retinopathy, rheumatoid arthritis, asthma, warts, and allergic

CC dermatitis. They may additionally be used for inhibiting cellular

CC proliferation, for modulating apoptosis and for treating a disease

CC related to abnormal angiogenesis. The survivin antisense oligonucleotides

CC of the invention are shorter than prior art survivin antisense

CC oligonucleotides (16-mers compared to 20-25-mers), therefore having

CC increased specificity and affinity for survivin mRNA, and also have

CC higher biostability and cell permeability. The present sequence

CC represents a specifically claimed antisense oligonucleotide targeted to

CC the human survivin cDNA target sequence shown in ADW09443.

XX

SQ Sequence 16 BP; 5 A; 5 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 38.6%; Score 11.2; DB 1; Length 16;

Best Local Similarity 81.2%; Pred. No. 80;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TCCACCTGCTGTGTGA 19

Db 16 TGCCACTGCTGTGTGA 1

RESULT 65

ADW09957/c

ID ADW09957 standard; DNA; 16 BP.

XX

AC ADW09957;

XX

DT 07-APR-2005 (first entry)

XX

DE Human survivin antisense oligonucleotide 93D, SEQ ID NO:515.

XX

KW Antisense therapy; apoptosis stimulation; neoplasm; carcinoma; melanoma;

KW basal cell carcinoma; ovary tumor; breast tumor;

KW non-small-cell lung cancer; renal cell carcinoma; bladder tumor;

KW stomach tumor; prostatic cancer; pancreas tumor; lung tumor;

KW uterine cervix tumor; cervical dysplasia; colon tumor; colorectal tumor;

KW sarcoma; osteosarcoma; Kaposi sarcoma; anti-HIV; glioma; cytostatic;

KW endocrine disease; gynecology and obstetrics; genitourinary disease;

KW respiratory disease; musculoskeletal disease; dermatological disease;

KW proliferative disorder; atherosclerosis; antiarteriosclerotic;

KW cardiovascular disease; metabolic disorder; psoriasis; antipsoriatic;

KW immune disorder; diabetic retinopathy; antidiabetic; ophthalmological;

KW cardiovascular disease; ocular disease; rheumatoid arthritis;

KW antiarthritic; antirheumatic; inflammation; asthma; antiasthmatic;

KW skin allergy; antiallergic; antiinflammatory; dermatological;

KW verruca vulgaris; virucide; cell proliferation; apoptosis modulation;

KW angiogenesis disorder; survivin; phosphorothioate;

KW antisense oligonucleotide; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT misc\_binding 1. .16

FT /\*tag= a

FT /bound\_moiety= "Bases 1248-1233 of human survivin cDNA

FT (SEQ ID NO:1)"

FT modified\_base 1. .16

FT /\*tag= b

FT /mod\_base= OTHER

FT /note= "Phosphorothioate linkages"

XX

PN US2005014712-A1.

XX

PD 20-JAN-2005.

XX

PF 10-FEB-2004; 2004US-00776934.

XX

PR 10-FEB-2003; 2003US-0446372P.

PR 19-NOV-2003; 2003US-0523591P.

XX

PA (HANS/) HANSEN B.

PA (THRU/) THRU C A.

PA (WEST/) WESTERGAARD M.

PA (PETE/) PETERSEN K D.

PA (WISS/) WISSENBACH M.

XX

PI Hansen B, Thru CA, Westergaard M, Petersen KD, Wissenbach M;  
XX WPI; 2005-100663/11.  
DR  
XX  
XX New oligomeric compound for the modulation of survivin, useful for  
PT treating e.g. cancers, atherosclerosis, psoriasis, diabetic retinopathy,  
PT rheumatoid arthritis, asthma, warts, or allergic dermatitis.  
XX  
XX  
PS Example 10; SEQ ID NO 515; 264pp; English.  
XX  
CC The invention relates to antisense oligonucleotides consisting of 8-50  
CC nucleotides and/or nucleotide analogs which inhibit expression of human  
CC survivin, an inhibitor of apoptosis which is also essential for cell  
CC division and angiogenesis. The antisense oligonucleotides comprise a  
CC subsequence of 8 or more nucleotides or nucleotide analogs, wherein the  
CC subsequence is located within a sequence selected from ADW09444-ADW09586.  
CC The oligonucleotides preferably contain one or more (preferably 6-10)  
CC nucleotide analogs, especially a locked nucleic acid (LNA), and also  
CC preferably contain a linkage group selected from a phosphate group, a  
CC phosphorothioate group or a boranophosphate group. The invention also  
CC relates to a conjugate comprising a survivin antisense oligonucleotide of  
CC the invention and one or more non-nucleotide or non-polynucleotide  
CC moieties covalently attached to the oligonucleotide; and a pharmaceutical  
CC composition comprising a survivin antisense oligonucleotide or conjugate  
CC of the invention, optionally further comprising a chemotherapeutic agent.  
CC The survivin antisense oligonucleotides, and conjugates and compositions  
CC containing them, are useful in the treatment of cancers such as  
CC carcinomas (e.g., malignant melanoma, basal cell carcinoma, ovarian  
CC carcinoma, breast carcinoma, non-small cell lung cancer, renal cell  
CC carcinoma, bladder carcinoma, recurrent superficial bladder cancer,  
CC stomach carcinoma, prostatic carcinoma, pancreatic carcinoma, lung  
CC carcinoma, cervical carcinoma, cervical dysplasia, laryngeal  
CC papillomatosis, colon carcinoma, colorectal carcinoma and carcinoma  
CC tumors); sarcomas (e.g., osteosarcoma, Ewing's sarcoma, chondrosarcoma,  
CC malignant fibrous histiocytoma, fibrosarcoma, and Kaposi's sarcoma); or  
CC gliomas. The survivin antisense oligonucleotides are also useful in the  
CC treatment of conditions such as atherosclerosis, psoriasis, diabetic  
CC retinopathy, rheumatoid arthritis, asthma, warts, and allergic  
CC dermatitis. They may additionally be used for inhibiting cellular  
CC proliferation, for modulating apoptosis and for treating a disease  
CC related to abnormal angiogenesis. The survivin antisense oligonucleotides  
CC of the invention are shorter than prior art survivin antisense  
CC oligonucleotides (16-mers compared to 20-25-mers), therefore having  
CC increased specificity and affinity for survivin mRNA, and also have  
CC higher biostability and cell permeability. The present sequence  
CC represents an antisense oligonucleotide targeted to the human survivin  
CC cDNA target sequence shown in ADW09443 used in an example of the  
CC invention.  
XX  
SQ Sequence 16 BP; 5 A; 5 C; 4 G; 2 T; 0 U; 0 Other;  
Query Match 38.6%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 80;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 4 TCCACCTGCTGTGTA 19  
Db 16 TGCCACTGCTGTGTA 1  
RESULT 66  
AAZ48742  
ID AAZ48742 standard; DNA; 12 BP.  
XX  
AC AAZ48742;  
XX  
DT 15-MAR-2000 (first entry)  
XX  
DE PCR primer for human alpha1-antitrypsin gene sequence.  
XX  
KW PCR primer; oligonucleotide detection; diagnosis; disease screening; COP;  
KW competitive oligonucleotide priming; genetic polymorphism detection;  
KW genetic disease diagnosis; linkage analysis; tissue typing; gene mapping;

KW human; alpha1-antitrypsin; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP333465-A.  
XX  
PD 20-SEP-1989.  
XX  
PF 15-MAR-1989; 89EP-003025569.  
XX  
PR 18-MAR-1988; 88US-00170214.  
XX  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
XX  
PI Caskey CT, Gibbs RAL;  
XX  
DR WPI; 1989-272222/38.  
XX  
PT Detection of mutations in DNA - by adding competitive oligo:nucleotide  
PT primers to nucleic acids, hybridising, etc.  
XX  
PS Example 4; Page 12; 21pp; English.  
XX  
CC This sequence represents a PCR primer for the human alpha1-antitrypsin  
CC gene sequence. The invention relates to a method for detecting the  
CC presence or absence of a specific known oligonucleotide, or  
CC distinguishing between specific and different nucleic acid (NA)  
CC sequences, comprising: (1) addition of at least two oligonucleotide  
CC primers to a sample or mixture of NA where one primer (a) is  
CC substantially complementary to a specific NA sequence and the other  
CC primer (b) has a single base mismatch with the specific sequence; (2)  
CC preferentially hybridising (a) to the specific NA sequence under  
CC competitive conditions; (3) extension of (a) from its 3' terminus to  
CC produce an extension product complementary to the strand hybridised to by  
CC (a); and (4) identifying the extension product by determining the  
CC presence or absence of labels attached to at least one of the primers.  
CC The method (referred to as competitive oligonucleotide priming (COP)) can  
CC be used in detecting genetic polymorphisms, particularly in detecting  
CC genetic diseases, screening for disease association by linkage analysis,  
CC tissue typing, gene mapping, screening for neoplasms, detection of known  
CC pathogens, determining purity of animal strains, and disease screening in  
CC animals. With this method, primers may be used that are shorter than  
CC those used in PCR, as the binding to template is competitive its sequence  
CC can be inferred. The target sequence of the gene need not be precisely  
CC known as only the specific sequence for the primers is required  
XX  
SQ Sequence 12 BP; 4 A; 2 C; 3 G; 3 T; 0 U; 0 Other;  
Query Match 37.9%; Score 11; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 64;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 19 ACCTGGTAAAT 29  
Db 1 ACCTGGTAAAT 11  
RESULT 67  
AAQ04007  
ID AAQ04007 standard; DNA; 12 BP.  
XX  
AC AAQ04007;  
XX  
DT 25-MAR-2003 (revised)  
DT 03-SEP-1990 (first entry)  
XX  
DE Primer used in detecting alpha1-antitrypsin deficiency.  
XX  
KW X-chromosome; ornithine transcarbamylase deficiency; muscular dystrophy;  
KW dystrophin; ds.  
XX  
OS Synthetic.  
XX

PN EP364255-A.  
XX 18-APR-1990.  
PD  
XX 11-OCT-1989; 89EP-00310424.  
PF  
XX 12-OCT-1988; 88US-00256689.  
PR  
XX (BAYU ) BAYLOR COLLEGE MEDICINE.  
PA  
PI Caskey CT, Chamberlain JS, Gibbs RAL, Rainer JE, Nguyen PN;  
XX WPI; 1990-117752/16.  
DR  
XX Multiplex genomic DNA amplification for deletion detection - useful for  
XX detecting X-linked diseases such as ornithine transcarbamylase deficiency  
PT and X-linked muscular dystrophy.  
PT  
XX Example 8; Page 18; 32pp; English.  
PS  
XX Paired oligonucleotide primers are used in detecting deletions  
CC specifically of the X and Y chromosomes. Probe may be used to recognise  
CC mutant (S) allele of alpha-1-antitrypsin. (Updated on 25-MAR-2003 to  
CC correct PA field.)  
CC  
XX Sequence 12 BP; 4 A; 2 C; 3 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 37.9%; Score 11; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 64;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 19 ACCTGGTAAAT 29  
DB 1 ACCTGGTAAAT 11  
RESULT 68  
AAF69397  
ID AAF69397 standard; DNA; 15 BP.  
XX  
AC AAF69397;  
XX  
DT 18-APR-2001 (first entry)  
XX  
DE Human IL4Ralpha gene probe #37.  
XX  
KW Polymorphism; human; interleukin 4 receptor-alpha; IL4R-alpha;  
KW allergic disease; probe; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200104270-A1.  
XX  
PD 18-JAN-2001.  
XX  
PF 13-JUL-2000; 2000WO-US019094.  
XX  
PR 13-JUL-1999; 99US-0143435P.  
XX  
XX (GENA-) GENAISSANCE PHARM INC.  
PA  
XX Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;  
PI Windemuth AK;  
PI  
XX WPI; 2001-103078/11.  
DR  
XX New isolated polynucleotide useful for the identification of therapeutics  
XX in allergic diseases is new.  
PT  
PT Claim 15; Page 42; 188pp; English.  
PS  
XX The present invention relates to polymorphisms of the human interleukin 4  
CC receptor-alpha gene (IL4R-alpha; see AAF57718 for the reference  
CC

CC sequence). Polynucleotides comprising polymorphic gene variants are  
CC useful for therapeutic purposes. For example, where a patient may benefit  
CC from expression of a particular IL4Ralpha protein isoform, an expression  
CC vector encoding the isoform may be administered to the patient. It may  
CC desirable to decrease or block expression of a particular IL4Ralpha  
CC isogene, which may be done by turning off by transforming a targeted  
CC organ, tissue or cell population with an expression vector that expresses  
CC high levels of untranslatable mRNA for the isogene. Specific therapeutics  
CC identified by these methods may be useful for allergic diseases. The  
CC present sequence is a probe for human IL4R-alpha  
XX Sequence 15 BP; 1 A; 4 C; 5 G; 5 T; 0 U; 0 Other;  
SQ  
Query Match 37.9%; Score 11; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 81;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CACCTGCTGTG 16  
DB 1 CACCTGCTGTG 11  
RESULT 69  
ABA99295/c  
ID ABA99295 standard; DNA; 15 BP.  
XX  
AC ABA99295;  
XX  
DT 13-MAY-2002 (first entry)  
XX  
DE Human ALDH5 allele-specific oligonucleotide SEQ ID No 15.  
XX  
KW ALDH5; human; gene; polymorphism; haplotype; aldehyde dehydrogenase 5;  
KW binding affinity; drug targeting; alcoholism; alcohol-induced disorder;  
KW antialcoholic; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200192279-A2.  
XX  
PD 06-DEC-2001.  
XX  
PF 29-MAY-2001; 2001WO-US017253.  
XX  
PR 26-MAY-2000; 2000US-0207508P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Duda A, Finkel K, Kazemi A, Messer C, Sanchis A;  
XX WPI; 2002-122054/16.  
DR  
XX New genetic variants with polymorphisms in the aldehyde dehydrogenase 5  
XX (ALDH5) gene, useful for studying the function of ALDH5, and for  
PT expressing ALDH5 protein which is useful in screening drugs for treating  
PT ALDH5-related diseases.  
XX  
PS Claim 17; Page 77; 96pp; English.  
XX  
CC This invention describes a novel isolated genes and haplotypes of the  
CC human aldehyde dehydrogenase 5 (ALDH5) gene containing polymorphic sites.  
CC The polymorphic ALDH5 variant is useful in studying the effect of the  
CC variation on the biological activity of ALDH5 and on the binding affinity  
CC of candidate drugs targeting ALDH5 for the treatment of alcoholism and  
CC alcohol-induced disorders. Polynucleotides comprising a polymorphic gene  
CC variant or fragment may be used for therapeutic purposes. ALDH5 protein  
CC isoforms may be used in assays to measure the binding affinities of one  
CC or more candidate drugs targeting the ALDH5 protein. ALDH5 proteins may  
CC be used to generate antibodies. Haplotyping method can be used by  
CC scientists to validate ALDH5 as a candidate target for treating a  
CC specific condition or disease predicted to be associated with ALDH5  
CC activity, and in the design of clinical trials of candidate drugs for  
CC treating a specific condition or disease predicted to be associated with



CC ALDH5 activity. Information on polymorphisms on the ALDH5 gene can be  
CC applied for studying the biological function of ALDH5 as well as in  
CC identifying drugs targeting this protein for the treatment of disorders  
CC related to its abnormal expression or function. The products of the  
CC invention have antialcoholic activity. This sequence represents a human  
CC ALDH5 allele-specific oligonucleotide described in the disclosure of the  
CC invention  
XX  
SQ Sequence 15 BP; 3 A; 4 C; 4 G; 3 T; 0 U; 1 Other;  
  
Query Match 37.9%; Score 11; DB 1; Length 15;  
Best Local Similarity 84.6%; Pred. No. 81;  
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 CATCCACCTGCTG 14  
|||||:|||||  
Db 14 CATCCAYGTGCTG 2  
  
RESULT 70  
ABL45833  
ID ABL45833 standard; DNA; 15 BP.  
XX  
AC ABL45833;  
XX  
DT 26-APR-2002 (first entry)  
XX  
DE Human EDG6 gene allele specific primer SEQ ID NO: 27.  
XX  
KW Human; endothelial differentiation, G-protein coupled receptor 6; EDG6;  
KW haplotype; cancer; angiogenesis; inflammation; chromosome 19p13.3;  
KW cytostatic; antiinflammatory; gene therapy; SNP;  
KW single nucleotide polymorphism; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200206446-A2.  
XX  
PD 24-JAN-2002.  
XX  
PF 17-JUL-2001; 2001WO-US022523.  
XX  
PR 17-JUL-2000; 2000US-0218727P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Kliem SE, Koshiy B;  
XX  
DR WPI; 2002-171804/22.  
XX  
PT New genetic variants of endothelial differentiation, G-protein coupled  
PT receptor-6 gene for studying expression, function of the gene and  
PT expressing EDG6 protein for use in screening drugs to treat cancer,  
PT inflammation.  
XX  
PS Claim 16; Page 13; 111pp; English.  
XX  
CC The present invention provides the gene, protein and cDNA sequences of  
CC the human endothelial differentiation, G-protein coupled receptor 6  
CC (EDG6). Also identified are single nucleotide polymorphisms (SNPs) found  
CC within the sequences. The sequences can be used in the identification of  
CC the haplotype of an individual, and in the treatment of cancer,  
CC angiogenesis and inflammation. The present sequence is an allele specific  
CC primer for the EDG6 gene, which is found on chromosome 19p13.3  
XX  
SQ Sequence 15 BP; 1 A; 4 C; 4 G; 5 T; 0 U; 1 Other;  
  
Query Match 37.9%; Score 11; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 81;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 8 CCTGCTGTGTG 18  
|||||

Db 1 CCTGCTGTGTG 11  
  
RESULT 71  
AAS16726/c  
ID AAS16726 standard; DNA; 15 BP.  
XX  
AC AAS16726;  
XX  
DT 14-FEB-2002 (first entry)  
XX  
DE Human APOA4 allele specific oligonucleotide, ASO, probe #9.  
XX  
KW Human; ss; APOA4; apolipoprotein A-IV; antiatherosclerotic; cardiant;  
KW haplotype; chromosome 11q23-qter; coronary heart disease; obesity;  
KW atherosclerosis; probe.  
XX  
OS Homo sapiens.  
XX  
PN WO200177124-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 03-APR-2001; 2001WO-US010670.  
XX  
PR 05-APR-2000; 2000US-0194362P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Bentivegna SC, Choi JY, Kliem SE, Koshiy B;  
XX  
DR WPI; 2002-041281/05.  
XX  
PT New haplotypes of the human apolipoprotein A-IV gene, useful to diagnose  
PT and treat disorders associated with its abnormal expression or function  
PT such as coronary artery disease.  
XX  
PS Claim 16; Page 15; 71pp; English.  
XX  
CC The invention relates to haplotyping the human apolipoprotein A-IV  
CC (APOA4) gene of an individual, comprising determining if the individual  
CC has one of the APOA4 haplotypes or haplotype pairs fully defined in the  
CC specification. Also disclosed are genotyping oligonucleotides (or allele  
CC specific oligonucleotides, ASO) as well as methods for correlating a  
CC particular haplotype pair with a trait e.g. obesity, in a population. The  
CC APOA4 gene is located on chromosome 11q23-qter. The methods of the  
CC invention are useful to diagnose and develop treatment for disorders  
CC associated with abnormal APOA4 expression or function, for example  
CC coronary heart disease and atherosclerosis. The APOA4 isogenes and  
CC screened compounds are useful for the treatment of disorders associated  
CC with abnormal APOA4 expression or function such as coronary artery  
CC disease. The present sequence is an APOA4 allele specific  
CC oligonucleotide, ASO, probe used to detect an APOA4 polymorphism  
XX  
SQ Sequence 15 BP; 4 A; 3 C; 6 G; 1 T; 0 U; 1 Other;  
  
Query Match 37.9%; Score 11; DB 1; Length 15;  
Best Local Similarity 84.6%; Pred. No. 81;  
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 CATCCACCTGCTG 14  
|||||:|||||  
Db 15 CCTCCACYTGTGCTG 3  
  
RESULT 72  
AAL39723  
ID AAL39723 standard; DNA; 15 BP.  
XX  
AC AAL39723;  
XX  
DT 05-SEP-2002 (first entry)  
XX



DE SMOH polymorphism detecting primer SEQ ID No 38.  
XX  
KW Cytostatic; polymorphic variant; single nucleotide polymorphism; SMOH;  
KW human smoothened Drosophila homologue; basal cell carcinoma; BCC;  
KW gene therapy; antisense gene therapy; PCR; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200229004-A2.  
XX  
PD 11-APR-2002.  
XX  
XX 04-OCT-2001; 2001WO-US031304.  
PF  
XX 04-OCT-2000; 2000US-0237871P.  
PR  
XX (GENA-) GENAISSANCE PHARM INC.  
PA  
XX Bentivegna SC, Choi JY, Koshy B, Lee HH, Sausker EA;  
PI  
XX WPI; 2002-519113/55.  
DR  
XX New genetic variants of smoothened Drosophila homolog (SMOH) gene useful  
PT for therapeutic purposes and for expressing SMOH protein useful in  
PT identifying drugs to treat basal cell carcinomas.  
XX  
PS Claim 15; Page 14; 179pp; English.  
XX  
CC The invention relates to an isolated polynucleotide comprising a sequence  
CC which is a polymorphic variant of a reference sequence for the human  
CC smoothened Drosophila homologue (SMOH) gene or its fragment, or a  
CC polymorphic variant of a reference sequence for a SMOH cDNA or its  
CC fragment. A new isolated polypeptide is useful for screening for drugs  
CC targeting the polypeptide. A new method is useful for identifying an  
CC association between a trait such as a clinical response to a drug  
CC targeting SMOH and a haplotype or haplotype pair of SMOH gene. The  
CC methods have applicability in developing diagnostic tests and therapeutic  
CC treatments for basal cell carcinomas (BCCs). The isolated polynucleotide  
CC is useful for studying the expression and function of SMOH and expressing  
CC SMOH protein for use in screening for candidate drugs to treat diseases  
CC related to SMOH activity. The polymorphism and haplotype data are useful  
CC for validating whether SMOH is a suitable target for drugs to treat BCCs,  
CC screening for the drugs and reducing bias in clinical trials of the  
CC drugs. The isolated polynucleotide is useful for therapeutic purposes.  
CC The new method, an oligonucleotide and kit of the invention are useful  
CC for determining whether an individual has one of the haplotypes or the  
CC haplotype pairs. The polynucleotides of the invention can be used to  
CC treat disorders by gene therapy and antisense gene therapy. This  
CC polynucleotide sequence represents a primer used for detecting human  
CC smoothened Drosophila homologue gene polymorphisms of the invention  
XX  
SQ Sequence 15 BP; 0 A; 5 C; 5 G; 4 T; 0 U; 1 Other;  
Query Match 37.9%; Score 11; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 81;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 CCTGCTGTGTG 18  
| | | | | | | | | |  
Db 2 CCTGCTGTGTG 12  
RESULT 73  
ACF57574/c  
ID ACF57574 standard; DNA; 15 BP.  
XX  
AC ACF57574;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Human ALDOB gene allele-specific probe SEQ ID NO: 25.  
XX  
KW Human; ALDOB; fructose-bisphosphate aldolase B; SNP;

KW single nucleotide polymorphism; primer; probe; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2003091454-A1.  
XX  
PD 06-NOV-2003.  
XX  
PF 26-APR-2002; 2002WO-US013328.  
XX  
PR 26-APR-2002; 2002WO-US013328.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Chew A, Kazemi A, Koshy B;  
XX WPI; 2003-877338/81.  
DR  
XX Claim 39; Page 14; 0pp; English.  
PS  
XX The present invention provides the protein and coding sequences of human  
CC fructose-bisphosphate aldolase B (ALDOB) and single nucleotide  
CC polymorphisms (SNPs) which have been identified in each sequence. The  
CC method of haplotyping the sequences is useful for haplotyping the  
CC fructose-bisphosphate aldose B (ALDOB) gene of an individual or for  
CC validating the ALDOB protein as a candidate target for treating a medical  
CC condition predicted to be associated with ALDOB activity. The present  
CC sequence is an allele-specific primer/probe used to identify the  
CC haplotype of the human ALDOB gene in the exemplification of the invention  
XX  
SQ Sequence 15 BP; 4 A; 3 C; 2 G; 5 T; 0 U; 1 Other;  
Query Match 37.9%; Score 11; DB 1; Length 15;  
Best Local Similarity 84.6%; Pred. No. 81;  
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 7 ACCTGCTGTGTGA 19  
| | | | | | | | | |  
Db 15 AACTGCTKTGTGA 3  
RESULT 74  
ADQ30419/c  
ID ADQ30419 standard; DNA; 15 BP.  
XX  
AC ADQ30419;  
XX  
DT 09-SEP-2004 (first entry)  
XX  
DE Human VR1 exon 1d transcription factor binding fragment #138.  
XX  
KW ds; VR1 receptor; vanilloid receptor type 1; modulator;  
KW pain transmission; primary sensory neuron; transcription factor;  
KW detection; MZF1; NFkappaB; NFAT; GATA1; sensitivity disorder; analgesia;  
KW hypalgesia; hyperalgesia; neuralgia; myalgia; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2004053120-A2.  
XX  
PD 24-JUN-2004.  
XX  
PF 01-DEC-2003; 2003WO-EP013522.  
XX  
PR 09-DEC-2002; 2002DE-01057421.  
XX  
PA (CHEF ) GRUENENTHAL GMBH.  
XX  
PI Weihe E, Bieller A, Schaefer MKH;  
XX  
DR WPI; 2004-468868/44.  
XX  
PT New nucleic acid that modulates expression of the vanilloid receptor-1,

PT useful for control of pain or sensitivity disorders, comprises sequences  
PT from control regions of the receptor gene.  
PS Disclosure; Page 54; 68pp; German.  
XX This invention describes a novel nucleic acid containing a specific  
CC segment having at least one region that modulates expression of the VR1  
CC (vanilloid receptor type 1) receptor, or a functional derivative, allele  
CC or fragment of this region, or a sequence that hybridises to it under  
CC standard conditions. The VR1 modulator is derived from one or more of  
CC positions 221931-223344 of GenBank AL670399, 31673-36359 of AL663116, or  
CC 44731-43231 or 36616-33151 of AF168787 and is involved in transmission of  
CC pain, particularly in primary sensory neurons. The invention also  
CC describes a vector that contains the VR1 modulator, host cells containing  
CC this vector (other than human germ or embryonal stem cells) and a method  
CC for modulating expression of the VR1 receptor by introducing the  
CC modulator or the vector into a cell that contains the VR1 gene. The  
CC products of the invention are used for detecting a transcription factor  
CC from its binding to a regulatory sequence (or a double-stranded  
CC oligonucleotide fragment of it), e.g. by Western blotting or enzyme-  
CC linked immunosorbant assay, particularly for diagnosis of diseases  
CC associated with overexpression or underexpression of the transcription  
CC factor. The region that modulates VR1 receptor expression includes a  
CC binding site for a transcription factor, e.g. MZF1, NFKappaB, NFAT or  
CC GATA1. The nucleic acids of the invention, or vectors containing them,  
CC are used for prevention or treatment of pain, also for treating  
CC sensitivity disorders, e.g. analgesia, hypalgesia or hyperalgesia, also  
CC neuralgia and myalgia, that are associated with activity of the VR1  
CC receptor. This sequence represents a fragment of human VR1 exon 1d DNA  
CC which is capable of binding to a transcription factor.  
XX  
SQ Sequence 15 BP; 4 A; 1 C; 8 G; 2 T; 0 U; 0 Other;  
  
Query Match 37.9%; Score 11; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 81;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 CATCCACCTGC 12  
Db 14 CATCCACCTGC 4  
  
RESULT 75  
AAV92814  
ID AAV92814 standard; RNA; 14 BP.  
XX  
AC AAV92814;  
XX  
DT 18-FEB-1999 (first entry)  
XX  
DE Human A-raf target sequence nucleotide position 1828.  
XX  
KW Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;  
KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;  
KW screening; identification; synthesis; deprotection; purification; cancer;  
KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;  
KW restenosis; rheumatoid arthritis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9850530-A2.  
XX  
PD 12-NOV-1998.  
XX  
PF 05-MAY-1998; 98WO-US009249.  
XX  
PR 09-MAY-1997; 97US-0046059P.  
PR 09-JUN-1997; 97US-0049002P.  
PR 03-JUL-1997; 97US-0051718P.  
PR 22-AUG-1997; 97US-0056808P.  
PR 02-OCT-1997; 97US-0061321P.  
PR 02-OCT-1997; 97US-0061324P.  
PR 05-NOV-1997; 97US-0064866P.

PR 19-DEC-1997; 97US-0068212P.  
XX (RIBO-) RIBOZYME PHARM INC.  
PA  
PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;  
PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;  
PI Thompson J, Workman CT, Beaudry A, Sweedler D;  
XX  
XX WPI; 1999-009494/01.  
XX  
PT Identifying new catalytic nucleic acid that modulates selected processes  
PT - especially ribozymes that cleave Raf RNA for treating cancer,  
PT restenosis, and also new ribozymes and modified nucleoside triphosphates  
PT used as antiviral agents and synthons.  
XX  
PS Claim 179; Page 164; 259pp; English.  
XX  
CC A method has been developed for the identification of a nucleic acid  
CC capable of modulating a process in a biological system. The method  
CC comprises: (a) introducing into the system a random library of nucleic  
CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising  
CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC  
CC in systems where modulation has occurred and/or determining the sequence  
CC of at least part of the SBDs in such systems. Nucleic acid molecules with  
CC endonuclease activity and catalytic activity, from the present invention,  
CC are used to modulate gene expression in plant and mammalian cells and to  
CC cleave target nucleic acid, particularly for treating systemic diseases  
CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic  
CC ascites and infection. They may also be used to detect genetic drift and  
CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs  
CC with RNA-cleaving activity that modulate expression of the Raf gene, are  
CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or  
CC generally any condition associated with the level of c-raf. Introduction  
CC of sugar/phosphate modifications increases stability against nuclease and  
CC activity. AAV90922 to AAV93877 represent NACs that can be used in the  
CC method, specifically for modulating the expression of a Raf gene  
XX  
SQ Sequence 14 BP; 1 A; 5 C; 4 G; 0 T; 4 U; 0 Other;  
  
Query Match 37.2%; Score 10.8; DB 1; Length 14;  
Best Local Similarity 57.1%; Pred. No. 83;  
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
  
QY 6 CACCTGCTGTGTGA 19  
Db 1 CGCCUGCUGUCUGA 14  
  
RESULT 76  
AAV48782  
ID AAV48782 standard; DNA; 15 BP.  
XX  
AC AAV48782;  
XX  
DT 15-OCT-1998 (first entry)  
XX  
DE ErbB-2 gene antisense oligonucleotide ErbB-2-74.  
XX  
KW ErbB-2; antisense oligonucleotide; modulate; gene expression; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN EP856579-A1.  
XX  
PD 05-AUG-1998.  
XX  
PF 31-JAN-1997; 97EP-00101531.  
XX  
PR 31-JAN-1997; 97EP-00101531.  
XX  
PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
XX

PI Schlingensiepen K, Brysch W;  
XX WPI; 1998-400910/35.  
DR  
XX  
PT Preparation of antisense oligo:nucleotide(s) which lack long runs of  
PT consecutive guanosine or inosine - and have specific ratio of residues  
PT able to form two or three hydrogen bonds, have greater activity and  
PT reduced toxicity, used therapeutically or to modulate growth of cells in  
PT culture.  
XX  
XX Claim 10; Fig 6b; 286pp; English.  
PS  
XX  
CC AAV48709-886 represent antisense oligonucleotides directed against the  
CC ErbB-2 gene. Of these, only oligonucleotides AAV48709-91 resulted in  
CC significant reduction in ErbB-2 protein expression, while  
CC oligonucleotides AAV48792-886 had little effect. The oligonucleotides  
CC exemplify the invention. The specification describes oligonucleotides  
CC that contain 8-30 nucleotides, which contain at most 8 nucleotides that  
CC can each form three hydrogen bonds to cytosine; do not contain four  
CC consecutive nucleotides able to form three H-bonds each to four  
CC consecutive cytosines; do not contain two sequences of three consecutive  
CC nucleotides each able to form three H-bonds to three consecutive  
CC cytosines, and the ratio between residues able to form two H-bonds each  
CC (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The  
CC oligonucleotides are used to modulate expression of genes, particularly  
CC the genes for p53, ErbB-2, junB, junD, TGF-beta 1 or beta 2 to control  
CC proliferation of primary cell cultures (e.g. bone marrow stem, liver or  
CC kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The  
CC oligonucleotides can also be used to analyse function of proteins (by  
CC altering their expression or activity) and therapeutically, e.g. in cases  
CC of cancer or (targeting TGF) for stimulating the immune system  
XX  
SQ Sequence 15 BP; 3 A; 5 C; 3 G; 4 T; 0 U; 0 Other;  
  
Query Match 37.2%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 89;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 CCATCCACCTGCTG 14  
Db | | | | | | | | | |  
1 CCATCCACTTGATG 14  
  
RESULT 77  
AAZ62474/c  
ID AAZ62474 standard; RNA; 15 BP.  
XX  
AC AAZ62474;  
XX  
DT 28-MAR-2000 (first entry)  
XX  
DE Substrate for HH ribozyme HCV-1282 which cleaves HCV RNA at nt. 1282.  
XX  
KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;  
KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;  
KW autoimmune disease; ss.  
XX  
OS Hepatitis C virus.  
OS  
PN WO9955847-A2.  
XX  
PD 04-NOV-1999.  
XX  
PF 26-APR-1999; 99WO-US009027.  
XX  
PR 27-APR-1998; 98US-0083217P.  
PR 18-SEP-1998; 98US-0100842P.  
PR 25-FEB-1999; 99US-00257608.  
PR 23-MAR-1999; 99US-00274553.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;

XX WPI; 2000-062023/05.  
DR  
XX  
PT Novel ribozymes for the treatment of diseases and conditions related to  
PT hepatitis C infection.  
XX  
PS Claim 1; Page 52; 123pp; English.  
XX  
CC The present sequence represents the preferred target sequence of an  
CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves  
CC the Hepatitis C virus (HCV) RNA sequence at the base position given in  
CC the descriptor line. The HCV sequence was screened for optimal ribozyme  
CC target sites using a computer folding algorithm and regions of the mRNA  
CC which did not form secondary folding structures and contained potential  
CC ribozyme cleavage sites were identified. Ribozymes were synthesised to  
CC target these sites and their activities optimised by either varying the  
CC length of the binding arms or by modification to prevent degradation by  
CC nucleases. The ribozymes of the invention inhibit gene expression and/or  
CC viral replication, and are used to treat diseases associated with  
CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and  
CC hepatocellular carcinoma. The ribozymes may be used in combination with  
CC interferon to treat HCV infection, other infectious diseases, autoimmune  
CC diseases, and cancer  
XX  
SQ Sequence 15 BP; 4 A; 4 C; 3 G; 0 T; 4 U; 0 Other;  
  
Query Match 37.2%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 89;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 16 GTGACCTGGTAAAT 29  
Db | | | | | | | | | |  
15 GTGACCTGATACAT 2  
  
RESULT 78  
AAH18890  
ID AAH18890 standard; DNA; 15 BP.  
XX  
AC AAH18890;  
XX  
DT 21-JUN-2001 (first entry)  
XX  
DE UCP3 polymorphism detection allele specific primer #3.  
XX  
KW UCP3; uncoupling protein 3; polymorphism; obesity; diabetes mellitus; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200118232-A2.  
XX  
PD 15-MAR-2001.  
XX  
PF 08-SEP-2000; 2000WO-US024784.  
XX  
PR 08-SEP-1999; 99US-0152789P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
PA (STEP/) STEPHENS J C.  
XX  
PI Chew A, Choi JY, Denton RR, Nandabalan K;  
XX  
DR WPI; 2001-218562/22.  
XX  
PT Nucleic acids encoding uncoupling protein 3 (mitochondrial, proton  
PT carrier) (UCP3) proteins comprising single nucleotide polymorphisms,  
PT useful for the design of drugs for treating obesity.  
XX  
PS Claim 15; Page 22; 94pp; English.  
XX  
CC The present invention relates to the human uncoupling protein 3  
CC (mitochondrial, proton carrier) (UCP3) gene and polymorphisms. The  
CC polymorphisms are associated with obesity, especially diabetes mellitus

CC associated obesity. They polymorphisms may be identified and analysed to  
CC determine whether an individual is susceptible to obesity and may be used  
CC as the basis for targeted design of drugs to treat obesity. The present  
CC sequence was used in the identification and amplification of UCP3  
CC polymorphisms  
XX  
SQ Sequence 15 BP; 1 A; 8 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 37.2%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 89;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CCTGCTGTGTGACC 21  
||||| |||||  
Db 1 CCTGCCCTGTGACC 14

RESULT 79  
AAF52803  
ID AAF52803 standard; DNA; 15 BP.  
XX  
AC AAF52803;

XX  
DT 30-MAR-2001 (first entry)  
XX  
DE IGF-I oligonucleotide #3763.  
XX

KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
KW hyperneovascular condition; hyperplasia; kidney disease;  
KW neovascular condition of the retina; ss.  
XX

OS Homo sapiens.  
XX  
PN WO200078341-A1.  
XX

PD 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU000693.

XX 21-JUN-1999; 99US-0140345P.

XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wright CJ, Werther GA, Edmondson SR;

XX WPI; 2001-041421/05.

XX  
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
PT inhibits or reduces growth factor mediated cell proliferation and/or  
PT inflammation.

XX Example 8; Page 85; 201pp; English.

XX  
CC The present invention relates to a method for ameliorating the effects of  
CC skin disorders. The method comprises contacting the skin with an  
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
CC inhibiting or reducing growth factor mediated cell proliferation,  
CC inflammation and/or other disorders. The present sequence is an  
CC oligonucleotide which can be used to design the antisense

CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
CC F45161). The method is useful for ameliorating the effects of psoriasis,  
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
CC hyperneovascular condition such as a neovascular condition of the retina,  
CC brain or skin, growth factor-mediated malignancies, other sclerotic  
CC disease, kidney disease, hyperproliferation of the inside of blood

CC vessels or any other hyperplasia  
XX  
SQ Sequence 15 BP; 3 A; 2 C; 4 G; 6 T; 0 U; 0 Other;  
Query Match 37.2%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 89;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 TGCTGTGTGACCTG 23  
||||| |||||  
Db 2 TGCTGTTGAACTG 15

RESULT 80  
AAF45867/c  
ID AAF45867 standard; DNA; 15 BP.

XX AAF45867;

XX 30-MAR-2001 (first entry)

XX IGFBP2 oligonucleotide #706.

XX  
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
KW hyperneovascular condition; hyperplasia; kidney disease;  
KW neovascular condition of the retina; ss.  
XX

OS Homo sapiens.

XX WO200078341-A1.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU000693.

XX 21-JUN-1999; 99US-0140345P.

XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wright CJ, Werther GA, Edmondson SR;

XX WPI; 2001-041421/05.

XX  
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
PT inhibits or reduces growth factor mediated cell proliferation and/or  
PT inflammation.

XX Example 6; Page 38; 201pp; English.

XX  
CC The present invention relates to a method for ameliorating the effects of  
CC skin disorders. The method comprises contacting the skin with an  
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
CC inhibiting or reducing growth factor mediated cell proliferation,  
CC inflammation and/or other disorders. The present sequence is an  
CC oligonucleotide which can be used to design the antisense

CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
CC F45161). The method is useful for ameliorating the effects of psoriasis,  
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
CC hyperneovascular condition such as a neovascular condition of the retina,  
CC brain or skin, growth factor-mediated malignancies, other sclerotic  
CC disease, kidney disease, hyperproliferation of the inside of blood  
CC vessels or any other hyperplasia

XX Sequence 15 BP; 5 A; 3 C; 5 G; 2 T; 0 U; 0 Other;



Query Match 37.2%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 89;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 CTGCTGTGTGACCT 22  
Db 15 CTGCTCAGTGACCT 2

RESULT 81  
AAFS2804

ID AAF52804 standard; DNA; 15 BP.  
XX  
AC AAF52804;  
XX  
DT 30-MAR-2001 (first entry)  
XX  
DE IGF-I oligonucleotide #3764.  
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
KW hyperneovascular condition; hyperplasia; kidney disease;  
KW neovascular condition of the retina; ss.

OS Homo sapiens.  
XX  
PN WO200078341-A1.  
XX  
PD 28-DEC-2000.  
XX  
PF 21-JUN-2000; 2000WO-AU0000693.  
XX  
PR 21-JUN-1999; 99US-0140345P.  
XX  
PA (MURD-) MURDOCH CHILDRENS RES INST.  
XX  
PI Wraight CJ, Werther GA, Edmondson SR;  
XX  
DR WPI; 2001-041421/05.  
XX  
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
PT inhibits or reduces growth factor mediated cell proliferation and/or  
PT inflammation.

XX Example 8; Page 85; 201pp; English.  
XX  
CC The present invention relates to a method for ameliorating the effects of  
CC skin disorders. The method comprises contacting the skin with an  
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
CC inhibiting or reducing growth factor mediated cell proliferation,  
CC inflammation and/or other disorders. The present sequence is an  
CC oligonucleotide which can be used to design the antisense  
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
CC F45161). The method is useful for ameliorating the effects of psoriasis,  
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
CC hyperneovascular condition such as a neovascular condition of the retina,  
CC brain or skin, growth factor-mediated malignancies, other sclerotic  
CC disease, kidney disease, hyperproliferation of the inside of blood  
CC vessels or any other hyperplasia  
XX  
SQ Sequence 15 BP; 3 A; 2 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 37.2%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 89;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 TGCTGTGTGACCTG 23  
Db 1 TGCTGTTTGAAC TG 14

RESULT 82  
AAF45868/C  
ID AAF45868 standard; DNA; 15 BP.  
XX  
AC AAF45868;  
XX  
DT 30-MAR-2001 (first entry)  
XX  
DE IGFBP2 oligonucleotide #707.  
XX

KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
KW hyperneovascular condition; hyperplasia; kidney disease;  
KW neovascular condition of the retina; ss.

OS Homo sapiens.  
XX  
PN WO200078341-A1.  
XX  
PD 28-DEC-2000.  
XX  
PF 21-JUN-2000; 2000WO-AU0000693.  
XX  
PR 21-JUN-1999; 99US-0140345P.  
XX  
PA (MURD-) MURDOCH CHILDRENS RES INST.  
XX  
PI Wraight CJ, Werther GA, Edmondson SR;  
XX  
DR WPI; 2001-041421/05.  
XX  
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
PT inhibits or reduces growth factor mediated cell proliferation and/or  
PT inflammation.

XX Example 6; Page 38; 201pp; English.  
XX  
CC The present invention relates to a method for ameliorating the effects of  
CC skin disorders. The method comprises contacting the skin with an  
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
CC inhibiting or reducing growth factor mediated cell proliferation,  
CC inflammation and/or other disorders. The present sequence is an  
CC oligonucleotide which can be used to design the antisense  
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
CC F45161). The method is useful for ameliorating the effects of psoriasis,  
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
CC hyperneovascular condition such as a neovascular condition of the retina,  
CC brain or skin, growth factor-mediated malignancies, other sclerotic  
CC disease, kidney disease, hyperproliferation of the inside of blood  
CC vessels or any other hyperplasia  
XX  
SQ Sequence 15 BP; 4 A; 4 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 37.2%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 89;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 CTGCTGTGTGACCT 22  
Db 14 CTGCTCAGTGACCT 1



RESULT 83  
ADV35524/c  
ID ADV35524 standard; RNA; 15 BP.  
XX  
AC ADV35524;  
XX  
DT 10-FEB-2005 (first entry)  
XX  
DE Human anti-HER2 NCH ribozyme substrate sequence #155.  
XX  
KW Enzymatic nucleic acid molecule; gene expression; down regulation;  
KW protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase;  
KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;  
KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;  
KW amberzyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;  
KW diabetes; obesity; cardiac disease; heart disease; age-related disease;  
KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;  
KW ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200116312-A2.  
XX  
PD 08-MAR-2001.  
XX  
PF 30-AUG-2000; 2000WO-US023998.  
XX  
PR 31-AUG-1999; 99US-0151713P.  
PR 27-SEP-1999; 99US-00406643.  
PR 27-SEP-1999; 99US-0156236P.  
PR 27-SEP-1999; 99US-0156467P.  
PR 08-NOV-1999; 99US-00436430.  
PR 06-DEC-1999; 99US-0169100P.  
PR 29-DEC-1999; 99US-00474432.  
PR 29-DEC-1999; 99US-0173612P.  
PR 30-DEC-1999; 99US-00476387.  
PR 04-FEB-2000; 2000US-00498824.  
PR 20-MAR-2000; 2000US-00531025.  
PR 14-APR-2000; 2000US-0197769P.  
PR 23-MAY-2000; 2000US-00578223.  
PR 09-AUG-2000; 2000US-00636385.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Mcswiggen J, Usman N, Blatt L, Beigelman L, Burgin A;  
PI Karpeisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;  
PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;  
XX  
DR WPI; 2001-244406/25.  
XX  
PT Enzymatic nucleic acid molecules able to cleave separate RNA molecules  
PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,  
PT obesity and heart disease.  
XX  
PS Example 7; Page 474; 717pp; English.  
XX  
CC The present invention relates to the use of enzymatic nucleic acid  
CC molecules (e.g. ribozymes) to modulate gene expression. The invention  
CC also methods for their use to down regulate or inhibit the expression of  
CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine  
CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C  
CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor  
CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),  
CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic  
CC nucleic acid molecules used to inhibit the expression of the said genes  
CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,  
CC zinzyme, and/or DNAzyme motifs. The methods of the invention are useful  
CC for treating cancer, in particular breast cancer, Alzheimer's disease,  
CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related  
CC diseases, hepatitis B infections, and hepatitis and hepatocellular

carcinoma. The enzymatic nucleic acid molecules can also be used as  
diagnostic tools to examine genetic drift and mutations within diseased  
cells and to detect the presence of specific RNA in a cell. The present  
sequence represents a substrate/target sequence for an anti-HER2 NCH  
ribozyme used in the examples of the present invention. Note: Some SEQ ID  
Nos are repeated more than once in the specification, but these have  
different sequences associated with them.  
SQ Sequence 15 BP; 4 A; 5 C; 4 G; 0 T; 2 U; 0 Other;  
  
Query Match 37.2%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 89;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 9 CTGCTGTGTGACCT 22  
Db 14 CTGCAGTGGGACCT 1  
||||| ||||| |||||  
  
RESULT 84  
ADV35522/c  
ID ADV35522 standard; RNA; 15 BP.  
XX  
AC ADV35522;  
XX  
DT 10-FEB-2005 (first entry)  
XX  
DE Human anti-HER2 NCH ribozyme substrate sequence #153.  
XX  
KW Enzymatic nucleic acid molecule; gene expression; down regulation;  
KW protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase;  
KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;  
KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;  
KW amberzyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;  
KW diabetes; obesity; cardiac disease; heart disease; age-related disease;  
KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;  
KW ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200116312-A2.  
XX  
PD 08-MAR-2001.  
XX  
PF 30-AUG-2000; 2000WO-US023998.  
XX  
PR 31-AUG-1999; 99US-0151713P.  
PR 27-SEP-1999; 99US-00406643.  
PR 27-SEP-1999; 99US-0156236P.  
PR 27-SEP-1999; 99US-0156467P.  
PR 08-NOV-1999; 99US-00436430.  
PR 06-DEC-1999; 99US-0169100P.  
PR 29-DEC-1999; 99US-00474432.  
PR 29-DEC-1999; 99US-0173612P.  
PR 30-DEC-1999; 99US-00476387.  
PR 04-FEB-2000; 2000US-00498824.  
PR 20-MAR-2000; 2000US-00531025.  
PR 14-APR-2000; 2000US-0197769P.  
PR 23-MAY-2000; 2000US-00578223.  
PR 09-AUG-2000; 2000US-00636385.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Mcswiggen J, Usman N, Blatt L, Beigelman L, Burgin A;  
PI Karpeisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;  
PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;  
XX  
DR WPI; 2001-244406/25.  
XX  
PT Enzymatic nucleic acid molecules able to cleave separate RNA molecules  
PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,

PT obesity and heart disease.

XX Example 7; Page 474; 717pp; English.

PS The present invention relates to the use of enzymatic nucleic acid

XX molecules (e.g. ribozymes) to modulate gene expression. The invention

CC also methods for their use to down regulate or inhibit the expression of

CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine

CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C

CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor

CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),

CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic

CC nucleic acid molecules used to inhibit the expression of the said genes

CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,

CC zinzyme, and/or DNAzyme motifs. The methods of the invention are useful

CC for treating cancer, in particular breast cancer, Alzheimer's disease,

CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related

CC diseases, hepatitis B infections, and hepatitis and hepatocellular

CC carcinoma. The enzymatic nucleic acid molecules can also be used as

CC diagnostic tools to examine genetic drift and mutations within diseased

CC cells and to detect the presence of specific RNA in a cell. The present

CC sequence represents a substrate/target sequence for an anti-HER2 NCH

CC ribozyme used in the examples of the present invention. Note: Some SEQ ID

CC Nos are repeated more than once in the specification, but these have

CC different sequences associated with them.

XX

SQ Sequence 15 BP; 3 A; 6 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 37.2%; Score 10.8; DB 1; Length 15;

Best Local Similarity 85.7%; Pred. No. 89;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 TGCTGTGTGACCTG 23

DB 15 TGCAGTGGGACCTG 2

RESULT 85

ABX00325/c

ID ABX00325 standard; RNA; 15 BP.

XX

AC ABX00325;

XX

DT 23-DEC-2002 (first entry)

XX

DE Hepatitis C virus substrate #107 for HCV hammerhead ribozyme #107.

XX

KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;

KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;

KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;

KW type I interferon; interferon alpha; interferon beta; cytostatic;

KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;

KW substrate; hammerhead ribozyme; HH ribozyme; ss.

XX

OS Hepatitis C virus.

XX

PN US2002082225-A1.

XX

PD 27-JUN-2002.

XX

PF 23-MAR-1999; 99US-00274553.

XX

PR 23-MAR-1999; 99US-00274553.

XX

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.

PA (ROBE/) ROBERTS B.

PA (PAVC/) PAVCO P A.

PA (MACE/) MACEJACK D.

XX

PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;

XX WPI; 2002-617759/66.

DR

XX New ribozymes targeting RNA derived from hepatitis C virus inhibit viral

PT replication and are useful to treat hepatitis C virus infections and

PT cirrhosis, liver failure or hepatocellular carcinoma.

XX

PS Claim 1; Page 24; 80pp; English.

XX

CC The present invention relates to enzymatic nucleic acids which

CC specifically cleave RNA derived from Hepatitis C virus (HCV). The

CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin

CC (Hp) motif where the binding arms comprise sequences complementary to one

CC of the substrate sequences defined in the specification. The HCV

CC ribozymes are useful for modulating the expression and/or replication of

CC HCV. They can be used to treat cirrhosis, liver failure and/or

CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating

CC a condition associated with HCV infection in conjunction with one or more

CC other drug therapies, particularly type I interferon, especially

CC interferon alpha, beta or gamma or consensus interferon. The present

CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:

CC Some of the sequence data for this patent did not form part of the

CC printed specification. The complete sequence data for this patent was

CC obtained in electronic format directly from the USPTO web site at

CC seqdata.uspto.gov/psipsDIDEntry.html

XX

SQ Sequence 15 BP; 4 A; 4 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 37.2%; Score 10.8; DB 1; Length 15;

Best Local Similarity 85.7%; Pred. No. 89;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 GTGACCTGGTAAAT 29

DB 15 GTGACCTGATACAT 2

RESULT 86

AEB74235/c

ID AEB74235 standard; RNA; 15 BP.

XX

AC AEB74235;

XX

DT 22-SEP-2005 (first entry)

XX

DE Hepatitis C virus hammerhead ribozyme substrate sequence.

XX

KW ribozyme; enzymatic nucleic acid molecule; hepatitis C virus infection;

KW antiviral; gene therapy; substrate; ss.

XX

OS Hepatitis C virus.

XX

PN US2002013458-A1.

XX

PD 31-JAN-2002.

XX

PF 15-FEB-2000; 2000US-00504231.

XX

PR 23-MAR-1999; 99US-00274553.

XX

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.

PA (ROBE/) ROBERTS E.

PA (PAVO/) PAVO P A.

PA (MACE/) MACEJACK D.

XX

PI Blatt L, Mcswiggen JA, Roberts E, Pavo PA, Macejack D;

XX WPI; 2002-215899/27.

DR

XX New enzymatic nucleic acid molecule, which specifically cleaves minus

PT strand RNA derived from hepatitis C virus, useful for modulating the

PT expression and/or replication of hepatitis C virus.

XX

PS Example 1; Page 25; 65pp; English.

XX The invention relates to an enzymatic nucleic acid molecule which  
CC specifically cleaves minus strand RNA derived from hepatitis C virus  
CC (HCV). The binding arms of the molecule comprise ribozyme sequences. The  
CC molecule is selected from inozyme, G-cleaver, DNAzyme, Amberzyme, and  
CC Zinzyme motifs. Also described: (1) a pharmaceutical composition  
CC comprising the novel enzymatic nucleic acid; (2) a mammalian cell  
CC including a nucleic acid sequence encoding at least one enzymatic  
CC comprising a nucleic acid sequence encoding at least one enzymatic  
CC nucleic acid molecule, in a manner, which allows expression of that  
CC molecule; (4) a mammalian cell including an expression vector of (3); (5)  
CC methods for treating cirrhosis, liver failure or hepatocellular carcinoma  
CC by administering to a patient the novel enzymatic nucleic acid or the  
CC vector of (3); (6) a method of treating a patient having a condition  
CC associated with HCV infection, by contacting cells of the patient with  
CC the nucleic acid molecule, and further employing one or more drug  
CC therapies; (7) a method for inhibiting HCV replication in a mammalian  
CC cell by administering the novel enzymatic nucleic acid; and (8) a method  
CC of cleaving a separate RNA molecule by contacting the novel enzymatic  
CC nucleic acid with the separate RNA molecule. The enzymatic nucleic acid  
CC is useful for modulating the expression and/or replication of hepatitis C  
CC virus (HCV), and for inhibiting the expression of HCV minus strand. The  
CC nucleic acid may also be used to treat or prevent the occurrence of a  
CC disease state in a patient. The present sequence represents an HCV  
CC hammerhead ribozyme target substrate sequence which is used in the  
CC exemplification of the present invention.  
XX  
SQ Sequence 15 BP; 4 A; 4 C; 3 G; 0 T; 4 U; 0 Other;  
  
Query Match 37.2%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 89;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 16 GTGACCTGGTAAAT 29  
Db 15 GTGACCTGATACAT 2  
  
RESULT 87  
ABL88273/c  
ID ABL88273 standard; DNA; 15 BP.  
XX  
AC ABL88273;  
XX  
DT 20-MAY-2002 (first entry)  
XX  
DE Human CHRNE allele-specific oligonucleotide (ASO) probe, SEQ ID NO:7.  
XX  
KW Human; cholinergic receptor nicotinic epsilon polypeptide; CHRNE;  
KW chromosome 17p13-12; acetylcholine receptor; AChR;  
KW neuromuscular junction; skeletal muscle; postnatal development;  
KW congenital myasthenic syndrome; CMS; haplotyping; genotyping; haplotype;  
KW genetic variant; single nucleotide polymorphism; SNP; gene therapy;  
KW drug screening; allele-specific oligonucleotide; ASO; probe; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200198316-A2.  
XX  
PD 27-DEC-2001.  
XX  
PF 20-JUN-2001; 2001WO-US019835.  
XX  
PR 20-JUN-2000; 2000US-0212870P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Amaro E, Bieglecki KM, Kliem SE, Koshy B, Tanguay DA;  
XX  
XX WPI; 2002-130787/17.  
XX  
PT Novel genetic variants of cholinergic receptor, nicotinic, epsilon  
PT polypeptide gene useful in studying expression and function of the

PT protein, and for screening drugs to treat diseases e.g. congenital  
PT myasthenic syndrome.  
XX  
PS Claim 17; Page 14; 104pp; English.  
XX  
CC The invention relates to a method for haplotyping the cholinergic  
CC receptor, nicotinic, epsilon polypeptide (CHRNE) gene (ABL88268) of an  
CC individual, and also describes 17 novel polymorphic sites within the  
CC human CHRNE gene. The CHRNE gene is located on chromosome 17p13-12 and  
CC contains 12 exons which encode a 493 amino acid protein (ABB49112). The  
CC CHRNE protein is one of the 5 subunits of mammalian acetylcholine  
CC receptors (AChRs) found at neuromuscular junctions in juveniles and  
CC adults, and is essential for the normal postnatal development of skeletal  
CC muscle. Mutations in the CHRNE gene are associated with congenital  
CC myasthenic syndrome (CMS). CHRNE gene sequences can therefore be used in  
CC gene therapy. The CHRNE gene is also useful for studying the expression  
CC and function of CHRNE, and in expressing CHRNE protein for use in  
CC screening for candidate drugs to treat diseases related to CHRNE. The  
CC method of the invention is useful for haplotyping the CHRNE gene in an  
CC individual, and can also be used in pharmaceutical research to validate  
CC CHRNE as a candidate target for, and in design of clinical trials of  
CC candidate drugs for, treating a specific condition drugs or disease  
CC predicted to be associated with CHRNE activity such as CMS. Polymorphisms  
CC in the target region may be determined by the use of allele-specific  
CC oligonucleotides (ASOs; ABL88370-ABL88320) as probes and primers, and by  
CC primer extension using oligonucleotide primers comprising sequences  
CC ABL88371-ABL88354. The CHRNE protein is useful for improving the  
CC efficiency and reliability of several steps in the discovery and  
CC development of drugs for treating diseases associated with CHRNE  
CC activity, and may be used to screen drugs which target CHRNE. Sequences  
CC ABL88270-ABL88286 represent specifically claimed allele-specific  
CC oligonucleotide (ASO) probes used for detecting polymorphisms in the  
CC CHRNE gene  
XX  
SQ Sequence 15 BP; 5 A; 5 C; 4 G; 0 T; 0 U; 1 Other;  
  
Query Match 36.6%; Score 10.6; DB 1; Length 15;  
Best Local Similarity 90.9%; Pred. No. 97;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 8 CCTGCTGTGTG 18  
Db 15 CCTGCTGYGTG 5  
  
RESULT 88  
ABK12178  
ID ABK12178 standard; DNA; 15 BP.  
XX  
AC ABK12178;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Human Tachykinin Receptor 1 allele specific oligonucleotide probe #8.  
XX  
KW Human; ss; probe; TACR1; Tachykinin receptor 1; chromosome 2; SNP;  
KW single nucleotide polymorphism; gene therapy; haplotype; pain;  
KW depression; vomiting; acute inflammatory diarrhoea; ASO;  
KW opiate addiction; drug screening; allele specific oligonucleotide.  
XX  
OS Homo sapiens.  
XX  
PN WO200216399-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 27-AUG-2001; 2001WO-US026663.  
XX  
PR 25-AUG-2000; 2000US-0227815P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Anastasio AE, Kazemi A;

XX WPI; 2002-280907/32.

XX Novel isolated polynucleotide which is a polymorphic variant of

PT tachykinin receptor 1 (TACR1) gene useful for expressing TACR1 protein

PT isoform used in screening drug candidates to treat pain, depression,

PT vomiting.

XX Claim 17; Page 14; 89pp; English.

XX The invention relates to an isolated polynucleotide sequence which

CC comprises a tachykinin receptor 1 (TACR1) isogene (SG) that is any one of

CC 16 SG as given in specification, where each SG comprises specific regions

CC of the TACR1 genomic DNA appearing as ABK12169, and is defined by

CC polymorphisms at positions (P) 3164, 3319, 3906, 4339, 4444, 92915,

CC 94601, 94821, 94892, 94960. Also included are fragments of the TACR1

CC isogenes and TACR1 cDNA, a transgenic non-human animal transformed with

CC the TACR1 isogene or coding region, haplotyping (or genotyping) the TACR1

CC of an individual by determining either the haplotype of one or both

CC copies of the TACR1 gene, predicting the haplotype pair for the TACR1

CC gene of an individual, identifying an association between a trait and a

CC haplotype pair, an isolated oligonucleotide for detecting the

CC polymorphisms, a computer system for storing and analysing polymorphism

CC data and a genome anthology for TACR1 gene. The TACR1 isogene is useful

CC for studying expression and function of TACR1 and expressing TACR1

CC protein for use in screening for candidate drugs to treat diseases

CC related to TACR1 activity. The polymorphism and haplotype data is useful

CC for validating whether TACR1 is a suitable target for drugs to treat

CC pain, depression, vomiting, acute inflammatory diarrhoea and opiate

CC addiction, screening for such drugs and reducing bias in clinical trials

CC of such drugs. The genotyping method is useful for determining whether an

CC individual has one of the haplotype pairs. The haplotyping method is

CC useful for improving efficiency and outcome of several steps in discovery

CC and development of drugs for treating the diseases. The haplotyping

CC method is also useful for validating TACR1 as a candidate target for

CC treating a specific condition or disease predicted to be associated with

CC TACR1 activity. The method is also useful for screening compounds to

CC treat a specific condition or disease predicted to be associated with

CC TACR1 activity. The methods are useful for identifying an association

CC between susceptibility to a disease, staging of a disease, or response to

CC a drug. The gene for TACR1 is located on human chromosome 2. The present

CC sequence is an allele specific oligonucleotide (ASO) probe used to detect

CC polymorphisms in the TACR1 gene

XX SQ Sequence 15 BP; 3 A; 3 C; 3 G; 5 T; 0 U; 1 Other;

Query Match 36.6%; Score 10.6; DB 1; Length 15;

Best Local Similarity 90.9%; Pred. No. 97;

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 TGCTGTGTGAC 20

Db 2 TGCTGKTGAC 12

RESULT 89

ACC70394/c

ID ACC70394 standard; DNA; 13 BP.

XX ACC70394;

XX 11-AUG-2003 (first entry)

DT Cytoprotective response element from a shear stress-regulated gene.

DE

XX Cytoprotective response element; CPRE; oxidative stress;

KW cytoprotective enzyme; hemodynamic shear stress; inflammatory disorder;

KW cardiovascular disease; hyperproliferative disorder; neoplasm;

KW lymphoblastic leukemia; skin cancer; radiation therapy;

KW shear stress-regulated gene; ss.

XX Unidentified.

OS

XX

PN WO2003033662-A2.

XX 24-APR-2003.

PD 16-OCT-2002; 2002WO-US033006.

XX 16-OCT-2001; 2001US-0329870P.

PR (ATHE-) ATHEROGENICS INC.

XX Kunsch C, Varner SE, Chen X, Luchoomun J;

PI WPI; 2003-403211/38.

XX Novel isolated cytoprotective response element nucleic acid for inducing

PT coordinate activation of genes that protect cells from damaging effects

PT of oxidative stress, e.g. during conditions of hemodynamic shear stress.

XX Claim 2; Fig 6; 133pp; English.

XX The present sequence represents a cytoprotective response element (CPRE).

CC The CPRE is an inducer of the coordinate activation of certain genes that

CC protect cells from damaging effects of oxidative stress. It is also a

CC regulator of cytoprotective effects and an inducer of expression of

CC cytoprotective enzymes. The CPRE is useful for inducing the coordinate

CC activation of certain genes that protect cells from damaging effects of

CC oxidative stress, for example during conditions of hemodynamic shear

CC stress. It is useful as a reagent for the identification of a compound

CC (preferably, a drug) with which it directly or indirectly interacts, or

CC for regulating cytoprotective effects by inducing the expression of

CC cytoprotective enzymes or other factors. A compound identified in this

CC way is useful for treating inflammatory disorders, cardiovascular

CC diseases, hyperproliferative disorders (such as neoplasms, lymphoblastic

CC leukemia, skin cancer, or to protect normal tissues and organs from the

CC damaging effects of chemotherapeutic drugs, radiation therapy and disease

CC processes

XX SQ Sequence 13 BP; 4 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 35.9%; Score 10.4; DB 1; Length 13;

Best Local Similarity 91.7%; Pred. No. 91;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTGCTGTGTGAC 20

Db 12 CTGCTGTGTGAC 1

RESULT 90

ADL72846

ID ADL72846 standard; DNA; 13 BP.

XX ADL72846;

AC 17-JUN-2004 (first entry)

DT CDNA tag for gene expression analysis method primer SEQ ID NO: 46.

XX ss; cDNA tag; gene expression; restriction enzyme; primer; PCR.

OS Synthetic.

XX WO2004024953-A1.

PN 25-MAR-2004.

XX 05-AUG-2003; 2003WO-JP009901.

XX 12-SEP-2002; 2002JP-00267163.

XX (KURE ) KUREHA CHEM IND CO LTD.

PA (YAMA/) YAMAMOTO M.

PA (YAMA/) YAMAMOTO N.



XX Yamamoto M, Yamamoto N, Hirose K, Sakai J;  
PI WPI; 2004-270062/25.  
XX  
DR Preparation of cDNA tags for identifying expressed genes, useful in  
PT analyzing gene expression, by providing complementary deoxyribonucleic  
PT acids and cleaving the cDNAs with a type II restriction enzyme.  
XX  
PS Example 1; Page 63; 70pp; English.  
XX  
CC The present invention relates to a method for the preparation of cDNA  
CC tags for identifying expressed genes, which comprises providing  
CC complementary deoxyribonucleic acids (cDNAs) and cleaving the cDNAs with  
CC a type II restriction enzyme to prepare cDNA fragments. The method is  
CC useful in the preparation of cDNA tags for identifying expressed genes.  
CC The methods and kits are useful in analyzing gene expression. The present  
CC sequence is a PCR primer for use in the method of the invention.  
XX  
SQ Sequence 13 BP; 2 A; 2 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 35.9%; Score 10.4; DB 1; Length 13;  
Best Local Similarity 91.7%; Pred. No. 91;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 TGTGTGACCTGG 24  
Db 2 TGTATGACCTGG 13  
||| |||||

RESULT 91  
AAQ78352/c  
ID AAQ78352 standard; DNA; 14 BP.  
XX  
AC AAQ78352;  
XX  
DT 25-MAR-2003 (revised)  
DT 27-JUN-1995 (first entry)  
XX  
DE Antisense oligonucleotide hybridising to TGF-beta gene.  
XX  
KW Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;  
KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;  
KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;  
KW immunosuppression; oligonucleotide; ss.  
XX  
OS Synthetic.  
XX  
PN WO9425588-A2.  
XX  
PD 10-NOV-1994.  
XX  
PF 29-APR-1994; 94WO-EP001362.  
XX  
PR 30-APR-1993; 93EP-00107089.  
PR 13-MAY-1993; 93EP-00107849.  
XX  
PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
XX  
PI Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;  
PI Bogdahn U;  
XX  
DR WPI; 1994-358266/44.  
XX  
PT New transforming growth factor beta antisense oligo:nucleotide(s) - for  
PT treating immunosuppression, tumours, etc.  
XX  
PS Claim 6; Page 24; 74pp; English.  
XX  
CC The antisense oligonucleotides are useful in the treatment of tumours in  
CC which expression of TGF-beta is of relevance for pathogenicity and/or  
CC inhibition of pathological angiogenesis. They are used especially for the  
CC treatment of the immunosuppressive effect of TGF-beta, augmentation of

CC the proliferation of cytotoxic lymphocytes, treatment of endogenous  
CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas  
CC and malignant gliomas, including glioblastomas, treatment and prophylaxis  
CC of skin carcinogenesis, and treatment of oesophageal and gastric  
CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESEQ files  
CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-  
CC beta 1. The sequences given in GENESEQ files AAQ78408-78487 are antisense  
CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate  
CC analogues. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 14 BP; 3 A; 1 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 35.9%; Score 10.4; DB 1; Length 14;  
Best Local Similarity 91.7%; Pred. No. 98;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCCACCTGC 12  
Db 13 CTATCCACCTGC 2  
|||||

RESULT 92  
AAV57016/c  
ID AAV57016 standard; cDNA; 14 BP.  
XX  
AC AAV57016;  
XX  
DT 25-MAR-2003 (revised)  
DT 21-DEC-1998 (first entry)  
XX  
DE Human Notch3 gene exon 8/intron 8 boundary sequence.  
XX  
KW Human; Notch3; transmembrane receptor; lateral inhibition; regulation;  
KW developmental cascade; neurogenic gene; mutant; neurological disorder;  
KW cerebral autosomal dominant arteriopathy; subcortical infarct; CADASIL;  
KW leukoencephalopathy; therapy; intron; exon; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT exon 1. .6  
FT /\*tag= a  
FT /number= 8  
FT intron 7. .14  
FT /\*tag= b  
FT /number= 8  
XX  
PN FR2751986-A1.  
XX  
PD 06-FEB-1998.  
XX  
PF 16-APR-1997; 97FR-00004680.  
XX  
PR 01-AUG-1996; 96FR-00009733.  
XX  
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
XX  
PI Tournier LE, Joutel A, Bousser MG, Bach JF;  
XX WPI; 1998-133138/13.  
DR  
XX Human Notch3 nucleic acids - and methods for identifying pre-disposition  
PT to cerebral autosomal dominant arteriopathy with sub-cortical infarcts  
PT and leukoencephalopathy.  
XX  
PS Example 3; Page 20; 45pp; French.  
XX  
CC This sequence represents the boundary between exon 8 and intron 8 of the  
CC human Notch3 gene. Notch3 is a transmembrane receptor protein involved in  
CC lateral inhibition and regulating developmental cascades of neurogenic  
CC genes. Mutated Notch3 proteins are thought to be involved in neurological  
CC disorders, especially of the cerebral autosomal dominant arteriopathy  
CC with subcortical infarcts and leukoencephalopathy (CADASIL) type.



CC Blocking expression of a mutated Notch3 gene or by substitution therapy  
CC with non-mutated Notch3 gene or protein can be used to treat CADASIL or  
CC related disorders. (Updated on 25-MAR-2003 to correct PI field.)  
XX  
SQ Sequence 14 BP; 1 A; 1 C; 9 G; 3 T; 0 U; 0 Other;  
  
Query Match 35.9%; Score 10.4; DB 1; Length 14;  
Best Local Similarity 91.7%; Pred. No. 98;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 CCATCCACCTGC 12  
Db 14 CCACCCACCTGC 3  
  
RESULT 93  
AAV92815  
ID AAV92815 standard; RNA; 14 BP.  
XX  
AC AAV92815;  
XX  
DT 18-FEB-1999 (first entry)  
XX  
DE Human A-raf target sequence nucleotide position 1831.  
XX  
KW Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;  
KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;  
KW screening; identification; synthesis; deprotection; purification; cancer;  
KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;  
KW restenosis; rheumatoid arthritis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9850530-A2.  
XX  
PD 12-NOV-1998.  
XX  
PF 05-MAY-1998; 98WO-US009249.  
XX  
PR 09-MAY-1997; 97US-0046059P.  
PR 09-JUN-1997; 97US-0049002P.  
PR 03-JUL-1997; 97US-0051718P.  
PR 22-AUG-1997; 97US-0056808P.  
PR 02-OCT-1997; 97US-0061321P.  
PR 02-OCT-1997; 97US-0061324P.  
PR 05-NOV-1997; 97US-0064866P.  
PR 19-DEC-1997; 97US-0068212P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;  
PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;  
PI Thompson J, Workman CT, Beaudry A, Sweedler D;  
XX  
DR WPI; 1999-009494/01.  
XX  
PT Identifying new catalytic nucleic acid that modulates selected processes  
PT - especially ribozymes that cleave Raf RNA for treating cancer,  
PT restenosis, and also new ribozymes and modified nucleoside triphosphates  
PT used as antiviral agents and synthons.  
XX  
PS Claim 179; Page 164; 259pp; English.  
XX  
CC A method has been developed for the identification of a nucleic acid  
CC capable of modulating a process in a biological system. The method  
CC comprises: (a) introducing into the system a random library of nucleic  
CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising  
CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC  
CC in systems where modulation has occurred and/or determining the sequence  
CC of at least part of the SBDs in such systems. Nucleic acid molecules with  
CC endonuclease activity and catalytic activity, from the present invention,  
CC are used to modulate gene expression in plant and mammalian cells and to  
CC cleave target nucleic acid, particularly for treating systemic diseases

CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic  
CC ascites and infection. They may also be used to detect genetic drift and  
CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs  
CC with RNA-cleaving activity that modulate expression of the Raf gene, are  
CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or  
CC generally any condition associated with the level of c-raf. Introduction  
CC of sugar/phosphate modifications increases stability against nuclease and  
CC activity. AAV90922 to AAV93877 represent NACs that can be used in the  
CC method, specifically for modulating the expression of a Raf gene  
XX  
SQ Sequence 14 BP; 1 A; 4 C; 4 G; 0 T; 5 U; 0 Other;  
  
Query Match 35.9%; Score 10.4; DB 1; Length 14;  
Best Local Similarity 58.3%; Pred. No. 98;  
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
  
QY 9 CTGCTGTGTGAC 20  
Db 1 CUGCUGUCUGAC 12  
  
RESULT 94  
ABQ83257  
ID ABQ83257 standard; DNA; 14 BP.  
XX  
AC ABQ83257;  
XX  
DT 18-JAN-2003 (first entry)  
XX  
DE Expressed gene identification cDNA tag related oligonucleotide SEQ:30.  
XX  
KW cDNA tag; identification; gene expression analysis; linker;  
KW expressed gene identification; EGI; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200274951-A1.  
XX  
PD 26-SEP-2002.  
XX  
PF 13-MAR-2002; 2002WO-JP002338.  
XX  
PR 15-MAR-2001; 2001JP-00073959.  
XX  
PA (KURE ) KUREHA CHEM IND CO LTD.  
PA (YAMA/) YAMAMOTO M.  
PA (YAMA/) YAMAMOTO N.  
XX  
PI Yamamoto M, Yamamoto N, Hirose K, Kasai J;  
XX  
DR WPI; 2002-759896/82.  
XX  
PT Construction of cDNA tags for identifying expressed genes with specific  
PT linkers and recognition sequences, applicable in gene expression  
PT analysis, disease diagnosis and identifying target for gene therapy.  
XX  
PS Example 1; Page 22; 59pp; Japanese.  
XX  
CC The present invention describes a method for constructing a cDNA tag for  
CC identifying an expressed gene. The method comprises: (a) preparation of  
CC complementary deoxyribonucleic acid; (b) producing cDNA fragment by  
CC cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA  
CC fragment ligated material; (d) amplification of the linker X-cDNA tag-  
CC linker Y ligated material; and (e) cleaving the amplification product.  
CC The method can be used for the construction of cDNA tags for identifying  
CC expressed genes, which is applicable in gene expression analysis, disease  
CC diagnosis and identifying target for gene therapy, including the  
CC clarification of difference in function or morphology of cells under  
CC physiological or pathological conditions. The cDNA or cells for assay can  
CC be specifically expressed, with reproducibility and accuracy in the  
CC detection of genes. The present sequence represents an expressed gene  
CC identification (EGI) cDNA tag related oligonucleotide which is used in an  
CC example from the present invention

XX SQ Sequence 14 BP; 3 A; 2 C; 5 G; 4 T; 0 U; 0 Other;  
Query Match 35.9%; Score 10.4; DB 1; Length 14;  
Best Local Similarity 91.7%; Pred. No. 98;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 13 TGTGTGACCTGG 24  
||| |||||  
Db 2 TGTATGACCTGG 13  
RESULT 95  
AAZ86497/c  
ID AAZ86497 standard; DNA; 10 BP.  
XX AAZ86497;  
XX 07-APR-2000 (first entry)  
XX Metastatic breast tumour cell downregulated transcript tag #5731.  
DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX Homo sapiens.  
XX WO9965928-A2.  
XX 23-DEC-1999.  
XX 18-JUN-1999; 99WO-US013647.  
XX 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX Roberts BL, Shankara S;  
PI WPI; 2000-106079/09.  
DR Isolated polynucleotides differentially expressed between metastatic and  
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX Claim 1; Page 209; 219pp; English.  
PS AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
XX that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC vaccines; for diagnosing breast cancer and for raising specific  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector

CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy  
XX Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;  
SQ Query Match 34.5%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 81;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 CCTGCTGTGT 17  
|||||  
Db 10 CCTGCTGTGT 1  
RESULT 96  
AAA95175/c  
ID AAA95175 standard; DNA; 10 BP.  
XX AAA95175;  
AC AAA95175;  
XX 12-JAN-2001 (first entry)  
DT Primer #22 for detection of TNFR1 polymorphism by primer extension.  
XX TNFR1; tumour necrosis factor receptor; polymorphism; human; tumour;  
DE cancer; apoptosis; bacterial infection; primer; primer extension; ss.  
KW Homo sapiens.  
XX WO200050436-A1.  
XX 31-AUG-2000.  
XX 23-FEB-2000; 2000WO-US004606.  
XX 23-FEB-1999; 99US-0121314P.  
PR (GENA-) GENAISSANCE PHARM INC.  
XX (NAND/) NANDABALAN K.  
PA (SCHU/) SCHULZ V P.  
PA (STEP/) STEPHENS J C.  
PA (CHEW/) CHEW A.  
XX Nandabalan K, Schulz VP, Stephens JC, Chew A;  
PI WPI; 2000-543909/49.  
XX Polynucleotides comprising polymorphic variants of a reference sequence  
PT for tumor necrosis factor receptor 1 (TNFR1), useful for studying the  
PT biological function of TNFR1 and identifying drugs targeting the protein  
PT for treating disorders.  
XX Claim 15; Page 21; 79pp; English.  
PS The present invention relates to polymorphic variants of the tumour  
XX necrosis factor receptor 1 (TNFR1) gene. The sequence of the gene is  
CC given in AAA95102, AAA95103 and AAA95104. The polymorphisms were  
CC identified by amplifying and sequencing regions of the gene. Twelve  
CC polymorphic loci were discovered. Of these twelve polymorphisms, four can  
CC cause a change in the TNFR1 protein. The present sequence is the terminal  
CC sequence of a primer used for detection of a TNFR1 gene polymorphism by  
CC primer extension. The TNFR1 polymorphisms may be useful for studying the  
CC biological function of TNFR1 as well as for identifying drugs targeting  
CC the protein for treatment of disorders related to its abnormal expression  
CC or function such as tumours, apoptosis related disorders and bacterial  
XX infection  
SQ Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;  
Query Match 34.5%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 81;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GTGACCTGGT 25  
Db 10 GTGACCTGGT 1

RESULT 97  
ADD71273/c  
ID ADD71273 standard; DNA; 10 BP.  
XX  
AC ADD71273;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Mouse ET gene 5' splice donor site from intron 9.  
XX  
KW Mouse; ethenolaminephosphate cytidilyl transferase; ET; ds;  
KW splice donor site; antilipemic; cardiant; anorectic;  
KW phosphatidylethanolamine; Zellweger's syndrome; lipid-related disease;  
KW cardiovascular disease; atherosclerosis; obesity.  
XX  
OS Mus musculus.  
XX  
PN US2003194795-A1.  
XX  
PD 16-OCT-2003.  
XX  
PF 21-MAR-2002; 2002US-00101957.  
XX  
PT New gene encoding a protein having ethanolaminephosphate  
PT cytidyltransferase activity, useful for treating Zellweger's syndrome, or  
PT lipid-related diseases such as cardiovascular diseases and obesity.  
XX  
PS Example 1; Page 6; 22pp; English.  
XX  
CC The invention relates to a mouse gene encoding a protein having  
CC ethanolaminephosphate cytidyltransferase (ET) activity appearing as  
CC ADD71226, a degenerate variant of the ET gene, or a sequence that  
CC hybridises to the complement of the ET gene under stringent conditions.  
CC Also included is a promoter of a human ethanolaminephosphate  
CC cytidyltransferase gene appearing as ADD71227. The gene and promoter are  
CC useful for producing a transgenic animal, and for identifying,  
CC preventing, and treating diseases (by gene therapy) related to  
CC inappropriate phosphatidylethanolamine production, e.g. Zellweger's  
CC syndrome, or lipid-related diseases such as cardiovascular diseases,  
CC atherosclerosis and obesity. The present sequence is a mouse ET gene 5'  
CC splice donor site.  
XX  
SQ Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 34.5%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 81;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GTGACCTGGT 25  
Db 10 GTGACCTGGT 1

RESULT 98  
ADD71297/c  
ID ADD71297 standard; DNA; 10 BP.  
XX  
AC ADD71297;  
XX

DT 15-JAN-2004 (first entry)  
XX  
DE Human ET gene 5' splice donor site from intron 8.  
XX  
KW Human; ethenolaminephosphate cytidilyl transferase; ET; ds;  
KW splice donor site; antilipemic; cardiant; anorectic;  
KW phosphatidylethanolamine; Zellweger's syndrome; lipid-related disease;  
KW cardiovascular disease; atherosclerosis; obesity; Chromosome 17.  
XX  
OS Homo sapiens.  
XX  
PN US2003194795-A1.  
XX  
PD 16-OCT-2003.  
XX  
PF 21-MAR-2002; 2002US-00101957.  
XX  
PR 21-MAR-2002; 2002US-00101957.  
XX  
PA (BAKO/) BAKOVIC M.  
PA (POLO/) POLOUMIENKO A.  
XX  
PI Bakovic M, Poloumienko A;  
XX  
DR WPI; 2003-844457/78.  
XX  
PT New gene encoding a protein having ethanolaminephosphate  
PT cytidyltransferase activity, useful for treating Zellweger's syndrome, or  
PT lipid-related diseases such as cardiovascular diseases and obesity.  
XX  
PS Example 1; Page 6; 22pp; English.  
XX  
CC The invention relates to a mouse gene encoding a protein having  
CC ethanolaminephosphate cytidyltransferase (ET) activity appearing as  
CC ADD71226, a degenerate variant of the ET gene, or a sequence that  
CC hybridises to the complement of the ET gene under stringent conditions.  
CC Also included is a promoter of a human ethanolaminephosphate  
CC cytidyltransferase gene appearing as ADD71227. The gene and promoter are  
CC useful for producing a transgenic animal, and for identifying,  
CC preventing, and treating diseases (by gene therapy) related to  
CC inappropriate phosphatidylethanolamine production, e.g. Zellweger's  
CC syndrome, or lipid-related diseases such as cardiovascular diseases,  
CC atherosclerosis and obesity. The human ET gene is located on chromosome  
CC 17. The present sequence is a human ET gene 5' splice donor site.  
XX  
SQ Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 34.5%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 81;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GTGACCTGGT 25  
Db 10 GTGACCTGGT 1

RESULT 99  
ABQ87100  
ID ABQ87100 standard; cDNA; 11 BP.  
XX  
AC ABQ87100;  
XX  
DT 10-SEP-2002 (first entry)  
XX  
DE Human skin stress/ageing related EST SEQ ID NO 855.  
XX  
KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253773-A2.  
XX  
PD 11-JUL-2002.

XX 20-DEC-2001; 2001WO-EP015178.  
PF 03-JAN-2001; 2001DE-01000121.  
XX (HENK ) HENKEL KGAA.  
PA Petersohn D, Conradt M, Hofmann K;  
XX WPI; 2002-528865/56.  
DR Identifying genes involved in skin stress and aging, useful e.g. in  
XX screening for cosmetic or therapeutic agents, based on differential gene  
PT expression.  
PT  
XX  
PS Claim 8; Page 73; 325pp; German.  
XX The invention relates to identifying (M1) genes in vitro that, in humans  
CC or animals, are important for skin ageing and/or skin stress by serial  
CC analysis of gene expression between mixtures of transcribed and  
CC optionally translated, genetically encoded factors (A) obtained from  
CC young and aged skin, to identify that genes that show strong differential  
CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is  
CC useful for: identifying markers of skin ageing and/or stress; determining  
CC skin ageing and/or stress; and identifying or determining the effects of  
CC pharmaceutical or cosmetic agents for control of skin ageing. The present  
CC sequence is one of a group of human skin ageing/stress related expressed  
CC sequence tags (ABQ86246-ABQ87680) of the invention  
XX  
SQ Sequence 11 BP; 2 A; 6 C; 1 G; 2 T; 0 U; 0 Other;  
Query Match 34.5%; Score 10; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 90;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 ATCCACCTGC 12  
DB 1 ATCCACCTGC 10  
RESULT 100  
ABV66313  
ID ABV66313 standard; cDNA; 11 BP.  
XX  
AC ABV66313;  
XX 21-OCT-2002 (first entry)  
DT Human skin EST 4099.  
XX  
DE Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX Homo sapiens.  
OS WPI; 2002-590638/63.  
XX WO200253774-A2.  
PN 11-JUL-2002.  
PD 20-DEC-2001; 2001WO-EP015179.  
XX 03-JAN-2001; 2001DE-01000127.  
PR (HENK ) HENKEL KGAA.  
XX Petersohn D, Conradt M, Hofmann K;  
PI WPI; 2002-590638/63.  
XX In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.

XX Disclosure; Page 138; 1345pp; German.  
PS The invention relates to in vitro identification (M1) of genes expressed  
XX in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 2 A; 5 C; 2 G; 2 T; 0 U; 0 Other;  
Query Match 34.5%; Score 10; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 90;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 CATCCACCTG 11  
DB 1 CATCCACCTG 10  
RESULT 101  
ABV65203  
ID ABV65203 standard; cDNA; 11 BP.  
XX  
AC ABV65203;  
XX 21-OCT-2002 (first entry)  
DT Human skin EST 2989.  
XX  
DE Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX Homo sapiens.  
OS WO200253774-A2.  
XX 11-JUL-2002.  
PD 20-DEC-2001; 2001WO-EP015179.  
XX 03-JAN-2001; 2001DE-01000127.  
PR (HENK ) HENKEL KGAA.  
XX Petersohn D, Conradt M, Hofmann K;  
PI WPI; 2002-590638/63.  
XX In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 108; 1345pp; German.  
XX The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the



CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 1 A; 1 C; 4 G; 5 T; 0 U; 0 Other;  
  
Query Match 34.5%; Score 10; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 90;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 10 TGCTGTGTGA 19  
Db 2 TGCTGTGTGA 11  
|||||  
  
RESULT 102  
ABV63737  
ID ABV63737 standard; cDNA; 11 BP.  
XX  
AC ABV63737;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 1523.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX WPI; 2002-590638/63.  
XX  
DR WO200253774-A2.  
XX  
PN 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX WPI; 2002-590638/63.  
XX  
DR In vitro identification of skin-expressed genes, useful for determining  
XX homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
PT  
XX  
PS Disclosure; Page 67; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 2 A; 6 C; 1 G; 2 T; 0 U; 0 Other;  
  
Query Match 34.5%; Score 10; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 90;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 ATCCACCTGC 12  
Db 1 ATCCACCTGC 10  
|||||  
  
RESULT 104  
AAD34268/c  
ID AAD34268 standard; DNA; 11 BP.  
XX  
AC AAD34268;  
XX  
DT 16-JUL-2002 (first entry)  
XX  
DE Human CYP2D6 gene polymorphic site 1255 detecting sense 5' oligo.  
XX  
KW Human; cytochrome P450 2D6; CYP2D6; enzyme; detection; xenobiotic;  
KW ligase-based sequenced determination; drug metabolism; chromosome 22; ss.

RESULT 103  
ABV71158  
ID ABV71158 standard; cDNA; 11 BP.  
XX  
AC ABV71158;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 8944.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX WPI; 2002-590638/63.  
XX  
DR In vitro identification of skin-expressed genes, useful for determining  
XX homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
PT  
XX  
PS Claim 24; Page 287; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 2 A; 6 C; 1 G; 2 T; 0 U; 0 Other;  
  
Query Match 34.5%; Score 10; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 90;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 ATCCACCTGC 12  
Db 1 ATCCACCTGC 10  
|||||  
  
RESULT 104  
AAD34268/c  
ID AAD34268 standard; DNA; 11 BP.  
XX  
AC AAD34268;  
XX  
DT 16-JUL-2002 (first entry)  
XX  
DE Human CYP2D6 gene polymorphic site 1255 detecting sense 5' oligo.  
XX  
KW Human; cytochrome P450 2D6; CYP2D6; enzyme; detection; xenobiotic;  
KW ligase-based sequenced determination; drug metabolism; chromosome 22; ss.



XX OS Homo sapiens.  
XX PN WO200218638-A2.  
XX PD 07-MAR-2002.  
XX PF 27-AUG-2001; 2001WO-IB001544.  
XX PR 30-AUG-2000; 2000GB-00021286.  
XX PA (GEMI-) GEMINI GENOMICS PLC.  
XX PI Risinger C, Andersson MK, Lewander T, Oliasson E;  
XX DR WPI; 2002-329785/36.  
XX PT New sequence determination oligonucleotides, useful for detecting  
PT polymorphic sites in a 5' flanking region of a CYP2D6 gene, as  
PT hybridization probes, as components of diagnostic assays, or in ligase-  
PT based sequence determination.  
XX PS Claim 2; Page 23; 63pp; English.  
XX CC The invention relates to sequence determination oligonucleotides for  
CC detecting polymorphic sites in a 5' flanking region of cytochrome P450  
CC 2D6 (CYP2D6) gene. CYP2D6 enzymes are involved in the metabolism of many  
CC different xenobiotics. Human CYP2D6 gene is located on chromosome 22. The  
CC oligonucleotides may be used as in situ hybridisation probes, in ligase-  
CC based sequenced determination, as components of diagnostic assays, as  
CC probes in sequence determination methods based on mismatches, as  
CC hybridisation-based diagnostic assays, and as components of diagnostic  
CC microarray. CYP2D6 is useful to predict variations in an individual's  
CC ability to metabolise certain drugs. The present sequence is a sense  
CC oligonucleotide used for detecting of human CYP2D6 gene 5' flanking  
CC region single nucleotide polymorphism (SNP)  
XX SQ Sequence 11 BP; 2 A; 0 C; 7 G; 2 T; 0 U; 0 Other;  
  
Query Match 34.5%; Score 10; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 90;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CCATCCACCT 10  
Db 11 CCATCCACCT 2  
  
RESULT 105  
ADQ30368  
ID ADQ30368 standard; DNA; 11 BP.  
XX AC ADQ30368;  
XX DT 09-SEP-2004 (first entry)  
XX DE Human VR1 exon 1d transcription factor binding fragment #87.  
XX KW ds; VR1 receptor; vanilloid receptor type 1; modulator;  
KW pain transmission; primary sensory neuron; transcription factor;  
KW detection; MZF1, NFKappaB, NFAT; GATA1; sensitivity disorder; analgesia;  
KW hypalgesia; hyperalgesia; neuralgia; myalgia; human.  
XX OS Homo sapiens.  
XX PN WO2004053120-A2.  
XX PD 24-JUN-2004.  
XX PF 01-DEC-2003; 2003WO-EP013522.  
XX PR 09-DEC-2002; 2002DE-01057421.  
XX XX

PA (CHEF ) GRUENTHAL GMBH.  
XX PI Weihe E, Bieller A, Schaefer MKH;  
XX DR WPI; 2004-468868/44.  
XX PT New nucleic acid that modulates expression of the vanilloid receptor-1,  
PT useful for control of pain or sensitivity disorders, comprises sequences  
PT from control regions of the receptor gene.  
XX PS Disclosure; Page 53; 68pp; German.  
XX CC This invention describes a novel nucleic acid containing a specific  
CC segment having at least one region that modulates expression of the VR1  
CC (vanilloid receptor type 1) receptor, or a functional derivative, allele  
CC or fragment of this region, or a sequence that hybridises to it under  
CC standard conditions. The VR1 modulator is derived from one or more of  
CC positions 221931-223344 of GenBank AL670399, 31673-36359 of AL663116, or  
CC 44731-43231 or 36616-33151 of AF168787 and is involved in transmission of  
CC pain, particularly in primary sensory neurons. The invention also  
CC describes a vector that contains the VR1 modulator, host cells containing  
CC this vector (other than human germ or embryonal stem cells) and a method  
CC for modulating expression of the VR1 receptor by introducing the  
CC modulator or the vector into a cell that contains the VR1 gene. The  
CC products of the invention are used for detecting a transcription factor  
CC from its binding to a regulatory sequence (or a double-stranded  
CC oligonucleotide fragment of it), e.g. by Western blotting or enzyme-  
CC linked immunosorbant assay, particularly for diagnosis of diseases  
CC associated with overexpression or underexpression of the transcription  
CC factor. The region that modulates VR1 receptor expression includes a  
CC binding site for a transcription factor, e.g. MZF1, NFKappaB, NFAT or  
CC GATA1. The nucleic acids of the invention, or vectors containing them,  
CC are used for prevention or treatment of pain, also for treating  
CC sensitivity disorders, e.g. analgesia, hypalgesia or hyperalgesia, also  
CC neuralgia and myalgia, that are associated with activity of the VR1  
CC receptor. This sequence represents a fragment of human VR1 exon 1d DNA  
CC which is capable of binding to a transcription factor.  
XX SQ Sequence 11 BP; 2 A; 6 C; 1 G; 2 T; 0 U; 0 Other;  
  
Query Match 34.5%; Score 10; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 90;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 ATCCACCTGC 12  
Db 1 ATCCACCTGC 10  
  
RESULT 106  
ABI43156  
ID ABI43156 standard; DNA; 12 BP.  
XX AC ABI43156;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 343129 for detecting SNP TSC0042904.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX XX

PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 343129; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;  
  
Query Match 34.5%; Score 10; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CCATCCACCT 10  
Db 3 CCATCCACCT 12  
  
RESULT 107  
ABI05465  
ID ABI05465 standard; DNA; 12 BP.  
XX  
AC ABI05465;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 305438 for detecting SNP TSC0021446.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 305438; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 7 C; 0 G; 2 T; 0 U; 0 Other;  
  
Query Match 34.5%; Score 10; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CCATCCACCT 10  
Db 2 CCATCCACCT 11  
  
RESULT 108  
ADQ30383/c  
ID ADQ30383 standard; DNA; 12 BP.  
XX  
AC ADQ30383;  
XX  
DT 09-SEP-2004 (first entry)  
XX  
DE Human VR1 exon 1d transcription factor binding fragment #102.  
XX  
KW ds; VR1 receptor; vanilloid receptor type 1; modulator;  
KW pain transmission; primary sensory neuron; transcription factor;  
KW detection; MZF1; NFkappaB; NFAT; GATA1; sensitivity disorder; analgesia;  
KW hypalgesia; hyperalgesia; neuralgia; myalgia; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2004053120-A2.  
XX  
PD 24-JUN-2004.  
XX  
PF 01-DEC-2003; 2003WO-EP013522.  
XX  
PR 09-DEC-2002; 2002DE-01057421.  
XX  
PA (CHEF ) GRUENENTHAL GMBH.  
XX  
PI Weihe E, Bieller A, Schaefer MKH;  
XX  
DR WPI; 2004-468868/44.  
XX  
PT New nucleic acid that modulates expression of the vanilloid receptor-1,  
PT useful for control of pain or sensitivity disorders, comprises sequences  
PT from control regions of the receptor gene.  
XX  
PS Disclosure; Page 53; 68pp; German.  
XX  
CC This invention describes a novel nucleic acid containing a specific  
CC segment having at least one region that modulates expression of the VR1  
CC (vanilloid receptor type 1) receptor, or a functional derivative, allele  
CC or fragment of this region, or a sequence that hybridises to it under  
CC standard conditions. The VR1 modulator is derived from one or more of  
CC positions 221931-223344 of GenBank AL670399, 31673-36359 of AL663116, or  
CC 44731-43231 or 36616-33151 of AF168787 and is involved in transmission of  
CC pain, particularly in primary sensory neurons. The invention also  
CC describes a vector that contains the VR1 modulator, host cells containing  
CC this vector (other than human germ or embryonal stem cells) and a method  
CC for modulating expression of the VR1 receptor by introducing the  
CC modulator or the vector into a cell that contains the VR1 gene. The  
CC products of the invention are used for detecting a transcription factor

CC from its binding to a regulatory sequence (or a double-stranded  
CC oligonucleotide fragment of it), e.g. by Western blotting or enzyme-  
CC linked immunosorbant assay, particularly for diagnosis of diseases  
CC associated with overexpression or underexpression of the transcription  
CC factor. The region that modulates VR1 receptor expression includes a  
CC binding site for a transcription factor, e.g. MZF1, NfkappaB, NFAT or  
CC GATA1. The nucleic acids of the invention, or vectors containing them,  
CC are used for prevention or treatment of pain, also for treating  
CC sensitivity disorders, e.g. analgesia, hypalgesia or hyperalgesia, also  
CC neuralgia and myalgia, that are associated with activity of the VR1  
CC receptor. This sequence represents a fragment of human VR1 exon 1d DNA  
CC which is capable of binding to a transcription factor.  
XX  
SQ Sequence 12 BP; 3 A; 1 C; 6 G; 2 T; 0 U; 0 Other;  
  
Query Match 34.5%; Score 10; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 ATCCACCTGC 12  
| | | | | | | |  
Db 12 ATCCACCTGC 3  
  
RESULT 109  
ADQ30420/C  
ID ADQ30420 standard; DNA; 12 BP.  
XX  
AC ADQ30420;  
XX  
DT 09-SEP-2004 (first entry)  
XX  
DE Human VR1 exon 1d transcription factor binding fragment #139.  
XX  
KW ds; VR1 receptor; vanilloid receptor type 1; modulator;  
KW pain transmission; primary sensory neuron; transcription factor;  
KW detection; MZF1; NfkappaB; NFAT; GATA1; sensitivity disorder; analgesia;  
KW hypalgesia; hyperalgesia; neuralgia; myalgia; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2004053120-A2.  
XX  
PD 24-JUN-2004.  
XX  
PF 01-DEC-2003; 2003WO-EP013522.  
XX  
PR 09-DEC-2002; 2002DE-01057421.  
XX  
PA (CHEF ) GRUENENTHAL GMBH.  
XX  
PI Weihe E, Bieller A, Schaefer MKH;  
XX  
DR WPI; 2004-468868/44.  
XX  
PT New nucleic acid that modulates expression of the vanilloid receptor-1,  
PT useful for control of pain or sensitivity disorders, comprises sequences  
PT from control regions of the receptor gene.  
XX  
PS Disclosure; Page 54; 68pp; German.  
XX  
CC This invention describes a novel nucleic acid containing a specific  
CC segment having at least one region that modulates expression of the VR1  
CC (vanilloid receptor type 1) receptor, or a functional derivative, allele  
CC or fragment of this region, or a sequence that hybridises to it under  
CC standard conditions. The VR1 modulator is derived from one or more of  
CC positions 221931-223344 of GenBank AL670399, 31673-36359 of AL663116, or  
CC 44731-43231 or 36616-33151 of AF168787 and is involved in transmission of  
CC pain, particularly in primary sensory neurons. The invention also  
CC describes a vector that contains the VR1 modulator, host cells containing  
CC this vector (other than human germ or embryonal stem cells) and a method  
CC for modulating expression of the VR1 receptor by introducing the  
CC modulator or the vector into a cell that contains the VR1 gene. The

CC products of the invention are used for detecting a transcription factor  
CC from its binding to a regulatory sequence (or a double-stranded  
CC oligonucleotide fragment of it), e.g. by Western blotting or enzyme-  
CC linked immunosorbant assay, particularly for diagnosis of diseases  
CC associated with overexpression or underexpression of the transcription  
CC factor. The region that modulates VR1 receptor expression includes a  
CC binding site for a transcription factor, e.g. MZF1, NfkappaB, NFAT or  
CC GATA1. The nucleic acids of the invention, or vectors containing them,  
CC are used for prevention or treatment of pain, also for treating  
CC sensitivity disorders, e.g. analgesia, hypalgesia or hyperalgesia, also  
CC neuralgia and myalgia, that are associated with activity of the VR1  
CC receptor. This sequence represents a fragment of human VR1 exon 1d DNA  
CC which is capable of binding to a transcription factor.  
XX  
SQ Sequence 12 BP; 3 A; 1 C; 6 G; 2 T; 0 U; 0 Other;  
  
Query Match 34.5%; Score 10; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 ATCCACCTGC 12  
| | | | | | | |  
Db 12 ATCCACCTGC 3  
  
RESULT 110  
ABC35433  
ID ABC35433 standard; DNA; 13 BP.  
XX  
AC ABC35433;  
XX  
DT 20-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 35450 for detecting SNP TSC0011230.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 35450; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF0010-ABF99989, ABH0010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

```
XX
SQ      Sequence 13 BP; 3 A; 7 C; 0 G; 3 T; 0 U; 0 Other;

      Query Match      34.5%; Score 10; DB 1; Length 13;
      Best Local Similarity 100.0%; Pred. No. 1.1e+02;
      Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATCCACCT 10
      |||||
Db      2 CCATCCACCT 11

RESULT 111
ABF12886/c
ID      ABF12886 standard; DNA; 13 BP.
XX
AC      ABF12886;
XX
DT      21-FEB-2002 (first entry)
XX
DE      Oligonucleotide SEQ ID NO 112883 for detecting SNP TSC0028229.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
AC      ABF12886;
XX
DT      21-FEB-2002 (first entry)
XX
DE      Oligonucleotide SEQ ID NO 112883 for detecting SNP TSC0028229.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.
XX
PR      07-APR-2000; 2000DE-01019173.
XX
PA      (EPIG-) EPIGENOMICS AG.
XX
PI      Olek A, Piepenbrock C, Berlin K;
XX
DR      WPI; 2001-657177/75.
XX
PT      Set of oligonucleotides, useful for diagnosis and cell typing, is
PT      designed to detect single-nucleotide polymorphisms and cytosine
PT      methylation status.
XX
PS      Claim 1; SEQ ID NO 112883; 29pp + Sequence Listing; German.
XX
CC      This invention describes novel oligonucleotide primers or peptide nucleic
CC      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC      and cytosine methylation status in chemically pretreated genomic DNA. The
CC      oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC      range of diseases including immune system, gastrointestinal, respiratory,
CC      central nervous system, cardiovascular and metabolic disorders. The
CC      oligomers are also used for detecting cell type differentiation. ABC00010
CC      -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC      represent the oligomers described in the invention. NOTE: The sequence
CC      data for this patent did not form part of the printed specification, but
CC      was obtained in electronic format from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
PS      Claim 1; SEQ ID NO 112883; 29pp + Sequence Listing; German.
XX
CC      This invention describes novel oligonucleotide primers or peptide nucleic
CC      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC      and cytosine methylation status in chemically pretreated genomic DNA. The
CC      oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC      range of diseases including immune system, gastrointestinal, respiratory,
CC      central nervous system, cardiovascular and metabolic disorders. The
CC      oligomers are also used for detecting cell type differentiation. ABC00010
CC      -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC      represent the oligomers described in the invention. NOTE: The sequence
CC      data for this patent did not form part of the printed specification, but
CC      was obtained in electronic format from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
SQ      Sequence 13 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 1 Other;

      Query Match      34.5%; Score 10; DB 1; Length 13;
      Best Local Similarity 100.0%; Pred. No. 1.1e+02;
      Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATCCACCT 10
      |||||
Db      10 CCATCCACCT 11

RESULT 112
```

```
ABC14106/c
ID      ABC14106 standard; DNA; 13 BP.
XX
AC      ABC14106;
XX
DT      20-FEB-2002 (first entry)
XX
DE      Oligonucleotide SEQ ID NO 14113 for detecting SNP TSC0003223.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.
XX
PR      07-APR-2000; 2000DE-01019173.
XX
PA      (EPIG-) EPIGENOMICS AG.
XX
PI      Olek A, Piepenbrock C, Berlin K;
XX
DR      WPI; 2001-657177/75.
XX
PT      Set of oligonucleotides, useful for diagnosis and cell typing, is
PT      designed to detect single-nucleotide polymorphisms and cytosine
PT      methylation status.
XX
PS      Claim 1; SEQ ID NO 14113; 29pp + Sequence Listing; German.
XX
CC      This invention describes novel oligonucleotide primers or peptide nucleic
CC      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC      and cytosine methylation status in chemically pretreated genomic DNA. The
CC      oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC      range of diseases including immune system, gastrointestinal, respiratory,
CC      central nervous system, cardiovascular and metabolic disorders. The
CC      oligomers are also used for detecting cell type differentiation. ABC00010
CC      -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC      represent the oligomers described in the invention. NOTE: The sequence
CC      data for this patent did not form part of the printed specification, but
CC      was obtained in electronic format from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
SQ      Sequence 13 BP; 2 A; 1 C; 7 G; 3 T; 0 U; 0 Other;

      Query Match      34.5%; Score 10; DB 1; Length 13;
      Best Local Similarity 100.0%; Pred. No. 1.1e+02;
      Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATCCACCT 10
      |||||
Db      13 CCATCCACCT 4

RESULT 113
ABC14104/c
ID      ABC14104 standard; DNA; 13 BP.
XX
AC      ABC14104;
XX
DT      20-FEB-2002 (first entry)
XX
DE      Oligonucleotide SEQ ID NO 14111 for detecting SNP TSC0003223.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
```



OS Homo sapiens.  
XX WO200177384-A2.  
XX 18-OCT-2001.  
XX 06-APR-2001; 2001WO-IB000713.  
XX 07-APR-2000; 2000DE-01019173.  
XX (EPIG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 14111; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 2 A; 0 C; 7 G; 4 T; 0 U; 0 Other;  
  
Query Match 34.5%; Score 10; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CCATCCACCT 10  
Db 13 CCATCCACCT 4  
  
RESULT 114  
ABH01641  
ID ABH01641 standard; DNA; 13 BP.  
XX  
AC ABH01641;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 201618 for detecting SNP TSC0049588.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 201618; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 3 A; 7 C; 0 G; 3 T; 0 U; 0 Other;  
  
Query Match 34.5%; Score 10; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CCATCCACCT 10  
Db 3 CCATCCACCT 12  
  
RESULT 115  
ABC14107  
ID ABC14107 standard; DNA; 13 BP.  
XX  
AC ABC14107;  
XX  
DT 20-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 14114 for detecting SNP TSC0003223.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 14114; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX



CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 3 A; 7 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 34.5%; Score 10; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCCACCT 10  
Db 1 CCATCCACCT 10  
|||||

RESULT 116  
ABC35432/c  
ID ABC35432 standard; DNA; 13 BP.  
XX  
AC ABC35432;  
XX  
DT 20-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 35449 for detecting SNP TSC0011230.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 35449; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 3 A; 0 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 34.5%; Score 10; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

QY 1 CCATCCACCT 10  
Db 1 CCATCCACCT 10  
|||||

RESULT 117  
ABC35432/c  
ID ABC35432 standard; DNA; 13 BP.  
XX  
AC ABC35432;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 112884 for detecting SNP TSC0028229.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 112884; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 1 Other;

Query Match 34.5%; Score 10; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCCACCT 10  
Db 4 CCATCCACCT 13  
|||||

RESULT 118  
ABH01640/c  
ID ABH01640 standard; DNA; 13 BP.  
XX  
AC ABH01640;  
XX

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCCACCT 10  
Db 12 CCATCCACCT 3  
|||||

RESULT 117  
ABF12887  
ID ABF12887 standard; DNA; 13 BP.  
XX  
AC ABF12887;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 112884 for detecting SNP TSC0028229.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 112884; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 1 Other;

Query Match 34.5%; Score 10; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCCACCT 10  
Db 4 CCATCCACCT 13  
|||||

RESULT 118  
ABH01640/c  
ID ABH01640 standard; DNA; 13 BP.  
XX  
AC ABH01640;  
XX

```
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 201617 for detecting SNP TSC0049588.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 201617; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 0 C; 7 G; 3 T; 0 U; 0 Other;
XX
Query Match 34.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATCCACCT 10
Db 11 CCATCCACCT 2

RESULT 119
ABC14105
ID ABC14105 standard; DNA; 13 BP.
XX
AC ABC14105;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 14112 for detecting SNP TSC0003223.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
```

```
XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 14112; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 7 C; 0 G; 2 T; 0 U; 0 Other;
XX
Query Match 34.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATCCACCT 10
Db 1 CCATCCACCT 10

RESULT 120
ADE14132
ID ADE14132 standard; DNA; 13 BP.
XX
AC ADE14132;
XX
DT 29-JAN-2004 (first entry)
XX
DE Optineurin promoter motif, repeat element or regulatory region #241.
XX
KW Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
KW SNP; glaucoma; progressive ocular hypertensive disorder;
KW glaucoma related disorder; motif; repeat element; regulatory region.
XX
OS Homo sapiens.
XX
PN US2003190617-A1.
XX
PD 09-OCT-2003.
XX
PF 06-MAR-2002; 2002US-00091281.
XX
PR 06-MAR-2002; 2002US-00091281.
XX
PA (SIEE/) SI E.
PA (RAYM/) RAYMOND V.
PA (MORI/) MORISSETTE J.
XX
PI Raymond V, Morissette J, Si E;
XX
DR WPI; 2003-864168/80.
XX
```

PT New nucleic acid sequences of the optineurin gene are useful to detect  
PT polymorphisms particularly single nucleotide polymorphisms in the  
PT optineurin promoter to diagnose, prognose and treat glaucoma and related  
PT disorders.  
XX  
PS Claim 11; SEQ ID NO 243; 159pp; English.  
XX  
CC The invention relates to an isolated nucleic acid (N1) comprising at  
CC least 20 but not more than 1500 consecutive nucleotides of the optineurin  
CC promoter appearing as ADE13890. Also included are the optineurin promoter  
CC operably linked to a heterologous nucleic acid, a nucleic acid capable of  
CC detecting a single nucleotide polymorphism (SNP) in the optineurin  
CC promoter, a host cell comprising the promoter operably linked to a  
CC heterologous sequence, diagnosing or prognosing glaucoma in a sample  
CC obtained from a cell or bodily fluid (comprising detecting a polymorphism  
CC in a promoter region of the optineurin gene, associated with a glaucoma  
CC phenotype), detecting a SNP sequence variation in a sample containing  
CC DNA, detecting the presence of an optineurin promoter sequence variation  
CC in a sample containing DNA, determining the presence or increased  
CC susceptibility to glaucoma or to a progressive ocular hypertensive  
CC disorder resulting in loss of visual field in a patient (or the severity  
CC or progression of glaucoma in a patient, comprising providing  
CC amplification reaction primers that direct amplification of a selected  
CC nucleic acid region containing the variation within the optineurin  
CC promoter and amplifying the DNA) and detecting a polymorphism (comprising  
CC obtaining a sample containing human genomic DNA, providing a nucleic acid  
CC capable of detecting a SNP located within an optineurin promoter, and  
CC detecting the polymorphism). The invention is used to diagnose and  
CC prognose glaucoma and also to treat glaucoma related disorders. The  
CC present sequence is an optineurin promoter motif, repeat element or  
CC putative regulatory region.  
XX  
SQ Sequence 13 BP; 2 A; 6 C; 2 G; 3 T; 0 U; 0 Other;  
  
Query Match 34.5%; Score 10; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 ATCCACCTGC 12  
Db 2 ATCCACCTGC 11  
  
RESULT 121  
AAV92770  
ID AAV92770 standard; RNA; 14 BP.  
XX  
AC AAV92770;  
XX  
DT 18-FEB-1999 (first entry)  
XX  
DE Human A-raf target sequence nucleotide position 366.  
XX  
KW Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;  
KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;  
KW screening; identification; synthesis; deprotection; purification; cancer;  
KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;  
KW restenosis; rheumatoid arthritis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9850530-A2.  
XX  
PD 12-NOV-1998.  
XX  
PF 05-MAY-1998; 98WO-US009249.  
XX  
PR 09-MAY-1997; 97US-0046059P.  
PR 09-JUN-1997; 97US-0049002P.  
PR 03-JUL-1997; 97US-0051718P.  
PR 22-AUG-1997; 97US-0056808P.  
PR 02-OCT-1997; 97US-0061321P.  
PR 02-OCT-1997; 97US-0061324P.

PR 05-NOV-1997; 97US-0064866P.  
PR 19-DEC-1997; 97US-0068212P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;  
PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;  
PI Thompson J, Workman CT, Beaudry A, Sweedler D;  
XX  
DR WPI; 1999-009494/01.  
XX  
PT Identifying new catalytic nucleic acid that modulates selected processes  
PT - especially ribozymes that cleave Raf RNA for treating cancer,  
PT restenosis, and also new ribozymes and modified nucleoside triphosphates  
PT used as antiviral agents and synthons.  
XX  
PS Claim 179; Page 163; 259pp; English.  
XX  
CC A method has been developed for the identification of a nucleic acid  
CC capable of modulating a process in a biological system. The method  
CC comprises: (a) introducing into the system a random library of nucleic  
CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising  
CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC  
CC in systems where modulation has occurred and/or determining the sequence  
CC of at least part of the SBDs in such systems. Nucleic acid molecules with  
CC endonuclease activity and catalytic activity, from the present invention,  
CC are used to modulate gene expression in plant and mammalian cells and to  
CC cleave target nucleic acid, particularly for treating systemic diseases  
CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic  
CC ascites and infection. They may also be used to detect genetic drift and  
CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs  
CC with RNA-cleaving activity that modulate expression of the Raf gene, are  
CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or  
CC generally any condition associated with the level of c-raf. Introduction  
CC of sugar/phosphate modifications increases stability against nuclease and  
CC activity. AAV90922 to AAV93877 represent NACs that can be used in the  
CC method, specifically for modulating the expression of a Raf gene  
XX  
SQ Sequence 14 BP; 1 A; 2 C; 7 G; 0 T; 4 U; 0 Other;  
  
Query Match 34.5%; Score 10; DB 1; Length 14;  
Best Local Similarity 60.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
  
QY 9 CTCGTGTGTG 18  
Db 4 CUGCUGUGUG 13  
  
RESULT 122  
AAZ64774  
ID AAZ64774 standard; RNA; 14 BP.  
XX  
AC AAZ64774;  
XX  
DT 28-MAR-2000 (first entry)  
XX  
DE Substrate for hairpin ribozyme which cleaves HCV at nt. 3887.  
XX  
KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;  
KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;  
KW autoimmune disease; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN WO9955847-A2.  
XX  
PD 04-NOV-1999.  
XX  
PF 26-APR-1999; 99WO-US009027.  
XX  
PR 27-APR-1998; 98US-0083217P.  
PR 18-SEP-1998; 98US-0100842P.

PR 25-FEB-1999; 99US-00257608.  
PR 23-MAR-1999; 99US-00274553.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PI Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;  
XX WPI; 2000-062023/05.  
DR  
XX Novel ribozymes for the treatment of diseases and conditions related to  
PT hepatitis C infection.  
XX  
PS Claim 2; Page 97; 123pp; English.  
XX  
CC The present sequence represents the preferred target sequence of an  
CC enzymatic nucleic acid, especially a hairpin ribozyme, which cleaves the  
CC Hepatitis C virus (HCV) RNA sequence at the base position given in the  
CC descriptor line. The HCV sequence was screened for optimal ribozyme  
CC target sites using a computer folding algorithm and regions of the mRNA  
CC which did not form secondary folding structures and contained potential  
CC ribozyme cleavage sites were identified. Ribozymes were synthesised to  
CC target these sites and their activities optimised by either varying the  
CC length of the binding arms or by modification to prevent degradation by  
CC nucleases. The ribozymes of the invention inhibit gene expression and/or  
CC viral replication, and are used to treat diseases associated with  
CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and  
CC hepatocellular carcinoma. The ribozymes may be used in combination with  
CC interferon to treat HCV infection, other infectious diseases, autoimmune  
CC diseases, and cancer  
XX  
SQ Sequence 14 BP; 0 A; 3 C; 7 G; 0 T; 4 U; 0 Other;

Query Match 34.5%; Score 10; DB 1; Length 14;  
Best Local Similarity 60.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 9 CTGCTGTGTG 18  
|:|:|:|:|  
Db 4 CUGCUGUGUG 13

RESULT 123  
AAZ37042  
ID AAZ37042 standard; DNA; 14 BP.  
XX  
AC AAZ37042;  
XX  
DT 27-MAR-2000 (first entry)  
XX  
DE Probe targeted to the conserved SNP 4.5S RNA of Escherichia coli.  
XX  
KW Signal recognition particle; SRP; 4.5S RNA; non-viral organism; probe;  
KW infection; screening; ss.  
XX  
OS Synthetic.  
OS Escherichia coli.  
XX  
PN WO9966079-A1.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013799.  
XX  
PR 19-JUN-1998; 98US-0090063P.  
XX  
PA (MOSA-) MOSAIC TECHNOLOGIES.  
XX  
PI Boles TC, Weir L, Stone BB;  
XX  
DR WPI; 2000-097755/08.  
XX  
PT Detecting non-viral organisms in samples, useful e.g. in medical  
PT diagnosis and for screening medical and food supplies.

XX Claim 19; Page 32; 49pp; English.  
PS  
XX  
CC AAZ37038-45 represent probes targeted to a sequence of the Escherichia  
CC coli signal recognition particle (SRP) 4.5S RNA which is conserved across  
CC bacteria (see AAZ37037). SRP RNA is found in all non-viral organisms, and  
CC has regions that are conserved in phylogenetic groups. Probes targeted to  
CC this region will therefore hybridise to all members of that group, but  
CC not to organism outside of the specified group. The probes are used in  
CC the method of the invention for the detection of a group (e.g. a kingdom  
CC or order) of non-viral organisms in a sample (in this case, E. coli). The  
CC method comprises using a nucleic acid probe with a SNP RNA from the group  
CC to be detected (where the probe is substantially complementary to a  
CC subsequence of the SRP RNA). The methods can be used to detect non-viral  
CC organisms in samples such as food, clinical, medical, environmental and  
CC assay control samples, useful e.g. in medical and veterinary diagnostics  
CC (e.g. to diagnose infection with specific organisms), screening medical  
CC and food supplies (e.g. to eliminate contaminants in medical supplies  
CC such as whole blood) and screening for soil and water contamination. The  
CC methods are especially useful to detect non-viral organisms in human  
CC samples  
XX  
SQ Sequence 14 BP; 3 A; 4 C; 4 G; 3 T; 0 U; 0 Other;  
  
Query Match 34.5%; Score 10; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 17 TGACCTGGTA 26  
|||||  
Db 5 TGACCTGGTA 14  
  
RESULT 124  
ABX01611  
ID ABX01611 standard; RNA; 14 BP.  
XX  
AC ABX01611;  
XX  
DT 23-DEC-2002 (first entry)  
XX  
DE Hepatitis C virus substrate #96 for HCV hairpin ribozyme #96.  
XX  
KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;  
KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;  
KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;  
KW type I interferon; interferon alpha; interferon beta; cytostatic;  
KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;  
KW substrate; hairpin ribozyme; HP ribozyme; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN US2002082225-A1.  
XX  
PD 27-JUN-2002.  
XX  
PF 23-MAR-1999; 99US-00274553.  
XX  
PR 23-MAR-1999; 99US-00274553.  
XX  
PA (BLAT/) BLATT L.  
PA (MCSW/) MCSWIGGEN J A.  
PA (ROBE/) ROBERTS B.  
PA (PAVC/) PAVCO P A.  
PA (MACE/) MACEJACK D.  
XX  
PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;  
XX  
DR WPI; 2002-617759/66.  
XX  
PT New ribozymes targeting RNA derived from hepatitis C virus inhibit viral  
PT replication and are useful to treat hepatitis C virus infections and  
PT cirrhosis, liver failure or hepatocellular carcinoma.







CC The present invention describes an array of nucleic acid probes  
CC immobilised on a solid support, which comprises: (1) a first probe set,  
CC comprising probes with a segment of at least 6 nucleotides complementary  
CC to the CFTR (cystic fibrosis transmembrane conductance regulator) gene,  
CC where the segment includes at least 1 interrogation position  
CC complementary to a nucleotide in the CFTR gene sequence; and (2) second,  
CC third and fourth probe sets, each comprising probes identical to those in  
CC (1) except that the interrogation position is occupied by a different  
CC nucleotide. AAA05991 to AAA06240 represent CFTR gene analysis  
CC oligonucleotide probes for use in the exemplification of the present  
CC invention. The present invention also describes a method of comparing a  
CC target nucleic acid with a reference sequence consisting of a  
CC predetermined sequence of nucleotides, comprising: (a) hybridising a  
CC sample comprising the target nucleic acid to an array of nucleic acid  
CC probes immobilised on a solid support; (b) comparing the relative  
CC specific binding of two corresponding probes from the first and second  
CC probe sets; (c) assigning a nucleotide in the target sequence as the  
CC complement of the interrogation position of the probe having the greater  
CC specific binding; and (d) repeating (b) and (c) by comparing the relative  
CC specific binding of a further two corresponding probes from the first and  
CC second probe sets until each nucleotide of interest in the target  
CC sequence has been assigned. The array is useful for analysis of the CFTR  
CC gene, e.g. detection of mutations  
XX  
SQ Sequence 13 BP; 0 A; 3 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 33.8%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 1.2e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 TGCTGTGTGACCT 22  
|| ||||| |||  
Db 1 TGGTGTGTGCCCT 13

RESULT 127  
ABF45366/c  
ID ABF45366 standard; DNA; 13 BP.

AC ABF45366;

XX 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 145363 for detecting SNP TSC0036590.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

XX Claim 1; SEQ ID NO 145363; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 3 A; 1 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 33.8%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 1.2e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCT 13  
||||| |||||  
Db 13 CCATCCGCCTACT 1

RESULT 128

ABF45367  
ID ABF45367 standard; DNA; 13 BP.

XX AC ABF45367;

XX 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 145364 for detecting SNP TSC0036590.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

XX Claim 1; SEQ ID NO 145364; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 2 A; 7 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 33.8%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 1.2e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCT 13  
||| ||| ||| |||  
Db 1 CCATCCGCCTACT 13

RESULT 129  
ABK28875  
ID ABK28875 standard; DNA; 13 BP.  
XX  
AC ABK28875;  
XX  
DT 09-APR-2002 (first entry)  
XX  
DE HPV blocker probe PZ-1.

XX  
KW HSV-1; HSV-2; HPV; ss; probe; microorganism classification;  
KW infectious disease; genetic abnormality; cancer; capture sequence;  
KW blocker probe.

OS Human papillomavirus.

XX  
PN WO200196608-A1.

XX  
PD 20-DEC-2001.

XX  
PF 15-JUN-2001; 2001WO-US019353.

XX  
PR 15-JUN-2000; 2000US-00594839.

XX  
PA (DIGE-) DIGENE CORP.

XX  
PI Anthony J, Lorincz A, Williams I, Troy J, Tang Y;

XX  
DR WPI; 2002-130748/17.

XX  
PT Detecting a target nucleic acid, for identifying microorganisms,  
PT diagnosing infections or detecting genetic abnormalities, comprises  
PT producing and detecting double-stranded hybrids between probes and the  
PT target nucleic acid.

XX  
PS Claim 53; Page 24; 128pp; English.

XX  
CC The invention relates to detecting a target nucleic acid comprising (a)  
CC hybridising a single-stranded or partially single-stranded target nucleic  
CC acid to a capture sequence probe and a signal sequence probe to form  
CC double-stranded hybrids between the probes and the target nucleic acid,  
CC where the capture sequence probe and the signal sequence probe are  
CC capable of hybridising to non-overlapping regions within the target  
CC nucleic acid and not hybridising to each other, (b) adding a blocker  
CC probe to the hybridisation reaction, where the blocker probe hybridises  
CC to excess non-hybridised capture sequence probes, (c) binding the hybrid  
CC to a solid phase to form a bound hybrid, and (d) detecting the bound  
CC hybrid. The method is used to detecting a target nucleic acid. The method  
CC is useful for identifying and classifying microorganisms, diagnosing  
CC infectious diseases, detecting and characterising genetic abnormalities,  
CC identifying genetic changes associated with cancer, studying genetic  
CC susceptibility to disease, and measuring response to various types of  
CC treatment. The method is also useful for detecting the presence of  
CC nucleic acid in test samples. The method is not only rapid and sensitive,  
CC but is also highly specific and capable of discriminating highly  
CC homologous nucleic acid target sequences. Blocker probes comprising  
CC oligonucleotides complementary to the capture sequence probes are used in  
CC the method to eliminate excess capture sequence probe, thus reducing the  
CC background signal in detection and increasing specificity of the assay.  
CC The present sequence is a blocker probe derived from HSV-1, HSV-2, HPV or  
CC HBV sequences

XX  
SQ Sequence 13 BP; 1 A; 7 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 33.8%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 1.2e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGT 17  
||| ||| ||| |||  
Db 1 CCACCTCCTGCGT 13

RESULT 130  
ABZ34180/c  
ID ABZ34180 standard; DNA; 13 BP.  
XX  
AC ABZ34180;  
XX  
DT 31-JAN-2003 (first entry)  
XX  
DE HIV-1 reverse transcriptase mutation detection probe SEQ ID NO:422.

XX  
KW Human immunodeficiency virus; HIV; reverse transcriptase; RT; enzyme;  
KW detection; mutation; anti-HIV drug resistance; polymorphism; resistance;  
KW probe; ss.

XX  
OS Human immunodeficiency virus 1.

OS Synthetic.

XX  
PN WO200255741-A2.

XX  
PD 18-JUL-2002.

XX  
PF 09-JAN-2002; 2002WO-EP000153.

XX  
PR 11-JAN-2001; 2001EP-00870005.

XX  
PR 20-APR-2001; 2001EP-00870085.

XX  
PR 24-APR-2001; 2001US-0286102P.

XX  
PA (INNO-) INNOGENETICS NV.

XX  
PI De Smet K, Stuyver L;

XX  
DR WPI; 2002-590680/63.

XX  
PT Detecting mutations associated with anti-HIV drug resistance comprises  
PT detecting at least one of the mutations in the HIV reverse transcriptase  
PT gene by using probes optimized to function together in a reverse-  
PT hybridization assay.

XX  
PS Claim 2; Page 27; 117pp; English.

XX  
CC The present invention describes a method for detecting mutations  
CC associated with anti-HIV drug resistance in a patient by detecting at  
CC least one of the mutations K103N/R, V106A/I/L, Y181C/I, M184V/I, Y188L,  
CC G190A/S/R, T215Y/F/D/S/A and/or Q151M/L in the reverse transcriptase (RT)  
CC of HIV strains in a biological sample using a specific set of probes  
CC optimised to function together in a reverse-hybridisation assay. The  
CC method and the nucleic acid sequences used in the method are useful for  
CC determining viral mutations and/or polymorphisms in the HIV RT gene  
CC associated with resistance. The probes are useful for the genetic  
CC detection, preferably in vitro detection of the mutations K103N/R,  
CC V106A/I/L, Y181C/I, Q151M/L, M184V/I, Y188L, G190A/S/R and/or  
CC T215Y/F/D/S/A in the RT of HIV strains in a biological sample, where the  
CC mutation is associated with anti-HIV drug resistance. The method provides  
CC a rapid, reliable and precise assay or determination and monitoring of  
CC antiviral drug resistance or mutations associated with drug resistance of  
CC viruses containing RT genes. ABZ33759 to ABZ34642 represent HIV RT  
CC sequences and probes which are used in the exemplification of the present  
CC invention

XX  
SQ Sequence 13 BP; 3 A; 2 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 33.8%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 1.2e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTG 14  
Db ||||| | |||  
13 CATCCACGTACTG 1

RESULT 131  
ABZ34155/c  
ID ABZ34155 standard; DNA; 13 BP.  
XX  
AC ABZ34155;  
XX  
DT 31-JAN-2003 (first entry)  
XX  
DE HIV-1 reverse transcriptase mutation detection probe SEQ ID NO:397.  
XX  
KW Human immunodeficiency virus; HIV; reverse transcriptase; RT; enzyme;  
KW detection; mutation; anti-HIV drug resistance; polymorphism; resistance;  
KW probe; ss.  
XX  
OS Human immunodeficiency virus 1.  
OS Synthetic.  
XX  
PN WO200255741-A2.  
XX  
PD 18-JUL-2002.  
XX  
PF 09-JAN-2002; 2002WO-EP000153.  
XX  
PR 11-JAN-2001; 2001EP-00870005.  
PR 20-APR-2001; 2001EP-00870085.  
PR 24-APR-2001; 2001US-0286102P.  
XX  
PA (INNO-) INNOGENETICS NV.  
XX  
PI De Smet K, Stuyver L;  
XX  
DR WPI; 2002-590680/63.  
XX  
PT Detecting mutations associated with anti-HIV drug resistance comprises  
PT detecting at least one of the mutations in the HIV reverse transcriptase  
PT gene by using probes optimized to function together in a reverse-  
PT hybridization assay.  
XX  
PS Claim 2; Page 26; 117pp; English.  
XX  
CC The present invention describes a method for detecting mutations  
CC associated with anti-HIV drug resistance in a patient by detecting at  
CC least one of the mutations K103N/R, V106A/I/L, Y181C/I, M184V/I, Y188L,  
CC G190A/S/R, T215Y/F/D/S/A and/or Q151M/L in the reverse transcriptase (RT)  
CC of HIV strains in a biological sample using a specific set of probes  
CC optimised to function together in a reverse-hybridisation assay. The  
CC method and the nucleic acid sequences used in the method are useful for  
CC determining viral mutations and/or polymorphisms in the HIV RT gene  
CC associated with resistance. The probes are useful for the genetic  
CC detection, preferably in vitro detection of the mutations K103N/R,  
CC V106A/I/L, Y181C/I, Q151M/L, M184V/I, Y188L, G190A/S/R and/or  
CC T215Y/F/D/S/A in the RT of HIV strains in a biological sample, where the  
CC mutation is associated with anti-HIV drug resistance. The method provides  
CC a rapid, reliable and precise assay or determination and monitoring of  
CC antiviral drug resistance or mutations associated with drug resistance of  
CC viruses containing RT genes. ABZ33759 to ABZ34642 represent HIV RT  
CC sequences and probes which are used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 13 BP; 3 A; 2 C; 5 G; 3 T; 0 U; 0 Other;  
Query Match 33.8%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 1.2e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTG 14  
Db ||||| | |||

Db 13 CATCCACGTACTG 1

RESULT 132  
ADF48833  
ID ADF48833 standard; DNA; 13 BP.  
XX  
AC ADF48833;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE DNA array associated oligonucleotide #25.  
XX  
KW ss; DNA array; microfabricated array; DNA chip; CFTR gene mutation;  
KW cystic fibrosis gene; uncharacterised mutation identification;  
KW simultaneous screening.  
XX  
OS Synthetic.  
XX  
PN US2003165823-A1.  
XX  
PD 04-SEP-2003.  
XX  
PF 22-FEB-2000; 2000US-00510378.  
XX  
PR 26-OCT-1993; 93US-00143312.  
PR 02-AUG-1994; 94US-00284064.  
PR 26-OCT-1994; 94WO-US012305.  
PR 02-AUG-1995; 95US-00510521.  
PR 10-OCT-1995; 95US-00544381.  
XX  
PA (CRON/) CRONIN M T.  
PA (MIYA/) MIYADA C G.  
PA (HUBB/) HUBBELL E A.  
PA (CHEE/) CHEE M.  
PA (FODO/) FODOR S P A.  
PA (HUAN/) HUANG X C.  
PA (LIPS/) LIPSHUTZ R J.  
PA (LOBB/) LOBBAN P E.  
PA (MORR/) MORRIS M S.  
PA (SHEL/) SHELDON E L.  
XX  
PI Cronin MT, Miyada CG, Hubbell EA, Chee M, Fodor SPA, Huang XC;  
PI Lipshutz RJ, Lobban PE, Morris MS, Sheldon EL;  
XX  
DR WPI; 2004-020546/02.  
XX  
PT Arrays of oligonucleotide probes immobilized in microfabricated patterns  
PT on chips used for detecting mutations in the cystic fibrosis  
PT transmembrane conductance regulator (CFTR) gene.  
XX  
PS Disclosure; SEQ ID NO 25; 123pp; English.  
XX  
CC The invention relates to an array of oligonucleotide probes immobilised  
CC on a solid support, the array comprising at least two sets of  
CC oligonucleotide probes (a microfabricated array or DNA chip). The arrays  
CC can be used in methods to detect uncommon mutations in the CFTR gene.  
CC Prior art methods for analysis of the cystic fibrosis gene do not monitor  
CC large regions of the CFTR gene. The invention uses a large number of  
CC probes and therefore permits the identification of uncharacterised  
CC mutations and the simultaneous screening of large numbers of mutations  
CC with a high degree of accuracy. The present sequence is used in the  
CC exemplification of the invention.  
XX  
SQ Sequence 13 BP; 0 A; 3 C; 5 G; 5 T; 0 U; 0 Other;  
Query Match 33.8%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 1.2e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 TGCTGTGTGACCT 22  
Db ||||| | |||  
1 TGCTGTGTGCCCT 13

RESULT 133  
AAQ78366  
ID AAQ78366 standard; DNA; 14 BP.  
XX  
AC AAQ78366;  
XX  
DT 25-MAR-2003 (revised)  
DT 27-JUN-1995 (first entry)  
XX  
DE Antisense oligonucleotide hybridising to TGF-beta gene.  
XX  
KW Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;  
KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;  
KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;  
KW immunosuppression; oligonucleotide; ss.  
XX  
OS Synthetic.  
OS  
XX WO9425588-A2.  
PN  
XX  
PD 10-NOV-1994.  
XX  
PF 29-APR-1994; 94WO-EP001362.  
XX  
PR 30-APR-1993; 93EP-00107089.  
PR 13-MAY-1993; 93EP-00107849.  
XX  
PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
XX  
PI Schlingensiepen G, Brysch W, Schlingensiepen R;  
PI Bogdahn U;  
XX  
DR WPI; 1994-358266/44.  
XX  
PT New transforming growth factor beta anti:sense oligo:nucleotide(s) - for  
PT treating immunosuppression, tumours, etc.  
XX  
PS Claim 6; Page 28; 74pp; English.  
XX  
CC The antisense oligonucleotides are useful in the treatment of tumours in  
CC which expression of TGF-beta is of relevance for pathogenicity and/or  
CC inhibition of pathological angiogenesis. They are used especially for the  
CC treatment of the immunosuppressive effect of TGF-beta, augmentation of  
CC the proliferation of cytotoxic lymphocytes, treatment of endogenous  
CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas  
CC and malignant gliomas, including glioblastomas, treatment and prophylaxis  
CC of skin carcinogenesis, and treatment of oesophageal and gastric  
CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESEQ files  
CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-  
CC beta 1. The sequences given in GENESEQ files AAQ78408-78487 are antisense  
CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate  
CC analogues. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 14 BP; 1 A; 3 C; 4 G; 6 T; 0 U; 0 Other;  
  
Query Match 33.8%; Score 9.8; DB 1; Length 14;  
Best Local Similarity 84.6%; Pred. No. 1.3e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 10 TGCTGTGTGACCT 22  
Db |||||  
1 TGCTGTGTGACT 13  
  
RESULT 134  
AAV48778  
ID AAV48778 standard; DNA; 14 BP.  
XX  
AC AAV48778;  
XX  
DT 15-OCT-1998 (first entry)

XX ErbB-2 gene antisense oligonucleotide ErbB-2-70.  
DE  
XX ErbB-2; antisense oligonucleotide; modulate; gene expression; ss.  
KW  
XX Synthetic.  
OS  
OS Homo sapiens.  
XX  
PN EP856579-A1.  
XX  
PD 05-AUG-1998.  
XX  
PF 31-JAN-1997; 97EP-00101531.  
XX  
PR 31-JAN-1997; 97EP-00101531.  
XX  
PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
XX  
PI Schlingensiepen K, Brysch W;  
XX  
DR WPI; 1998-400910/35.  
XX  
PT Preparation of antisense oligo:nucleotide(s) which lack long runs of  
PT consecutive guanosine or inosine - and have specific ratio of residues  
PT able to form two or three hydrogen bonds, have greater activity and  
PT reduced toxicity, used therapeutically or to modulate growth of cells in  
PT culture.  
XX  
PS Claim 10; Fig 6b; 286pp; English.  
XX  
CC AAV48709-886 represent antisense oligonucleotides directed against the  
CC ErbB-2 gene. Of these, only oligonucleotides AAV48709-91 resulted in  
CC significant reduction in ErbB-2 protein expression, while  
CC oligonucleotides AAV48792-886 had little effect. The oligonucleotides  
CC exemplify the invention. The specification describes oligonucleotides  
CC that contain 8-30 nucleotides, which contain at most 8 nucleotides that  
CC can each form three hydrogen bonds to cytosine; do not contain four  
CC consecutive nucleotides able to form three H-bonds each to four  
CC consecutive cytosines; do not contain two sequences of three consecutive  
CC nucleotides each able to form three H-bonds to three consecutive  
CC cytosines, and the ratio between residues able to form two H-bonds each  
CC (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The  
CC oligonucleotides are used to modulate expression of genes, particularly  
CC the genes for p53, ErbB-2, junB, junD, TGF-beta 1 or beta 2 to control  
CC proliferation of primary cell cultures (e.g. bone marrow stem, liver or  
CC kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The  
CC oligonucleotides can also be used to analyse function of proteins (by  
CC altering their expression or activity) and therapeutically, e.g. in cases  
CC of cancer or (targeting TGF) for stimulating the immune system  
XX  
SQ Sequence 14 BP; 2 A; 5 C; 4 G; 3 T; 0 U; 0 Other;  
  
Query Match 33.8%; Score 9.8; DB 1; Length 14;  
Best Local Similarity 84.6%; Pred. No. 1.3e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 11 GCTGTGTGACCTG 23  
Db |||||  
1 GCTGTGTCCACAG 13  
  
RESULT 135  
ABZ34156/c  
ID ABZ34156 standard; DNA; 14 BP.  
XX  
AC ABZ34156;  
XX  
DT 31-JAN-2003 (first entry)  
XX  
DE HIV-1 reverse transcriptase mutation detection probe SEQ ID NO:398.  
XX  
KW Human immunodeficiency virus; HIV; reverse transcriptase; RT; enzyme;  
KW detection; mutation; anti-HIV drug resistance; polymorphism; resistance;







XX PD 18-JUL-2002.  
XX PF 09-JAN-2002; 2002WO-EP000153.  
XX PR 11-JAN-2001; 2001EP-00870005.  
PR 20-APR-2001; 2001EP-00870085.  
PR 24-APR-2001; 2001US-0286102P.  
XX PA (INNO-) INNOGENETICS NV.  
XX PI De Smet K, Stuyver L;  
XX WPI; 2002-590680/63.  
XX  
PT Detecting mutations associated with anti-HIV drug resistance comprises  
PT detecting at least one of the mutations in the HIV reverse transcriptase  
PT gene by using probes optimized to function together in a reverse-  
PT hybridization assay.  
XX Claim 2; Page 26; 117pp; English.  
XX  
CC The present invention describes a method for detecting mutations  
CC associated with anti-HIV drug resistance in a patient by detecting at  
CC least one of the mutations K103N/R, V106A/I/L, Y181C/I, M184V/I, Y188L,  
CC G190A/S/R, T215Y/F/D/S/A and/or Q151M/L in the reverse transcriptase (RT)  
CC of HIV strains in a biological sample using a specific set of probes  
CC optimised to function together in a reverse-hybridisation assay. The  
CC method and the nucleic acid sequences used in the method are useful for  
CC determining viral mutations and/or polymorphisms in the HIV RT gene  
CC associated with resistance. The probes are useful for the genetic  
CC detection, preferably in vitro detection of the mutations K103N/R,  
CC V106A/I/L, Y181C/I, Q151M/L, M184V/I, Y188L, G190A/S/R and/or  
CC T215Y/F/D/S/A in the RT of HIV strains in a biological sample, where the  
CC mutation is associated with anti-HIV drug resistance. The method provides  
CC a rapid, reliable and precise assay or determination and monitoring of  
CC antiviral drug resistance or mutations associated with drug resistance of  
CC viruses containing RT genes. ABZ33759 to ABZ34642 represent HIV RT  
CC sequences and probes which are used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 14 BP; 3 A; 2 C; 5 G; 4 T; 0 U; 0 Other;  
  
Query Match 33.8%; Score 9.8; DB 1; Length 14;  
Best Local Similarity 84.6%; Pred. No. 1.3e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2 CATCCACCTGCTG 14  
Db ||||| | |||  
14 CATCCACGTACTG 2  
  
RESULT 138  
ABZ34170/c  
ID ABZ34170 standard; DNA; 14 BP.  
XX AC ABZ34170;  
XX DT 31-JAN-2003 (first entry)  
DE HIV-1 reverse transcriptase mutation detection probe SEQ ID NO:412.  
XX  
KW Human immunodeficiency virus; HIV; reverse transcriptase; RT; enzyme;  
KW detection; mutation; anti-HIV drug resistance; polymorphism; resistance;  
KW probe; ss.  
XX  
OS Human immunodeficiency virus 1.  
OS Synthetic.  
XX  
PN WO200255741-A2.  
XX PD 18-JUL-2002.  
XX PF 09-JAN-2002; 2002WO-EP000153.  
XX PR 11-JAN-2001; 2001EP-00870005.

PF 09-JAN-2002; 2002WO-EP000153.  
XX 11-JAN-2001; 2001EP-00870005.  
PR 20-APR-2001; 2001EP-00870085.  
PR 24-APR-2001; 2001US-0286102P.  
XX (INNO-) INNOGENETICS NV.  
PA De Smet K, Stuyver L;  
XX WPI; 2002-590680/63.  
XX  
PT Detecting mutations associated with anti-HIV drug resistance comprises  
PT detecting at least one of the mutations in the HIV reverse transcriptase  
PT gene by using probes optimized to function together in a reverse-  
PT hybridization assay.  
XX Claim 2; Page 27; 117pp; English.  
XX  
CC The present invention describes a method for detecting mutations  
CC associated with anti-HIV drug resistance in a patient by detecting at  
CC least one of the mutations K103N/R, V106A/I/L, Y181C/I, M184V/I, Y188L,  
CC G190A/S/R, T215Y/F/D/S/A and/or Q151M/L in the reverse transcriptase (RT)  
CC of HIV strains in a biological sample using a specific set of probes  
CC optimised to function together in a reverse-hybridisation assay. The  
CC method and the nucleic acid sequences used in the method are useful for  
CC determining viral mutations and/or polymorphisms in the HIV RT gene  
CC associated with resistance. The probes are useful for the genetic  
CC detection, preferably in vitro detection of the mutations K103N/R,  
CC V106A/I/L, Y181C/I, Q151M/L, M184V/I, Y188L, G190A/S/R and/or  
CC T215Y/F/D/S/A in the RT of HIV strains in a biological sample, where the  
CC mutation is associated with anti-HIV drug resistance. The method provides  
CC a rapid, reliable and precise assay or determination and monitoring of  
CC antiviral drug resistance or mutations associated with drug resistance of  
CC viruses containing RT genes. ABZ33759 to ABZ34642 represent HIV RT  
CC sequences and probes which are used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 14 BP; 3 A; 2 C; 5 G; 4 T; 0 U; 0 Other;  
  
Query Match 33.8%; Score 9.8; DB 1; Length 14;  
Best Local Similarity 84.6%; Pred. No. 1.3e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2 CATCCACCTGCTG 14  
Db ||||| | |||  
14 CATCCACGTACTG 2  
  
RESULT 139  
ABZ34179/c  
ID ABZ34179 standard; DNA; 14 BP.  
XX AC ABZ34179;  
XX DT 31-JAN-2003 (first entry)  
DE HIV-1 reverse transcriptase mutation detection probe SEQ ID NO:421.  
XX  
KW Human immunodeficiency virus; HIV; reverse transcriptase; RT; enzyme;  
KW detection; mutation; anti-HIV drug resistance; polymorphism; resistance;  
KW probe; ss.  
XX  
OS Human immunodeficiency virus 1.  
OS Synthetic.  
XX  
PN WO200255741-A2.  
XX PD 18-JUL-2002.  
XX PF 09-JAN-2002; 2002WO-EP000153.  
XX PR 11-JAN-2001; 2001EP-00870005.

PR 20-APR-2001; 2001EP-00870085.  
PR 24-APR-2001; 2001US-0286102P.  
XX  
PA (INNO-) INNOGENETICS NV.  
XX  
PI De Smet K, Stuyver L;  
XX  
DR WPI; 2002-590680/63.  
XX  
PI  
XX  
DR  
XX  
PT Detecting mutations associated with anti-HIV drug resistance comprises  
PT detecting at least one of the mutations in the HIV reverse transcriptase  
PT gene by using probes optimized to function together in a reverse-  
PT hybridization assay.  
XX  
PS Claim 2; Page 27; 117pp; English.  
XX  
CC The present invention describes a method for detecting mutations  
CC associated with anti-HIV drug resistance in a patient by detecting at  
CC least one of the mutations K103N/R, V106A/I/L, Y181C/I, M184V/I, Y188L,  
CC G190A/S/R, T215Y/F/D/S/A and/or Q151M/L in the reverse transcriptase (RT)  
CC of HIV strains in a biological sample using a specific set of probes  
CC optimised to function together in a reverse-hybridisation assay. The  
CC method and the nucleic acid sequences used in the method are useful for  
CC determining viral mutations and/or polymorphisms in the HIV RT gene  
CC associated with resistance. The probes are useful for the genetic  
CC detection, preferably in vitro detection of the mutations K103N/R,  
CC V106A/I/L, Y181C/I, Q151M/L, M184V/I, Y188L, G190A/S/R and/or  
CC T215Y/F/D/S/A in the RT of HIV strains in a biological sample, where the  
CC mutation is associated with anti-HIV drug resistance. The method provides  
CC a rapid, reliable and precise assay or determination and monitoring of  
CC antiviral drug resistance or mutations associated with drug resistance of  
CC viruses containing RT genes. ABZ33759 to ABZ34642 represent HIV RT  
CC sequences and probes which are used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 14 BP; 4 A; 2 C; 5 G; 3 T; 0 U; 0 Other;  
XX  
SQ  
Query Match 33.8%; Score 9.8; DB 1; Length 14;  
Best Local Similarity 84.6%; Pred. No. 1.3e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 CATCCACCTGCTG 14  
Db 13 CATCCACGTACTG 1  
RESULT 140  
ABZ34172/c  
ID ABZ34172 standard; DNA; 14 BP.  
XX  
AC ABZ34172;  
XX  
DT 31-JAN-2003 (first entry)  
XX  
DE HIV-1 reverse transcriptase mutation detection probe SEQ ID NO:414.  
XX  
KW Human immunodeficiency virus; HIV; reverse transcriptase; RT; enzyme;  
KW detection; mutation; anti-HIV drug resistance; polymorphism; resistance;  
KW probe; ss.  
XX  
OS Human immunodeficiency virus 1.  
OS Synthetic.  
XX  
PN WO200255741-A2.  
XX  
PD 18-JUL-2002.  
XX  
PF 09-JAN-2002; 2002WO-EP000153.  
XX  
XX 11-JAN-2001; 2001EP-00870005.  
PR 20-APR-2001; 2001EP-00870085.  
PR 24-APR-2001; 2001US-0286102P.  
XX

PA (INNO-) INNOGENETICS NV.  
XX  
PI De Smet K, Stuyver L;  
XX  
DR WPI; 2002-590680/63.  
XX  
PI  
XX  
DR  
XX  
PT Detecting mutations associated with anti-HIV drug resistance comprises  
PT detecting at least one of the mutations in the HIV reverse transcriptase  
PT gene by using probes optimized to function together in a reverse-  
PT hybridization assay.  
XX  
PS Claim 2; Page 27; 117pp; English.  
XX  
CC The present invention describes a method for detecting mutations  
CC associated with anti-HIV drug resistance in a patient by detecting at  
CC least one of the mutations K103N/R, V106A/I/L, Y181C/I, M184V/I, Y188L,  
CC G190A/S/R, T215Y/F/D/S/A and/or Q151M/L in the reverse transcriptase (RT)  
CC of HIV strains in a biological sample using a specific set of probes  
CC optimised to function together in a reverse-hybridisation assay. The  
CC method and the nucleic acid sequences used in the method are useful for  
CC determining viral mutations and/or polymorphisms in the HIV RT gene  
CC associated with resistance. The probes are useful for the genetic  
CC detection, preferably in vitro detection of the mutations K103N/R,  
CC V106A/I/L, Y181C/I, Q151M/L, M184V/I, Y188L, G190A/S/R and/or  
CC T215Y/F/D/S/A in the RT of HIV strains in a biological sample, where the  
CC mutation is associated with anti-HIV drug resistance. The method provides  
CC a rapid, reliable and precise assay or determination and monitoring of  
CC antiviral drug resistance or mutations associated with drug resistance of  
CC viruses containing RT genes. ABZ33759 to ABZ34642 represent HIV RT  
CC sequences and probes which are used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 14 BP; 3 A; 2 C; 6 G; 3 T; 0 U; 0 Other;  
XX  
SQ  
Query Match 33.8%; Score 9.8; DB 1; Length 14;  
Best Local Similarity 84.6%; Pred. No. 1.3e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 CATCCACCTGCTG 14  
Db 14 CATCCACGTACTG 2  
RESULT 141  
AEA60845  
ID AEA60845 standard; DNA; 14 BP.  
XX  
AC AEA60845;  
XX  
DT 11-AUG-2005 (first entry)  
XX  
DE Blood fluke Sjpp 5'-RACE PCR primer Sjpp-P.  
XX  
KW Sjpp; RACE; PCR; primer; ss.  
XX  
OS Fasciola sp.  
OS Synthetic.  
XX  
PN CN1563382-A.  
XX  
PD 12-JAN-2005.  
XX  
PF 16-APR-2004; 2004CN-00017743.  
XX  
PR 16-APR-2004; 2004CN-00017743.  
XX  
PA (SHAN-) SHANGHAI LIVESTOCK PARASTITIC DISEASE IN.  
XX  
PI Lin J, Yao L, Fu Z;  
XX  
DR WPI; 2005-307227/32.  
XX  
PT Gene of Chinese Mainland SJPP gene stock of Japanese blood fluke, clone,

PT expression and application.  
XX  
PS Example 1; Page 9; 25pp; Chinese.  
XX  
CC The invention relates to a novel blood fluke gene designated Sjpp. Also  
CC described are methods for cloning and expressing the Sjpp gene. The  
CC present sequence represents a 5'-RACE PCR primer for the blood fluke Sjpp  
CC gene, which is used in an example from the present invention.  
XX  
SQ Sequence 14 BP; 1 A; 4 C; 5 G; 4 T; 0 U; 0 Other;  
  
Query Match 33.8%; Score 9.8; DB 1; Length 14;  
Best Local Similarity 84.6%; Pred. No. 1.3e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 4 TCCACCTGCTGTG 16  
Db 2 TCCGCATGCTGTG 14  
  
RESULT 142  
AAZ18959  
ID AAZ18959 standard; DNA; 11 BP.  
XX  
AC AAZ18959;  
XX  
DT 22-OCT-1999 (first entry)  
XX  
DE Murine MRL SAGE tag 1334652.  
XX  
KW Wound healing; non-MRL healer mouse; quantitative trait locus; QTL;  
KW healing response; microsatellite marker; treatment; central nerve;  
KW peripheral nerve; nerve injury; SAGE tag; murine; ss.  
XX  
OS Mus sp.  
XX  
PN WO9941364-A2.  
XX  
PD 19-AUG-1999.  
XX  
PF 12-FEB-1999; 99WO-US002962.  
XX  
PR 13-FEB-1998; 98US-0074737P.  
PR 26-AUG-1998; 98US-0097937P.  
PR 28-SEP-1998; 98US-0102051P.  
XX  
PA (WIST-) WISTAR INST.  
XX  
PI Heber-Katz E;  
XX  
DR WPI; 1999-494533/41.  
XX  
PT New mammalian model for enhanced wound healing - useful for identifying  
PT enhanced wound healing genes.  
XX  
PS Claim 13; Page 73; 136pp; English.  
XX  
CC This invention describes a novel non-MRL healer mouse (M) having at least  
CC one quantitative trait locus selected from those given in the  
CC specification, exhibiting an enhanced healing response to a wound  
CC compared to mice (m) without the locus. The invention describes a novel  
CC method of identifying a gene involved in enhanced wound healing by  
CC identifying DNA microsatellite markers which can distinguish healer mice  
CC from non-healer mice and identifying microsatellite markers which  
CC segregate with enhanced wound healing in progeny of the mice, where a  
CC chromosomal locus containing at least one enhanced wound healing gene is  
CC identified. A method of treating a wound in a mammal is also disclosed.  
CC The new methods are useful for treating wounds, especially central and  
CC peripheral nerve wound. The methods of the invention are useful for  
CC restoring function after nerve injury in a mammal. (M) is useful as a  
CC mammalian model of enhanced wound healing, useful for identifying genes  
CC and gene products involved in enhanced wound healing, and to provide  
CC methods for wound healing. AAZ18691-Z19036 represent murine SAGE tags

CC from C57BL/6 and MRL mice which are used to illustrate the method of the  
CC invention  
XX Sequence 11 BP; 1 A; 6 C; 1 G; 3 T; 0 U; 0 Other;  
SQ  
  
Query Match 32.4%; Score 9.4; DB 1; Length 11;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 CCACCTGCTGT 15  
Db 1 CCACCTCCTGT 11  
  
RESULT 143  
AAZ18744/C  
ID AAZ18744 standard; DNA; 11 BP.  
XX  
AC AAZ18744;  
XX  
DT 22-OCT-1999 (first entry)  
XX  
DE Murine C57BL/6 SAGE tag 1217605.  
XX  
KW Wound healing; non-MRL healer mouse; quantitative trait locus; QTL;  
KW healing response; microsatellite marker; treatment; central nerve;  
KW peripheral nerve; nerve injury; SAGE tag; murine; ss.  
XX  
OS Mus sp.  
XX  
PN WO9941364-A2.  
XX  
PD 19-AUG-1999.  
XX  
PF 12-FEB-1999; 99WO-US002962.  
XX  
PR 13-FEB-1998; 98US-0074737P.  
PR 26-AUG-1998; 98US-0097937P.  
PR 28-SEP-1998; 98US-0102051P.  
XX  
PA (WIST-) WISTAR INST.  
XX  
PI Heber-Katz E;  
XX  
DR WPI; 1999-494533/41.  
XX  
PT New mammalian model for enhanced wound healing - useful for identifying  
PT enhanced wound healing genes.  
XX  
PS Claim 13; Page 56; 136pp; English.  
XX  
CC This invention describes a novel non-MRL healer mouse (M) having at least  
CC one quantitative trait locus selected from those given in the  
CC specification, exhibiting an enhanced healing response to a wound  
CC compared to mice (m) without the locus. The invention describes a novel  
CC method of identifying a gene involved in enhanced wound healing by  
CC identifying DNA microsatellite markers which can distinguish healer mice  
CC from non-healer mice and identifying microsatellite markers which  
CC segregate with enhanced wound healing in progeny of the mice, where a  
CC chromosomal locus containing at least one enhanced wound healing gene is  
CC identified. A method of treating a wound in a mammal is also disclosed.  
CC The new methods are useful for treating wounds, especially central and  
CC peripheral nerve wound. The methods of the invention are useful for  
CC restoring function after nerve injury in a mammal. (M) is useful as a  
CC mammalian model of enhanced wound healing, useful for identifying genes  
CC and gene products involved in enhanced wound healing, and to provide  
CC methods for wound healing. AAZ18691-Z19036 represent murine SAGE tags  
CC from C57BL/6 and MRL mice which are used to illustrate the method of the  
CC invention  
XX Sequence 11 BP; 4 A; 5 C; 2 G; 0 T; 0 U; 0 Other;  
SQ  
  
Query Match 32.4%; Score 9.4; DB 1; Length 11;

```
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 TGTGTGACCTG 23
Db 11 TGTGTGGCCTG 1

RESULT 144
AAA96508/c
ID AAA96508 standard; DNA; 11 BP.
XX
AC AAA96508;
XX
DT 08-FEB-2001 (first entry)
XX
DE Consensus sequence derived from the human VhIII gene domain.
XX
KW HIV-1; envelope glycoprotein; gp120; ss.
XX
OS Homo sapiens.
XX
PN EP1043407-A2.
XX
PD 11-OCT-2000.
XX
PF 04-APR-2000; 2000EP-00107333.
XX
PR 09-APR-1999; 99IT-MI000729.
XX
PA (DIAP-) DIAPHARM LTD.
XX
PI Veljkovic V, Veljkovic N, Prljic J, Metlas R;
XX
DR WPI; 2000-595765/57.
XX
PT New oligonucleotides for identifying human immunodeficiency virus-1 in
PT biological samples comprise an 8 bp sequence inserted between highly
PT conserved HIV-1 gp120 gene derived sequences.
XX
PS Disclosure; Page 3; 8pp; English.
XX
CC The present sequence represents a consensus sequence derived from the
CC human VhIII gene domain coding the FR1 region. The sequence used to
CC design primers which also contain the sequence GCTGTGG, inserted between
CC highly conserved sequences corresponding to the domain of Human
CC immunodeficiency virus type 1 (HIV-1) envelope glycoprotein gp120. The
CC primer comprises The PCR primer is used to detect the presence of HIV-1
CC isolates in a biological sample
XX
SQ Sequence 11 BP; 2 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 32.4%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCCACCTGCTG 14
Db 11 TCCACCAGCTG 1

RESULT 145
ABQ86330
ID ABQ86330 standard; cDNA; 11 BP.
XX
AC ABQ86330;
XX
DT 10-SEP-2002 (first entry)
XX
DE Human skin stress/ageing related EST SEQ ID NO 85.
XX
KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
```

```
OS Homo sapiens.
XX
PN WO200253773-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015178.
XX
PR 03-JAN-2001; 2001DE-01000121.
XX
PA (HENK ) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-528865/56.
XX
PT Identifying genes involved in skin stress and aging, useful e.g. in
PT screening for cosmetic or therapeutic agents, based on differential gene
PT expression.
XX
PS Claim 8; Page 40; 325pp; German.
XX
CC The invention relates to identifying (M1) genes in vitro that, in humans
CC or animals, are important for skin ageing and/or skin stress by serial
CC analysis of gene expression between mixtures of transcribed and
CC optionally translated, genetically encoded factors (A) obtained from
CC young and aged skin, to identify that genes that show strong differential
CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC useful for: identifying markers of skin ageing and/or stress; determining
CC skin ageing and/or stress; and identifying or determining the effects of
CC pharmaceutical or cosmetic agents for control of skin ageing. The present
CC sequence is one of a group of human skin ageing/stress related expressed
CC sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ Sequence 11 BP; 2 A; 2 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 32.4%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTGCTGTGTGA 19
Db 1 CTGCTGAGTGA 11

RESULT 146
ABV64871
ID ABV64871 standard; cDNA; 11 BP.
XX
AC ABV64871;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 2657.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK ) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
```



DR WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 99; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 2 A; 3 C; 3 G; 3 T; 0 U; 0 Other;  
  
Query Match 32.4%; Score 9.4; DB 1; Length 11;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 12 CTGTGTGACCT 22  
Db 1 CTGTGAGACCT 11  
|||||  
RESULT 147  
ABV66455  
ID ABV66455 standard; cDNA; 11 BP.  
XX  
AC ABV66455;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 4241.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 142; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to

CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 1 A; 2 C; 3 G; 5 T; 0 U; 0 Other;  
  
Query Match 32.4%; Score 9.4; DB 1; Length 11;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 7 ACCTGCTGTGT 17  
Db 1 ACTTGCTGTGT 11  
|||||  
RESULT 148  
ABV67092  
ID ABV67092 standard; cDNA; 11 BP.  
XX  
AC ABV67092;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 4878.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 159; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 1 A; 5 C; 1 G; 4 T; 0 U; 0 Other;  
  
Query Match 32.4%; Score 9.4; DB 1; Length 11;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



QY 5 CCACCTGCTGT 15  
Db 1 CCACCTGCTTT 11

RESULT 149  
ABV70439  
ID ABV70439 standard; cDNA; 11 BP.  
XX  
AC ABV70439;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 8225.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Claim 24; Page 263; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 1 A; 2 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 32.4%; Score 9.4; DB 1; Length 11;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 TGTGACCTGGT 25  
Db 1 TGTACCTGGT 11

RESULT 150  
ABV63018  
ID ABV63018 standard; cDNA; 11 BP.  
XX  
AC ABV63018;  
XX  
DT 21-OCT-2002 (first entry)

Query Match 32.4%; Score 9.4; DB 1; Length 11;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 TGTGACCTGGT 25  
Db 1 TGTACCTGGT 11

RESULT 151  
ABV65196  
ID ABV65196 standard; cDNA; 11 BP.  
XX  
AC ABV65196;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 2982.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX

XX Human skin EST 804.  
DE  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 47; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 1 A; 2 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 32.4%; Score 9.4; DB 1; Length 11;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 TGTGACCTGGT 25  
Db 1 TGTACCTGGT 11

RESULT 151  
ABV65196  
ID ABV65196 standard; cDNA; 11 BP.  
XX  
AC ABV65196;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 2982.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX

PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
XX In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 108; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 1 A; 5 C; 2 G; 3 T; 0 U; 0 Other;  
  
Query Match 32.4%; Score 9.4; DB 1; Length 11;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 ATCCACCTGCT 13  
Db 1 ATCCGCCTGCT 11  
  
RESULT 152  
ABV67859  
ID ABV67859 standard; cDNA; 11 BP.  
XX  
AC ABV67859;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 5645.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
XX In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.

XX Disclosure; Page 181; 1345pp; German.  
PS  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 2 A; 2 C; 4 G; 3 T; 0 U; 0 Other;  
  
Query Match 32.4%; Score 9.4; DB 1; Length 11;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 9 CTGCTGTGTGA 19  
Db 1 CTGCTGAGTGA 11  
  
RESULT 153  
ADQ34760  
ID ADQ34760 standard; DNA; 11 BP.  
XX  
AC ADQ34760;  
XX  
DT 23-SEP-2004 (first entry)  
XX  
DE Human facial skin-associated DNA fragment SEQ ID NO 2850.  
XX  
KW facial skin; human; serial analysis of gene expression; SAGE;  
KW homeostasis; biochip; cosmetic; pharmaceutical; ds.  
XX  
OS Homo sapiens.  
XX  
PN DE10260928-A1.  
XX  
PD 08-JUL-2004.  
XX  
PF 20-DEC-2002; 2002DE-01060928.  
XX  
PR 20-DEC-2002; 2002DE-01060928.  
XX  
XX (HENK ) HENKEL KGAA.  
PA  
XX Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;  
PI Conradt M, Hofmann K;  
XX  
DR WPI; 2004-518855/50.  
XX  
PT In vitro identification of genes important for facial skin, useful for  
PT assessing homeostasis and in screening for pharmaceutical or cosmetic  
PT agents, based on differential expression analysis.  
XX  
PS Claim 4; SEQ ID NO 2850; 577pp; German.  
XX  
CC This invention describes a novel in vitro method for identifying genes  
CC that are significant for facial skin in humans. The method comprises  
CC recovering, from facial skin, a first mixture of genetically expressed  
CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or  
CC their fragments), recovering a second, similar mixture from some other  
CC human tissue, preferably skin from a protected area, especially from the  
CC breast and subjecting the mixtures to serial analysis of gene expression  
CC (SAGE) to identify those genes for which expression is markedly different  
CC between facial skin and the other tissue. The invention also describes an  
CC in vitro method for determining homeostasis of human facial skin; a test

CC kit which comprises a solid support (flexible or rigid) on which are  
CC immobilised probes that bind specifically to the factors of interest and  
CC a biochip for determining homeostasis of human facial skin. The products  
CC of the invention are also used in a method which determines activity of  
CC cosmetic and pharmaceutical agents for use against disorders or  
CC disturbances of the homeostasis of human skin and a screening method for  
CC identifying cosmetic and pharmaceutical agents. The method allows  
CC identification of as many as possible of the genes important for facial  
CC skin and thus of a very wide range of potential therapeutic and cosmetic  
CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to  
CC identify the facial skin-associated genes described in the invention.  
XX  
SQ Sequence 11 BP; 1 A; 5 C; 1 G; 4 T; 0 U; 0 Other;  
  
Query Match 32.4%; Score 9.4; DB 1; Length 11;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 CCACCTGCTGT 15  
Db 1 CCACCTGCTTT 11  
  
RESULT 154  
ADQ33707  
ID ADQ33707 standard; DNA; 11 BP.  
XX  
AC ADQ33707;  
XX  
DT 23-SEP-2004 (first entry)  
XX  
DE Human facial skin-associated DNA fragment SEQ ID NO 1797.  
XX  
KW facial skin; human; serial analysis of gene expression; SAGE;  
KW homeostasis; biochip; cosmetic; pharmaceutical; ds.  
XX  
OS Homo sapiens.  
XX  
PN DE10260928-A1.  
XX  
PD 08-JUL-2004.  
XX  
PF 20-DEC-2002; 2002DE-01060928.  
XX  
PR 20-DEC-2002; 2002DE-01060928.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;  
PI Conradt M, Hofmann K;  
XX  
DR WPI; 2004-518855/50.  
XX  
PT In vitro identification of genes important for facial skin, useful for  
PT assessing homeostasis and in screening for pharmaceutical or cosmetic  
PT agents, based on differential expression analysis.  
XX  
PS Claim 5; SEQ ID NO 1797; 577pp; German.  
XX  
CC This invention describes a novel in vitro method for identifying genes  
CC that are significant for facial skin in humans. The method comprises  
CC recovering, from facial skin, a first mixture of genetically expressed  
CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or  
CC their fragments), recovering a second, similar mixture from some other  
CC human tissue, preferably skin from a protected area, especially from the  
CC breast and subjecting the mixtures to serial analysis of gene expression  
CC (SAGE) to identify those genes for which expression is markedly different  
CC between facial skin and the other tissue. The invention also describes an  
CC in vitro method for determining homeostasis of human facial skin; a test  
CC kit which comprises a solid support (flexible or rigid) on which are  
CC immobilised probes that bind specifically to the factors of interest and  
CC a biochip for determining homeostasis of human facial skin. The products  
CC of the invention are also used in a method which determines activity of

CC cosmetic and pharmaceutical agents for use against disorders or  
CC disturbances of the homeostasis of human skin and a screening method for  
CC identifying cosmetic and pharmaceutical agents. The method allows  
CC identification of as many as possible of the genes important for facial  
CC skin and thus of a very wide range of potential therapeutic and cosmetic  
CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to  
CC identify the facial skin-associated genes described in the invention.  
XX  
SQ Sequence 11 BP; 1 A; 5 C; 2 G; 3 T; 0 U; 0 Other;  
  
Query Match 32.4%; Score 9.4; DB 1; Length 11;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 ATCCACCTGCT 13  
Db 1 ATCCGCCCTGCT 11  
  
RESULT 155  
AAZ48741  
ID AAZ48741 standard; DNA; 12 BP.  
XX  
AC AAZ48741;  
XX  
DT 15-MAR-2000 (first entry)  
XX  
DE PCR primer for human alphasal-antitrypsin gene sequence.  
XX  
KW PCR primer; oligonucleotide detection; diagnosis; disease screening; COP;  
KW competitive oligonucleotide priming; genetic polymorphism detection;  
KW genetic disease diagnosis; linkage analysis; tissue typing; gene mapping;  
KW human; alphasal-antitrypsin; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP333465-A.  
XX  
PD 20-SEP-1989.  
XX  
PF 15-MAR-1989; 89EP-00302569.  
XX  
PR 18-MAR-1988; 88US-00170214.  
XX  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
XX  
PI Caskey CT, Gibbs RAL;  
XX  
DR WPI; 1989-272222/38.  
XX  
PT Detection of mutations in DNA - by adding competitive oligo:nucleotide  
PT primers to nucleic acids, hybridising, etc.  
XX  
PS Example 4; Page 12; 21pp; English.  
XX  
CC This sequence represents a PCR primer for the human alphasal-antitrypsin  
CC gene sequence. The invention relates to a method for detecting the  
CC presence or absence of a specific known oligonucleotide, or  
CC distinguishing between specific and different nucleic acid (NA)  
CC sequences, comprising: (1) addition of at least two oligonucleotide  
CC primers to a sample or mixture of NA where one primer (a) is  
CC substantially complementary to a specific NA sequence and the other  
CC primer (b) has a single base mismatch with the specific sequence; (2)  
CC preferentially hybridising (a) to the specific NA sequence under  
CC competitive conditions; (3) extension of (a) from its 3' terminus to  
CC produce an extension product complementary to the strand hybridised to by  
CC (a); and (4) identifying the extension product by determining the  
CC presence or absence of labels attached to at least one of the primers.  
CC The method (referred to as competitive oligonucleotide priming (COP)) can  
CC be used in detecting genetic polymorphisms, particularly in detecting  
CC genetic diseases, screening for disease association by linkage analysis,  
CC tissue typing, gene mapping, screening for neoplasms, detection of known  
CC pathogens, determining purity of animal strains, and disease screening in

CC animals. With this method, primers may be used that are shorter than  
CC those used in PCR, as the binding to template is competitive its sequence  
CC can be inferred. The target sequence of the gene need not be precisely  
CC known as only the specific sequence for the primers is required  
XX  
SQ Sequence 12 BP; 5 A; 2 C; 3 G; 2 T; 0 U; 0 Other;  
  
Query Match 32.4%; Score 9.4; DB 1; Length 12;  
Best Local Similarity 90.9%; Pred. No. 1.3e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 19 ACCTGGTAAAT 29  
Db 1 ACCTGGAAAT 11  
  
RESULT 156  
AAQ04006  
ID AAQ04006 standard; DNA; 12 BP.  
XX  
AC AAQ04006;  
XX  
DT 25-MAR-2003 (revised)  
DT 03-SEP-1990 (first entry)  
XX  
DE Primer used in detecting alpha-1-antitrypsin deficiency.  
XX  
KW X-chromosome; ornithine transcarbamylase deficiency; muscular dystrophy;  
KW dystrophin; ds.  
XX  
OS Synthetic.  
XX  
PN EP364255-A.  
XX  
PD 18-APR-1990.  
XX  
PF 11-OCT-1989; 89EP-00310424.  
XX  
PR 12-OCT-1988; 88US-00256689.  
XX  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
XX  
PI Caskey CT, Chamberlain JS, Gibbs RAL, Rainer JE, Nguyen PN;  
XX WPI; 1990-117752/16.  
DR  
XX Multiplex genomic DNA amplification for deletion detection - useful for  
PT detecting X-linked diseases such as ornithine transcarbamylase deficiency  
PT and X-linked muscular dystrophy.  
XX  
PS Example 8; Page 18; 32pp; English.  
XX  
CC Paired oligonucleotide primers are used in detecting deletions  
CC specifically of the X and Y chromosomes. Probe may be used to recognise  
CC normal (M) allele of alpha-1-antitrypsin. (Updated on 25-MAR-2003 to  
CC correct PA field.)  
XX  
SQ Sequence 12 BP; 5 A; 2 C; 3 G; 2 T; 0 U; 0 Other;  
  
Query Match 32.4%; Score 9.4; DB 1; Length 12;  
Best Local Similarity 90.9%; Pred. No. 1.3e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 19 ACCTGGTAAAT 29  
Db 1 ACCTGGAAAT 11  
  
RESULT 157  
AAV40900  
ID AAV40900 standard; DNA; 12 BP.  
XX  
AC AAV40900;

XX 25-SEP-1998 (first entry)  
DT  
XX Primer CBFBMVHA:1033L12 for abnormality detection.  
DE  
XX  
KW PCR primer; chromosomal abnormality; abnormality detection; leukaemia;  
KW lymphoma; carcinoma; adenocarcinoma; sarcoma; glioma; neuroblastoma;  
KW medullablastoma; malignant melanoma; malignant neoplastic condition; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9824928-A2.  
XX  
PD 11-JUN-1998.  
XX  
PF 08-DEC-1997; 97WO-DK000556.  
XX  
PR 06-DEC-1996; 96DK-00001401.  
XX  
PA (PALL/) PALLISGAARD N.  
XX  
PI Pallisgaard N, Hokland P;  
XX  
DR WPI; 1998-333344/29.  
XX  
PT Detection of chromosomal abnormalities - by subjecting patient sample  
PT nucleic acids to a multiplex molecular amplification procedure using  
PT primers specific for characteristic nucleic acid sequence.  
XX  
PS Claim 73; Page 58; 126pp; English.  
XX  
CC This sequence represents a primer used in the method of the invention for  
CC the detection of the presence or absence of chromosomal abnormalities,  
CC each abnormality being associated with a condition in a subject and each  
CC being defined by at least one characteristic nucleic acid sequence. The  
CC method comprises: (a) obtaining a sample of nucleic acids derived from a  
CC subject which may harbour one of the chromosomal abnormalities; (b)  
CC subjecting the sample to a multiplex molecular amplification (MMA)  
CC procedure, where a number of the characteristic sequences, if present in  
CC a sufficient amount, will be amplified; (c) retrieving the product(s)  
CC from step (b), and detecting the presence and/or absence of an amplicon  
CC characteristic of the abnormal sequences to detect the presence or  
CC absence of corresponding chromosomal abnormalities; where the MMA  
CC procedure comprises the use of at least 7 mutually distinct primers (MDP)  
CC in one single reaction mixture, each of the primers defining an end of at  
CC least one characteristic nucleic acid sequence, and where at least one of  
CC the primers defines the first end of at least two characteristic nucleic  
CC acid sequences, the characteristic nucleic acid sequences each being  
CC determined in their opposite ends by MDP selected from the remainder of  
CC the MDP. The methods can be used for detecting chromosomal abnormalities  
CC associated with diseases including numerous leukaemia's, lymphoma's,  
CC carcinoma's, adenocarcinoma's, sarcoma's, glioma's, neuroblastoma's,  
CC medullablastoma, malignant melanoma, and malignant neoplastic conditions  
XX  
SQ Sequence 12 BP; 1 A; 2 C; 6 G; 3 T; 0 U; 0 Other;  
  
Query Match 32.4%; Score 9.4; DB 1; Length 12;  
Best Local Similarity 90.9%; Pred. No. 1.3e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 9 CTGCTGTGTGA 19  
Db 1 CTGCTGGGTGA 11  
  
RESULT 158  
AAA06782  
ID AAA06782 standard; DNA; 12 BP.  
XX  
AC AAA06782;  
XX  
DT 05-JUN-2000 (first entry)



XX VEGF derived short oligonucleotide SEQ ID NO:91.  
DE  
XX  
KW Human; vascular endothelial growth factor; VEGF; phosphorothioate;  
KW antisense oligonucleotide; inhibition; cytostatic; angiogenic;  
KW gene therapy; abnormal vascular permeability; cell proliferation;  
KW cell permeation; angiogenesis; neovascularisation; tumour cell growth;  
KW metastasis; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN EP979869-A1.  
XX  
PD 16-FEB-2000.  
XX  
PF 07-AUG-1998; 98EP-00114853.  
XX  
PR 07-AUG-1998; 98EP-00114853.  
XX  
PA (HMRI ) HOECHST MARION ROUSSEL DEUT GMBH.  
XX  
PI Uhlmann E, Peyman A, Bitonti AJ, Woessner RD;  
XX  
DR WPI; 2000-258586/23.  
XX  
PF 07-AUG-1998; 98EP-00114853.  
XX  
PR 07-AUG-1998; 98EP-00114853.  
XX  
PA (HMRI ) HOECHST MARION ROUSSEL DEUT GMBH.  
XX  
PI Uhlmann E, Peyman A, Bitonti AJ, Woessner RD;  
XX  
DR WPI; 2000-258586/23.  
XX  
PT Novel oligonucleotides corresponding to a part of a vascular endothelial  
PT growth factor, useful for treating e.g. tumor cell growth and/or  
PT metastasis.  
XX  
PS Disclosure; Page 13; 73pp; English.  
XX  
CC The present invention describes oligonucleotides (I) of 10-15 residues  
CC corresponding to a part of a vascular endothelial growth factor (VEGF)  
CC comprising 1 of 6 sequences given in AAA06692 to AAA06697. AAA06698 to  
CC AAA06783 represent VEGF antisense oligonucleotides used in the  
CC exemplification of the present invention. The antisense oligonucleotides  
CC can contain phosphorothioate linkages. Oligonucleotides from the present  
CC invention have cytostatic and angiogenic activities, and can be used in  
CC gene therapy. The oligonucleotides are useful for inhibiting the  
CC expression of VEGF, e.g. for the treatment of diseases associated with  
CC abnormal vascular permeability, cell proliferation, cell permeation,  
CC angiogenesis, neovascularisation, tumour cell growth and/or metastasis.  
CC AAA06784 represents a human VEGF nucleotide sequence from which the  
CC oligonucleotides are derived  
XX  
SQ Sequence 12 BP; 1 A; 3 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 32.4%; Score 9.4; DB 1; Length 12;  
Best Local Similarity 90.9%; Pred. No. 1.3e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 GTGTGACCTGG 24  
Db 1 GTGCGACCTGG 11

RESULT 159  
AAA06783  
ID AAA06783 standard; DNA; 12 BP.  
XX  
AC AAA06783;  
XX  
DT 05-JUN-2000 (first entry)  
XX  
DE VEGF derived short oligonucleotide SEQ ID NO:92.  
XX  
KW Human; vascular endothelial growth factor; VEGF; phosphorothioate;  
KW antisense oligonucleotide; inhibition; cytostatic; angiogenic;  
KW gene therapy; abnormal vascular permeability; cell proliferation;  
KW cell permeation; angiogenesis; neovascularisation; tumour cell growth;  
KW metastasis; ss.  
XX

OS Homo sapiens.  
OS Synthetic.  
XX  
PN EP979869-A1.  
XX  
PD 16-FEB-2000.  
XX  
PF 07-AUG-1998; 98EP-00114853.  
XX  
PR 07-AUG-1998; 98EP-00114853.  
XX  
PA (HMRI ) HOECHST MARION ROUSSEL DEUT GMBH.  
XX  
PI Uhlmann E, Peyman A, Bitonti AJ, Woessner RD;  
XX  
DR WPI; 2000-258586/23.  
XX  
PT Novel oligonucleotides corresponding to a part of a vascular endothelial  
PT growth factor, useful for treating e.g. tumor cell growth and/or  
PT metastasis.  
XX  
PS Disclosure; Page 13; 73pp; English.  
XX  
CC The present invention describes oligonucleotides (I) of 10-15 residues  
CC corresponding to a part of a vascular endothelial growth factor (VEGF)  
CC comprising 1 of 6 sequences given in AAA06692 to AAA06697. AAA06698 to  
CC AAA06783 represent VEGF antisense oligonucleotides used in the  
CC exemplification of the present invention. The antisense oligonucleotides  
CC can contain phosphorothioate linkages. Oligonucleotides from the present  
CC invention have cytostatic and angiogenic activities, and can be used in  
CC gene therapy. The oligonucleotides are useful for inhibiting the  
CC expression of VEGF, e.g. for the treatment of diseases associated with  
CC abnormal vascular permeability, cell proliferation, cell permeation,  
CC angiogenesis, neovascularisation, tumour cell growth and/or metastasis.  
CC AAA06784 represents a human VEGF nucleotide sequence from which the  
CC oligonucleotides are derived  
XX  
SQ Sequence 12 BP; 1 A; 3 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 32.4%; Score 9.4; DB 1; Length 12;  
Best Local Similarity 90.9%; Pred. No. 1.3e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 GTGTGACCTGG 24  
Db 1 GTGTGACCCGG 11

RESULT 160  
ABH86901  
ID ABH86901 standard; DNA; 12 BP.  
XX  
AC ABH86901;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 286894 for detecting SNP TSC0012869.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.



XX Olek A, Piepenbrock C, Berlin K;  
PI WPI; 2001-657177/75.  
XX  
DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 286894; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;  
  
Query Match 32.4%; Score 9.4; DB 1; Length 12;  
Best Local Similarity 90.9%; Pred. No. 1.3e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 CATCCACCTGC 12  
Db |||||||  
2 CATCCACCTAC 12  
  
RESULT 161  
AAD54083  
ID AAD54083 standard; DNA; 12 BP.  
XX  
AC AAD54083;  
XX  
DT 17-JUN-2003 (first entry)  
XX  
DE HNF1-131-1 gene SNP detecting capture probe 1.  
XX  
KW Microfluidic analysis; biomolecule identification; sample analysis;  
KW single nucleotide polymorphism; SNP; genotyping; probe; HNF1-131-1; ss.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 2 /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "Methylated LNA nucleotide"  
FT modified\_base 6. .8  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "LNA nucleotides"  
FT modified\_base 6  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "Methylated"  
FT modified\_base 11  
FT /\*tag= d  
FT /mod\_base= OTHER  
FT /note= "LNA nucleotide"  
XX  
PN WO200297398-A2.  
XX  
PD 05-DEC-2002.  
XX  
PF 25-OCT-2001; 2001WO-IB002902.

XX 25-OCT-2000; 2000US-0243349P.  
PR 16-JUL-2001; 2001US-0305726P.  
XX  
PA (EXIQ-) EXIQON AS.  
XX  
PI Jakobsen MH, Kongsbak L;  
XX  
DR WPI; 2003-183891/18.  
XX  
PT Closed substrate platform has slide element comprising microfluidic  
PT analysis platform, enclosed within container having inlet port for  
PT introducing liquid into sample analysis area and vent for removing air  
PT from container.  
XX  
PS Example; Page 70; 49pp; English.  
XX  
CC The invention relates to a closed substrate platform which has a slide  
CC element comprising microfluidic analysis platform, enclosed within  
CC container having inlet port for introducing liquid into sample analysis  
CC area and vent for removing air from container. The invention is used for  
CC identifying a nucleic acid sequence capable of binding to a biomolecule  
CC such as a nucleic acid sequence or polypeptide. It is useful for  
CC identifying a polypeptide capable of binding to a biomolecule such as a  
CC nucleic acid sequence, polypeptide, multimeric polypeptide, an antibody,  
CC a receptor, a hormone, drug or drug candidate. It is also useful for  
CC sample analysis, especially liquid, and is useful for detecting DNA  
CC sequence variation, DNA sequencing, deletion analysis, single nucleotide  
CC polymorphism (SNP) analysis, gene expression, genotyping, etc. The  
CC present sequence is a capture probe used for detecting HNF1-131-1 gene  
CC SNP. This sequence is used in the exemplification of the invention  
XX  
SQ Sequence 12 BP; 1 A; 5 C; 2 G; 4 T; 0 U; 0 Other;  
  
Query Match 32.4%; Score 9.4; DB 1; Length 12;  
Best Local Similarity 90.9%; Pred. No. 1.3e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 CCACCTGCTGT 15  
Db |||||||  
2 CCTCCTGCTGT 12  
  
RESULT 162  
AAL51397/c  
ID AAL51397 standard; DNA; 12 BP.  
XX  
AC AAL51397;  
XX  
DT 27-MAR-2003 (first entry)  
XX  
DE Human polyamine oxidase (PAO) exon-intron junction, SEQ ID No 24.  
XX  
KW Human; gene; ds; enzyme; polyamine oxidase; PAO; exon-intron junction;  
KW polyamine oxidase-related disease.  
XX  
OS Homo sapiens.  
XX  
PN WO2002100884-A2.  
XX  
PD 19-DEC-2002.  
XX  
PF 13-JUN-2002; 2002WO-US018666.  
XX  
PR 13-JUN-2001; 2001US-0297815P.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
XX  
PI Casero RA, Wang Y;  
XX  
DR WPI; 2003-156944/15.  
XX  
PT New purified mammalian polyamine oxidase enzyme, useful as a diagnostic

PT or prognostic tool, e.g. for determining the etiology and predicting the  
PT optimal treatment regimens for diseases caused by abnormal expression of  
PT this enzyme.  
XX  
PS Disclosure; Fig 2C; 45pp; English.  
XX  
CC The invention comprises the amino acid and coding sequence of human  
CC polyamine oxidase (PAO) proteins. The PAO DNA and protein sequences of  
CC the invention are useful as diagnostic and prognostic tools, particularly  
CC to determine the etiology of and predict the optimal treatment regimens  
CC for disease states caused by abnormal expression of this enzyme. The  
CC present DNA sequence represents an exon-intron junction from the human  
CC PAO gene  
XX  
SQ Sequence 12 BP; 2 A; 3 C; 6 G; 1 T; 0 U; 0 Other;  
  
Query Match 32.4%; Score 9.4; DB 1; Length 12;  
Best Local Similarity 90.9%; Pred. No. 1.3e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 TCCACCTGCTG 14  
Db 11 TCCACCTGCGG 1  
  
RESULT 163  
AAA54184/c  
ID AAA54184 standard; cDNA; 13 BP.  
XX  
AC AAA54184;  
XX  
DT 08-FEB-2001 (first entry)  
XX  
DE 5' exon-intron junction of exon 8 of BSMAP.  
XX  
KW Brain specific membrane anchored protein; BSMAP; dopamine; GABA;  
KW receptor; agonist; antagonist; central nervous system; CNS;  
KW brain disease; chromosome 19; CLF-I; depression; dyslexia; dystonia;  
KW eating disorder; epilepsy; migraine; headache; panic disorder;  
KW schizophrenia; obsessive disorder; compulsive disorder;  
KW amyotrophic lateral sclerosis; multiple sclerosis; Alzheimer's disease;  
KW brain tumour; Huntington's disease; Parkinson's disease; stroke; human;  
KW exon; intron; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200055317-A1.  
XX  
PD 21-SEP-2000.  
XX  
PF 16-MAR-2000; 2000WO-IB000360.  
XX  
PR 16-MAR-1999; 99EP-00400636.  
XX  
PA (FABR ) FABRE MEDICAMENT SA PIERRE.  
XX  
PI Elson G, Bonnefoy J, Gauchat J;  
XX  
DR WPI; 2000-638200/61.  
XX  
PT Novel nucleic acid encoding Brain-Specific Membrane Anchored Protein  
PT useful for treating central nervous system associated disorders and  
PT diseases.  
XX  
PS Disclosure; Page 13; 45pp; English.  
XX  
CC Several receptors (dopamine receptors, the 5-HT family of receptors and  
CC GABA receptors) have been shown to be useful targets by agonist and  
CC antagonist compounds to treat and/or prevent CNS disorders. Brain  
CC receptors in general are attractive candidates for finding new therapies  
CC for brain diseases. Human chromosome 19 is a short chromosome with a  
CC relatively high GC content which has been found to be involved in CNS  
CC functions. The gene for type I cytokine receptor homologue CLF-1 was

CC recently localised to chromosome 19. Unexpectedly seven other exons  
CC coding in the reverse orientation located adjacent to the CLF-1 exons  
CC have also been found. This new gene was designated brain-specific  
CC membrane anchored protein (BSMAP). Antagonistic compounds directed  
CC against BSMAP are useful for preparing medicaments for treating and/or  
CC preventing central nervous system disorders such as depression, dyslexia,  
CC dystonia, eating disorders, epilepsy, migraine, headache, panic disorder,  
CC schizophrenia, obsessive and compulsive disorders, amyotrophic lateral  
CC sclerosis, multiple sclerosis, Alzheimer's disease, brain tumors,  
CC Huntington's disease, Parkinson's disease and stroke  
XX  
SQ Sequence 13 BP; 1 A; 2 C; 7 G; 3 T; 0 U; 0 Other;  
  
Query Match 32.4%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 1.4e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 CCATCCACCTG 11  
Db 13 CCACCCACCTG 3  
  
RESULT 164  
ABC87602/c  
ID ABC87602 standard; DNA; 13 BP.  
XX  
AC ABC87602;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 87619 for detecting SNP TSC0022039.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 87619; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF0010-ABF99989, ABH0010-ABH99989 and ABI0010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 3 A; 0 C; 5 G; 5 T; 0 U; 0 Other;

```

Query Match      32.4%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 ATCCACCTGCT 13
Db      11 ATCCACCTACT 1

RESULT 165
ABC87603
ID ABC87603 standard; DNA; 13 BP.
XX
AC ABC87603;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 87620 for detecting SNP TSC0022039.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 87620; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 5 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

Query Match      32.4%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 ATCCACCTGCT 13
Db      3 ATCCACCTACT 13

RESULT 166
ACC70395/c
ID ACC70395 standard; DNA; 13 BP.
XX
```

```

AC ACC70395;
XX
DT 11-AUG-2003 (first entry)
XX
DE Cytoprotective response element from a shear stress-regulated gene.
XX
KW Cytoprotective response element; CPRE; oxidative stress;
KW cytoprotective enzyme; hemodynamic shear stress; inflammatory disorder;
KW cardiovascular disease; hyperproliferative disorder; neoplasm;
KW lymphoblastic leukemia; skin cancer; radiation therapy;
KW shear stress-regulated gene; ss.
XX
OS Unidentified.
XX
PN WO2003033662-A2.
XX
PD 24-APR-2003.
XX
PF 16-OCT-2002; 2002WO-US033006.
XX
PR 16-OCT-2001; 2001US-0329870P.
XX
PA (ATHE-) ATHEROGENICS INC.
XX
PI Kunsch C, Varner SE, Chen X, Luchoomun J;
XX
DR WPI; 2003-403211/38.
XX
PT Novel isolated cytoprotective response element nucleic acid for inducing
PT coordinate activation of genes that protect cells from damaging effects
PT of oxidative stress, e.g. during conditions of hemodynamic shear stress.
XX
PS Claim 2; Fig 6; 133pp; English.
XX
CC The present sequence represents a cytoprotective response element (CPRE).
CC The CPRE is an inducer of the coordinate activation of certain genes that
CC protect cells from damaging effects of oxidative stress. It is also a
CC regulator of cytoprotective effects and an inducer of expression of
CC cytoprotective enzymes. The CPRE is useful for inducing the coordinate
CC activation of certain genes that protect cells from damaging effects of
CC oxidative stress, for example during conditions of hemodynamic shear
CC stress. It is useful as a reagent for the identification of a compound
CC (preferably, a drug) with which it directly or indirectly interacts, or
CC for regulating cytoprotective effects by inducing the expression of
CC cytoprotective enzymes or other factors. A compound identified in this
CC way is useful for treating inflammatory disorders, cardiovascular
CC diseases, hyperproliferative disorders (such as neoplasms, lymphoblastic
CC leukemia, skin cancer, or to protect normal tissues and organs from the
CC damaging effects of chemotherapeutic drugs, radiation therapy and disease
CC processes
XX
SQ Sequence 13 BP; 5 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

Query Match      32.4%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9 CTGCTGTGTGA 19
Db      12 CTGCTGTGTCA 2

RESULT 167
AAZ79202
ID AAZ79202 standard; DNA; 10 BP.
XX
AC AAZ79202;
XX
DT 10-APR-2000 (first entry)
XX
DE Human dendritic cell SAGE tag, SEQ ID NO:1630.
XX
KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
```

KW APC; monocyte-derived dendritic cell; differential gene expression;  
KW immunostimulatory cofactor; costimulatory factor; CTL;  
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965924-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013800.  
XX  
PR 19-JUN-1998; 98US-0089833P.  
PR 19-JUN-1998; 98US-0089844P.  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089878P.  
PR 19-JUN-1998; 98US-0089991P.  
PR 19-JUN-1998; 98US-0089992P.  
PR 19-JUN-1998; 98US-0089993P.  
PR 19-JUN-1998; 98US-0089994P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0089999P.  
PR 19-JUN-1998; 98US-0090000P.  
PR 19-JUN-1998; 98US-0090003P.  
PR 19-JUN-1998; 98US-0090035P.  
PR 19-JUN-1998; 98US-0090036P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
PR 19-JUN-1998; 98US-0090042P.  
PR 19-JUN-1998; 98US-0090043P.  
PR 19-JUN-1998; 98US-0090044P.  
PR 19-JUN-1998; 98US-0090045P.  
PR 19-JUN-1998; 98US-0090047P.  
PR 19-JUN-1998; 98US-0090048P.  
PR 19-JUN-1998; 98US-0090072P.  
PR 19-JUN-1998; 98US-0090076P.  
PR 19-JUN-1998; 98US-0090077P.  
PR 19-JUN-1998; 98US-0090078P.  
PR 19-JUN-1998; 98US-0090079P.  
PR 19-JUN-1998; 98US-0090080P.  
PR 08-DEC-1998; 98US-0111715P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106077/09.  
XX  
PT Isolated polynucleotides differentially expressed in antigen-presenting  
PT cells, useful in gene vaccines against cancer.  
XX  
PS Claim 1; Page 111; 130pp; English.  
XX  
CC Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene  
CC expression) tags used to identify mRNA transcripts encoding  
CC immunostimulatory cofactor proteins which are preferentially or  
CC differentially expressed in monocyte-derived dendritic cells compared  
CC with monocytes. Some of the transcripts correspond to known genes or ESTs  
CC (expressed sequence tags) which were previously unknown to be  
CC preferentially or differentially expressed in dendritic cells, while  
CC other transcripts correspond to novel genes. Antigen-presenting cell  
CC (APC)-associated costimulatory factors play an important role in the  
CC activation of the cytotoxic immune response, particularly against tumour  
CC cells. Tumour antigen presentation via the MHC (major histocompatibility  
CC complex) and subsequent recognition by T-cell receptors is alone  
CC insufficient to activate a robust cytotoxic immune response that can lyse  
CC the tumour cells, immunostimulatory cofactors also being required for  
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid  
CC sequences identified using the SAGE tags have several potential uses.  
CC They may be used in vaccines to induce an immune response, particularly  
CC against a tumour antigen; to modulate the genotype of an APC; to screen

CC for agents that modulate expression of differentially expressed genes in  
CC an APC; and as hybridisation probes/amplification primers for the  
CC diagnosis, prognosis and monitoring of diseases related to abnormal  
CC expression of these genes. Detection of the dendritic cell differentially  
CC expressed genes, or of their encoded proteins, can be used to identify  
CC cells as belonging to the monocyte lineage. Cells containing these genes  
CC can be used in active immunotherapy (or to stimulate production of a  
CC population of antigen-specific effector cells) and vectors containing  
CC them are used in gene therapy. Co-administration of tumour antigens and  
CC APC-associated costimulatory factors ensures adequate antigen  
CC presentation to endogenous APCs and upregulates the APCs for the  
CC presentation of co-stimulatory signals, migration to T cell-rich sites,  
CC secretion of T cell growth factors and secretion of chemokines for  
CC recruitment of immune effector cells

SQ Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 31.0%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CTGTGTGAC 20  
Db 1 CTGTGTGAC 9  
|||||||

RESULT 168

AAZ78009  
ID AAZ78009 standard; DNA; 10 BP.

XX AAZ78009;

XX 10-APR-2000 (first entry)

DE Human dendritic cell SAGE tag, SEQ ID NO:437.

KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;  
KW APC; monocyte-derived dendritic cell; differential gene expression;  
KW immunostimulatory cofactor; costimulatory factor; CTL;  
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.  
XX

OS Homo sapiens.

XX WO9965924-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013800.

PR 19-JUN-1998; 98US-0089833P.

PR 19-JUN-1998; 98US-0089844P.

PR 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-0089878P.

PR 19-JUN-1998; 98US-0089991P.

PR 19-JUN-1998; 98US-0089992P.

PR 19-JUN-1998; 98US-0089993P.

PR 19-JUN-1998; 98US-0089994P.

PR 19-JUN-1998; 98US-0089997P.

PR 19-JUN-1998; 98US-0089999P.

PR 19-JUN-1998; 98US-0090000P.

PR 19-JUN-1998; 98US-0090035P.

PR 19-JUN-1998; 98US-0090036P.

PR 19-JUN-1998; 98US-0090039P.

PR 19-JUN-1998; 98US-0090040P.

PR 19-JUN-1998; 98US-0090041P.

PR 19-JUN-1998; 98US-0090042P.

PR 19-JUN-1998; 98US-0090043P.

PR 19-JUN-1998; 98US-0090044P.

PR 19-JUN-1998; 98US-0090045P.

PR 19-JUN-1998; 98US-0090047P.

PR 19-JUN-1998; 98US-0090048P.

PR 19-JUN-1998; 98US-0090072P.

PR 19-JUN-1998; 98US-0090076P.



PR 19-JUN-1998; 98US-00900077P.  
PR 19-JUN-1998; 98US-00900078P.  
PR 19-JUN-1998; 98US-00900079P.  
PR 19-JUN-1998; 98US-00900080P.  
PR 08-DEC-1998; 98US-0111715P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106077/09.  
XX  
PT Isolated polynucleotides differentially expressed in antigen-presenting  
cells, useful in gene vaccines against cancer.  
XX  
PS Claim 1; Page 77; 130pp; English.  
XX  
CC Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene  
expression) tags used to identify mRNA transcripts encoding  
immunostimulatory cofactor proteins which are preferentially or  
differentially expressed in monocyte-derived dendritic cells compared  
with monocytes. Some of the transcripts correspond to known genes or ESTs  
(expressed sequence tags) which were previously unknown to be  
preferentially or differentially expressed in dendritic cells, while  
other transcripts correspond to novel genes. Antigen-presenting cell  
(APC)-associated costimulatory factors play an important role in the  
activation of the cytotoxic immune response, particularly against tumour  
cells. Tumour antigen presentation via the MHC (major histocompatibility  
complex) and subsequent recognition by T-cell receptors is alone  
insufficient to activate a robust cytotoxic immune response that can lyse  
the tumour cells, immunostimulatory cofactors also being required for  
efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid  
sequences identified using the SAGE tags have several potential uses.  
They may be used in vaccines to induce an immune response, particularly  
against a tumour antigen; to modulate the genotype of an APC; to screen  
for agents that modulate expression of differentially expressed genes in  
an APC; and as hybridisation probes/amplification primers for the  
diagnosis, prognosis and monitoring of diseases related to abnormal  
expression of these genes. Detection of the dendritic cell differentially  
expressed genes, or of their encoded proteins, can be used to identify  
cells as belonging to the monocyte lineage. Cells containing these genes  
can be used in active immunotherapy (or to stimulate production of a  
population of antigen-specific effector cells) and vectors containing  
them are used in gene therapy. Co-administration of tumour antigens and  
APC-associated costimulatory factors ensures adequate antigen  
presentation to endogenous APCs and upregulates the APCs for the  
presentation of co-stimulatory signals, migration to T cell-rich sites,  
secretion of T cell growth factors and secretion of chemokines for  
recruitment of immune effector cells  
XX  
SQ Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 31.0%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCTGCT 13  
|||||||  
Db 1 CCACCTGCT 9

RESULT 169  
AAZ78129  
ID AAZ78129 standard; DNA; 10 BP.  
XX  
AC AAZ78129;  
XX  
DT 10-APR-2000 (first entry)  
XX  
DE Human dendritic cell SAGE tag, SEQ ID NO:557.  
XX

KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;  
KW APC; monocyte-derived dendritic cell; differential gene expression;  
KW immunostimulatory cofactor; costimulatory factor; CTL;  
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965924-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013800.  
XX  
PR 19-JUN-1998; 98US-0089833P.  
PR 19-JUN-1998; 98US-0089844P.  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089878P.  
PR 19-JUN-1998; 98US-0089991P.  
PR 19-JUN-1998; 98US-0089992P.  
PR 19-JUN-1998; 98US-0089993P.  
PR 19-JUN-1998; 98US-0089994P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0089999P.  
PR 19-JUN-1998; 98US-0090000P.  
PR 19-JUN-1998; 98US-0090035P.  
PR 19-JUN-1998; 98US-0090036P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
PR 19-JUN-1998; 98US-0090042P.  
PR 19-JUN-1998; 98US-0090043P.  
PR 19-JUN-1998; 98US-0090044P.  
PR 19-JUN-1998; 98US-0090045P.  
PR 19-JUN-1998; 98US-0090047P.  
PR 19-JUN-1998; 98US-0090048P.  
PR 19-JUN-1998; 98US-0090072P.  
PR 19-JUN-1998; 98US-0090076P.  
PR 19-JUN-1998; 98US-0090077P.  
PR 19-JUN-1998; 98US-0090078P.  
PR 19-JUN-1998; 98US-0090079P.  
PR 19-JUN-1998; 98US-0090080P.  
PR 08-DEC-1998; 98US-0111715P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106077/09.  
XX  
PT Isolated polynucleotides differentially expressed in antigen-presenting  
cells, useful in gene vaccines against cancer.  
XX  
PS Claim 1; Page 81; 130pp; English.  
XX  
CC Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene  
expression) tags used to identify mRNA transcripts encoding  
immunostimulatory cofactor proteins which are preferentially or  
differentially expressed in monocyte-derived dendritic cells compared  
with monocytes. Some of the transcripts correspond to known genes or ESTs  
(expressed sequence tags) which were previously unknown to be  
preferentially or differentially expressed in dendritic cells, while  
other transcripts correspond to novel genes. Antigen-presenting cell  
(APC)-associated costimulatory factors play an important role in the  
activation of the cytotoxic immune response, particularly against tumour  
cells. Tumour antigen presentation via the MHC (major histocompatibility  
complex) and subsequent recognition by T-cell receptors is alone  
insufficient to activate a robust cytotoxic immune response that can lyse  
the tumour cells, immunostimulatory cofactors also being required for  
efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid  
sequences identified using the SAGE tags have several potential uses.  
They may be used in vaccines to induce an immune response, particularly



CC against a tumour antigen; to modulate the genotype of an APC; to screen  
CC for agents that modulate expression of differentially expressed genes in  
CC an APC; and as hybridisation probes/amplification primers for the  
CC diagnosis, prognosis and monitoring of diseases related to abnormal  
CC expression of these genes. Detection of the dendritic cell differentially  
CC expressed genes, or of their encoded proteins, can be used to identify  
CC cells as belonging to the monocyte lineage. Cells containing these genes  
CC can be used in active immunotherapy (or to stimulate production of a  
CC population of antigen-specific effector cells) and vectors containing  
CC them are used in gene therapy. Co-administration of tumour antigens and  
CC APC-associated costimulatory factors ensures adequate antigen  
CC presentation to endogenous APCs and upregulates the APCs for the  
CC presentation of co-stimulatory signals, migration to T cell-rich sites,  
CC secretion of T cell growth factors and secretion of chemokines for  
CC recruitment of immune effector cells  
XX  
SQ Sequence 10 BP; 0 A; 2 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 31.0%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 TGCTGTGTG 18  
Db 1 TGCTGTGTG 9  
|||||||

RESULT 170  
AAZ85467/c  
ID AAZ85467 standard; DNA; 10 BP.  
XX  
AC AAZ85467;  
XX  
DT 07-APR-2000 (first entry)  
XX  
DE Metastatic breast tumour cell downregulated transcript tag #4701.  
XX  
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965928-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013647.  
XX  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106079/09.  
XX  
PT Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX  
PS Claim 1; Page 185; 219pp; English.  
XX  
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are

CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC vaccines; for diagnosing breast cancer and for raising specific  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy  
XX  
SQ Sequence 10 BP; 2 A; 0 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 31.0%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATCCACCT 10  
Db 10 CATCCACCT 2  
|||||||

RESULT 171  
AAZ86332/c  
ID AAZ86332 standard; DNA; 10 BP.  
XX  
AC AAZ86332;  
XX  
DT 07-APR-2000 (first entry)  
XX  
DE Metastatic breast tumour cell downregulated transcript tag #5566.  
XX  
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965928-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013647.  
XX  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106079/09.  
XX  
PT Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX  
PS Claim 1; Page 206; 219pp; English.  
XX  
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour

CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy  
XX  
SQ Sequence 10 BP; 4 A; 5 C; 1 G; 0 T; 0 U; 0 Other;  
  
Query Match 31.0%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 10 TGCTGTGTG 18  
Db 9 TGCTGTGTG 1  
|||||  
TGCTGTGTG 1  
  
RESULT 172  
AAZ81042  
ID AAZ81042 standard; DNA; 10 BP.  
XX  
AC AAZ81042;  
XX  
DT 07-APR-2000 (first entry)  
XX  
DE Metastatic breast tumour cell upregulated transcript tag #276.  
XX  
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; Gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX Homo sapiens.  
OS  
XX  
XX WO9965928-A2.  
PN  
XX  
PD 23-DEC-1999.  
XX  
XX 18-JUN-1999; 99WO-US013647.  
PF  
XX  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX  
XX (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
XX Roberts BL, Shankara S;  
PI  
XX  
DR WPI; 2000-106079/09.  
XX  
XX Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX  
PS Claim 1; Page 65; 219pp; English.  
XX

CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy  
XX  
SQ Sequence 10 BP; 0 A; 2 C; 4 G; 4 T; 0 U; 0 Other;  
  
Query Match 31.0%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 10 TGCTGTGTG 18  
Db 1 TGCTGTGTG 9  
|||||  
TGCTGTGTG 9  
  
RESULT 173  
AAZ82620  
ID AAZ82620 standard; DNA; 10 BP.  
XX  
AC AAZ82620;  
XX  
DT 07-APR-2000 (first entry)  
XX  
DE Metastatic breast tumour cell upregulated transcript tag #1854.  
DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
XX non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
KW Homo sapiens.  
OS  
XX  
XX WO9965928-A2.  
PN  
XX  
PD 23-DEC-1999.  
XX  
XX 18-JUN-1999; 99WO-US013647.  
PF  
XX  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX  
XX (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
XX Roberts BL, Shankara S;  
PI  
XX  
DR WPI; 2000-106079/09.  
XX  
XX Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX  
PS Claim 1; Page 65; 219pp; English.  
XX

PS Claim 1; Page 108; 219pp; English.

XX

CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts

CC that are preferentially transcribed in the metastatic breast tumour

CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942

CC to AAZ86677 represent tags corresponding to distinct transcripts that are

CC preferentially transcribed in the primary or non-metastatic breast tumour

CC tissue (i.e. are downregulated in metastatic breast tumour cells). These

CC transcripts can be used for diagnosis, prognosis, monitoring and

CC treatment of breast cancer, particularly where metastatic. Diagnosis is

CC by standard immunoassays or hybridisation/amplification reactions.

CC Compounds that modulate expression of the transcripts are potentially

CC useful for treatment of (metastatic) breast cancer, while promoters from

CC the transcripts are used to direct expression, in selected cell types, of

CC e.g. therapeutic genes (also ribozymes or antisense sequences),

CC particularly an antigen-encoded sequence for use in gene or cell-based

CC vaccines. Polypeptides encoded by the transcripts are also useful in

CC vaccines; for diagnosing breast cancer and for raising specific

CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic

CC agents. Host cells that produce the polypeptides can be used to expand

CC and isolate populations of educated, antigen-specific immune effector

CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive

CC immunotherapy

XX

SQ Sequence 10 BP; 0 A; 1 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 31.0%; Score 9; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 TGCTGTGTG 18

|||||

Db 2 TGCTGTGTG 10

RESULT 174

AAH63185/c

ID AAH63185 standard; cDNA; 10 BP.

XX

AC AAH63185;

XX

DT 20-SEP-2001 (first entry)

XX

DE Human colon epithelium specific transcriptome sequence SEQ ID NO: 25.

XX

KW Human; transcriptome; gene expression pattern; cancer; drug screening;

KW cancer diagnosis; cell specific gene expression; ss.

XX

OS Homo sapiens.

XX

PN WO200138577-A2.

XX

PD 31-MAY-2001.

XX

PF 21-NOV-2000; 2000WO-US031922.

XX

PR 24-NOV-1999; 99US-00448480.

XX

PA (UYJO ) UNIV JOHNS HOPKINS.

XX

PI Velculescu VE, Vogelstein B, Kinzler KW;

XX

DR WPI; 2001-367706/38.

XX

XX New isolated polynucleotides, useful for identifying specific cell type,

PT such as cancer cell, comprises transcriptomes expressed in particular

PT cell types.

XX

PS Claim 11; Page 39; 94pp; English.

XX

CC The present invention describes a method of identifying the type of cell

CC in a sample, involving determining which of the sequences AAH63161-

CC AAH64724 is expressed by the cell. The transcriptomes described in the

CC invention are cell-type specific, cancer specific or ubiquitously

CC expressed in humans. They can also be used to screen for drugs, reduce

CC cancer specific gene expression, standardise expression and restore the

CC function of a diseased cell or tissue. The present sequence is one of the

CC transcriptomes described in the exemplification of the invention

XX

SQ Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 31.0%; Score 9; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GTGACCTGG 24

|||||

Db 10 GTGACCTGG 2

RESULT 175

AAS57316

ID AAS57316 standard; DNA; 10 BP.

XX

AC AAS57316;

XX

DT 16-JAN-2002 (first entry)

XX

DE Human CHRNA2 allele specific oligonucleotide PCR primer terminus #41.

XX

KW Human; cholinergic receptor, nicotinic, beta polypeptide 2; neuronal;

KW CHRNA2; memory disorder; Alzheimer's disease; epilepsy; learning;

KW chromosome 1q21; schizophrenia; attention deficit/hyperactivity disorder;

KW ADHD; autosomal dominant nocturnal frontal lobe epilepsy; ADNFLE; ss;

KW allele specific oligonucleotide; ASO; PCR primer.

XX

OS Homo sapiens.

XX

PN WO200174833-A2.

XX

PD 11-OCT-2001.

XX

PF 03-APR-2001; 2001WO-US010666.

XX

PR 03-APR-2000; 2000US-0194155P.

PR 13-JUL-2000; 2000US-0217952P.

XX

PA (GENA-) GENAISSANCE PHARM INC.

XX

PI Choi JY, Kliem SE, Koshy B, Lee HH, Sanchis A;

XX

DR WPI; 2001-626374/72.

XX

PT Genotyping cholinergic receptor, nicotinic, beta-polypeptide 2 gene of an

PT individual involves determining for two copies of the gene, the identity

PT of nucleotide pair at polymorphic sites selected from PS1-24.

XX

PS Claim 17; Page 15; 82pp; English.

XX

CC The invention relates to genotyping/haplotyping the cholinergic receptor,

CC nicotinic, beta-polypeptide 2 (neuronal) (CHRNA2) gene of an individual,

CC comprising determining for the two copies of the CHRNA2 gene present in

CC the individual, the identity of the nucleotide pair at one or more

CC polymorphic sites selected from PS1-24. Also include are oligonucleotides

CC for performing the method and the nucleotide sequence of the polymorphic

CC variants of CHRNA2. The method is useful for detecting novel CHRNA2

CC polymorphisms and for determining if an individual has a haplotype or

CC haplotype pairs defined in the specification and to validate CHRNA2 as a

CC candidate agent for treating a specific condition or disease predicted to

CC be associated with CHRNA2 activity (e.g. a memory disorder, Alzheimer's

CC disease, epilepsy, a learning disorder, schizophrenia, attention

CC deficit/hyperactivity disorder, (ADHD) and autosomal dominant nocturnal

CC frontal lobe epilepsy (ADNFLE)), and in the design of clinical trials of

CC candidate drugs for treating a specific condition or disease predicted to

CC be associated with CHRNA2 activity. The method is useful to screen for

CC compounds targeting CHRNA2 to treat a specific conditions or disease

CC associated with CHRN2 activity. The polymorphic nucleic acids are useful  
CC in studying the expression and function of CHRN2, and in expressing  
CC CHRN2 protein for use in screening for candidate drugs to treat diseases  
CC related to CHRN2 activity and are useful for therapeutic purposes. The  
CC CHRN2 gene is located on chromosome 1q21. The present sequence is an  
CC allele specific oligonucleotide (ASO) PCR primer (3' terminus) for  
CC performing the method of the invention  
XX  
SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 31.0%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GTGACCTGG 24  
|||||  
Db 1 GTGACCTGG 9

RESULT 176  
AAH32728  
ID AAH32728 standard; cDNA; 10 BP.

XX AAH32728;  
DT 13-AUG-2001 (first entry)  
DE LPS activated human monocyte expression gene cDNA tag SEQ:101.

XX Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;  
KW expressed sequence tag; diagnosis; human disease; treatment; ss.

XX Homo sapiens.  
XX JP2001069993-A.  
XX  
PD 21-MAR-2001.  
XX  
PF 28-APR-2000; 2000JP-00131079.  
XX  
PR 08-JUL-1999; 99JP-00195103.  
XX  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX  
DR WPI; 2001-304369/32.

XX LPS activated human monocyte expression gene group.  
XX  
PS Claim 10; Page 24; 52pp; Japanese.

XX The present invention describes an lipopolysaccharide (LPS) activated  
CC human monocyte expression gene group consisting of the high-ranking 50  
CC genes of the highest expression among the genes expressed by human  
CC monocyte stimulated by LPS in which the cDNA of each gene has the base  
CC sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-  
CC CATG-3' nearest to the polyA region. The gene group is useful for the  
CC development of new means for the diagnosis and the treatment of various  
CC human diseases in which human monocyte plays an important role. AAH32628  
CC to AAH32943 represent specifically claimed LPS activated human monocyte  
CC expression gene cDNA tags from the present invention. AAH32944 represents  
CC an LPS activated human monocyte expression gene cDNA sequence encoding  
CC AAB98009, which are given in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 31.0%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTGTGACCT 22  
|||||  
Db 2 GTGTGACCT 10

RESULT 177  
ABA81652  
ID ABA81652 standard; DNA; 10 BP.  
XX  
AC ABA81652;  
XX  
DT 24-JAN-2002 (first entry)  
XX  
DE Human phospholipid transfer protein gene PCR primer SEQ ID NO: 101.  
XX  
KW Human; phospholipid transfer protein; PLTP; SNP; atherosclerosis;  
KW single nucleotide polymorphism; high-density lipoprotein metabolism;  
KW PCR primer; ss.

XX Homo sapiens.  
XX WO200172761-A2.  
XX  
PD 04-OCT-2001.

XX 15-MAR-2001; 2001WO-US008283.  
XX 24-MAR-2000; 2000US-0192127P.  
XX (GENA-) GENAISSANCE PHARM INC.

XX Chew A, Choi JY, Koshy B;  
PI WPI; 2001-662922/76.  
XX

PT Genotyping phospholipid transfer protein gene of individual for  
PT haplotyping individual's gene, comprises determining identity of  
PT nucleotide pair at polymorphic sites for two copies of PLTP gene present  
PT in the individual.

XX Claim 17; Page 14; 98pp; English.

XX The present invention relates to a method for haplotyping the human  
CC phospholipid transfer protein (PLTP) gene, involving determining the  
CC identity of the nucleotide present at one or more of the 25 polymorphic  
CC sites within the gene. This can be used to aid drug development for the  
CC treatment of diseases associated with different haplotypes of the PLTP  
CC gene, possibly including atherosclerosis. The present sequence is a PCR  
CC primer used for detecting polymorphisms in the PLTP gene

SQ Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 31.0%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GCTGTGTGA 19  
|||||  
Db 1 GCTGTGTGA 9

RESULT 178  
AAF35559  
ID AAF35559 standard; DNA; 10 BP.

XX  
AC AAF35559;  
XX  
DT 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2298.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.



|                                                            |                                                                           |  |  |
|------------------------------------------------------------|---------------------------------------------------------------------------|--|--|
| XX                                                         | WO2000077214-A2.                                                          |  |  |
| PN                                                         |                                                                           |  |  |
| XX                                                         |                                                                           |  |  |
| PD                                                         | 21-DEC-2000.                                                              |  |  |
| XX                                                         |                                                                           |  |  |
| PF                                                         | 14-JUN-2000; 2000WO-US016223.                                             |  |  |
| XX                                                         |                                                                           |  |  |
| PR                                                         | 16-JUN-1999; 99US-00335032.                                               |  |  |
| XX                                                         |                                                                           |  |  |
| PA                                                         | (UYJO ) UNIV JOHNS HOPKINS.                                               |  |  |
| XX                                                         |                                                                           |  |  |
| PI                                                         | Velculescu V, Vogelstein B, Kinzler K;                                    |  |  |
| XX                                                         |                                                                           |  |  |
| DR                                                         | WPI; 2001-061874/07.                                                      |  |  |
| XX                                                         |                                                                           |  |  |
| PT                                                         | Yeast gene coding sequences comprising NORF genes with serial analysis of |  |  |
| PT                                                         | gene expression (SAGE) tags, useful for studying, monitoring and          |  |  |
| PT                                                         | affecting phases of the cell cycle.                                       |  |  |
| XX                                                         |                                                                           |  |  |
| PS                                                         | Example; Page 82; 419pp; English.                                         |  |  |
| XX                                                         |                                                                           |  |  |
| CC                                                         | The present invention describes an isolated DNA molecule comprising a     |  |  |
| CC                                                         | coding sequence of a yeast gene selected from a group of 745 NORF (not    |  |  |
| CC                                                         | previously assigned open reading frame; or nonannotated ORF) genes        |  |  |
| CC                                                         | comprising a SAGE (serial analysis of gene expression) tag. Also          |  |  |
| CC                                                         | described are: (1) a method (M1) of using NORF genes to affect the cell   |  |  |
| CC                                                         | cycle comprising administering a NORF gene whose expression varies by at  |  |  |
| CC                                                         | least 10% between any two phases of the cell cycle selected from log      |  |  |
| CC                                                         | phase, S phase and G2/M; (2) a method (M2) for screening candidate        |  |  |
| CC                                                         | antifungal drugs comprising: (a) contacting a test substance with a yeast |  |  |
| CC                                                         | cell; and (b) monitoring expression of a NORF gene whose expression       |  |  |
| CC                                                         | varies as in M1, where a test substance which modifies the expression of  |  |  |
| CC                                                         | the yeast gene is a candidate antifungal drug; (3) a method (M3) for      |  |  |
| CC                                                         | identifying human genes which are involved in cell cycle progression      |  |  |
| CC                                                         | comprising contacting human DNA with a probe which comprises at least 10  |  |  |
| CC                                                         | contiguous nucleotides of a NORF gene whose expression varies as in M1;   |  |  |
| CC                                                         | and (4) a method (M4) for identifying a candidate drug as a member of a   |  |  |
| CC                                                         | class of drugs having a characteristic effect on gene expression in a     |  |  |
| CC                                                         | yeast cell comprising contacting a yeast cell with a candidate drug and   |  |  |
| CC                                                         | monitoring expression in the yeast cell of at least 1 NORF gene whose     |  |  |
| CC                                                         | expression is affected by the class of drugs. The NORF genes may be used  |  |  |
| CC                                                         | to study, monitor and affect phases of the cell cycle, the differentially |  |  |
| CC                                                         | expressed genes may be used as markers of phases of the cell cycle. The   |  |  |
| CC                                                         | methods may be used to identify candidate drugs which affect the cell     |  |  |
| CC                                                         | cycle and for identification of antifungal drugs. AAF33268 to AAF44064    |  |  |
| CC                                                         | represent SAGE tags used in the exemplification of the present invention. |  |  |
| CC                                                         | AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE   |  |  |
| CC                                                         | method, in the exemplification of the present invention                   |  |  |
| XX                                                         |                                                                           |  |  |
| SQ                                                         | Sequence 10 BP; 3 A; 2 C; 2 G; 3 T; 0 U; 0 Other;                         |  |  |
| Query Match 31.0%; Score 9; DB 1; Length 10;               |                                                                           |  |  |
| Best Local Similarity 100.0%; Pred. No. 1.3e+02;           |                                                                           |  |  |
| Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                                                                           |  |  |
| QY                                                         | 21 CTGGTAAAT 29                                                           |  |  |
|                                                            |                                                                           |  |  |
| Db                                                         | 1 CTGGTAAAT 9                                                             |  |  |
| RESULT 179                                                 |                                                                           |  |  |
| AAF34581                                                   |                                                                           |  |  |
| ID                                                         | AAF34581 standard; DNA; 10 BP.                                            |  |  |
| XX                                                         |                                                                           |  |  |
| AC                                                         | AAF34581;                                                                 |  |  |
| XX                                                         |                                                                           |  |  |
| DT                                                         | 23-MAR-2001 (first entry)                                                 |  |  |
| XX                                                         |                                                                           |  |  |
| DE                                                         | Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1320.                  |  |  |
| XX                                                         |                                                                           |  |  |
| KW                                                         | Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;      |  |  |
| KW                                                         | nor previously assigned open reading frame; nonannotated ORF; SAGE;       |  |  |
| KW                                                         | serial analysis of gene expression; antifungal; tag; identification;      |  |  |
|                                                            |                                                                           |  |  |
| KW                                                         | linker; PCR primer; ds.                                                   |  |  |
| XX                                                         |                                                                           |  |  |
| OS                                                         | Saccharomyces cerevisiae.                                                 |  |  |
| XX                                                         |                                                                           |  |  |
| PN                                                         | WO2000077214-A2.                                                          |  |  |
| XX                                                         |                                                                           |  |  |
| PD                                                         | 21-DEC-2000.                                                              |  |  |
| XX                                                         |                                                                           |  |  |
| PF                                                         | 14-JUN-2000; 2000WO-US016223.                                             |  |  |
| XX                                                         |                                                                           |  |  |
| PR                                                         | 16-JUN-1999; 99US-00335032.                                               |  |  |
| XX                                                         |                                                                           |  |  |
| PA                                                         | (UYJO ) UNIV JOHNS HOPKINS.                                               |  |  |
| XX                                                         |                                                                           |  |  |
| PI                                                         | Velculescu V, Vogelstein B, Kinzler K;                                    |  |  |
| XX                                                         |                                                                           |  |  |
| DR                                                         | WPI; 2001-061874/07.                                                      |  |  |
| XX                                                         |                                                                           |  |  |
| PT                                                         | Yeast gene coding sequences comprising NORF genes with serial analysis of |  |  |
| PT                                                         | gene expression (SAGE) tags, useful for studying, monitoring and          |  |  |
| PT                                                         | affecting phases of the cell cycle.                                       |  |  |
| XX                                                         |                                                                           |  |  |
| PS                                                         | Example; Page 47; 419pp; English.                                         |  |  |
| XX                                                         |                                                                           |  |  |
| CC                                                         | The present invention describes an isolated DNA molecule comprising a     |  |  |
| CC                                                         | coding sequence of a yeast gene selected from a group of 745 NORF (not    |  |  |
| CC                                                         | previously assigned open reading frame; or nonannotated ORF) genes        |  |  |
| CC                                                         | comprising a SAGE (serial analysis of gene expression) tag. Also          |  |  |
| CC                                                         | described are: (1) a method (M1) of using NORF genes to affect the cell   |  |  |
| CC                                                         | cycle comprising administering a NORF gene whose expression varies by at  |  |  |
| CC                                                         | least 10% between any two phases of the cell cycle selected from log      |  |  |
| CC                                                         | phase, S phase and G2/M; (2) a method (M2) for screening candidate        |  |  |
| CC                                                         | antifungal drugs comprising: (a) contacting a test substance with a yeast |  |  |
| CC                                                         | cell; and (b) monitoring expression of a NORF gene whose expression       |  |  |
| CC                                                         | varies as in M1, where a test substance which modifies the expression of  |  |  |
| CC                                                         | the yeast gene is a candidate antifungal drug; (3) a method (M3) for      |  |  |
| CC                                                         | identifying human genes which are involved in cell cycle progression      |  |  |
| CC                                                         | comprising contacting human DNA with a probe which comprises at least 10  |  |  |
| CC                                                         | contiguous nucleotides of a NORF gene whose expression varies as in M1;   |  |  |
| CC                                                         | and (4) a method (M4) for identifying a candidate drug as a member of a   |  |  |
| CC                                                         | class of drugs having a characteristic effect on gene expression in a     |  |  |
| CC                                                         | yeast cell comprising contacting a yeast cell with a candidate drug and   |  |  |
| CC                                                         | monitoring expression in the yeast cell of at least 1 NORF gene whose     |  |  |
| CC                                                         | expression is affected by the class of drugs. The NORF genes may be used  |  |  |
| CC                                                         | to study, monitor and affect phases of the cell cycle, the differentially |  |  |
| CC                                                         | expressed genes may be used as markers of phases of the cell cycle. The   |  |  |
| CC                                                         | methods may be used to identify candidate drugs which affect the cell     |  |  |
| CC                                                         | cycle and for identification of antifungal drugs. AAF33268 to AAF44064    |  |  |
| CC                                                         | represent SAGE tags used in the exemplification of the present invention. |  |  |
| CC                                                         | AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE   |  |  |
| CC                                                         | method, in the exemplification of the present invention                   |  |  |
| XX                                                         |                                                                           |  |  |
| SQ                                                         | Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;                         |  |  |
| Query Match 31.0%; Score 9; DB 1; Length 10;               |                                                                           |  |  |
| Best Local Similarity 100.0%; Pred. No. 1.3e+02;           |                                                                           |  |  |
| Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                                                                           |  |  |
| QY                                                         | 21 CTGGTAAAT 29                                                           |  |  |
|                                                            |                                                                           |  |  |
| Db                                                         | 1 CTGGTAAAT 9                                                             |  |  |
| RESULT 180                                                 |                                                                           |  |  |
| AAF37646/c                                                 |                                                                           |  |  |
| ID                                                         | AAF37646 standard; DNA; 10 BP.                                            |  |  |
| XX                                                         |                                                                           |  |  |
| AC                                                         | AAF37646;                                                                 |  |  |
| XX                                                         |                                                                           |  |  |
| DT                                                         | 23-MAR-2001 (first entry)                                                 |  |  |
| XX                                                         |                                                                           |  |  |
| DE                                                         | Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4385.                  |  |  |
| XX                                                         |                                                                           |  |  |



|    |                                                                           |  |
|----|---------------------------------------------------------------------------|--|
| KW | Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;      |  |
| KW | nor previously assigned open reading frame; nonannotated ORF; SAGE;       |  |
| KW | serial analysis of gene expression; antifungal; tag; identification;      |  |
| KW | linker; PCR primer; ds.                                                   |  |
| XX | Saccharomyces cerevisiae.                                                 |  |
| OS |                                                                           |  |
| XX | WO200077214-A2.                                                           |  |
| PN |                                                                           |  |
| XX | 21-DEC-2000.                                                              |  |
| PD |                                                                           |  |
| XX | 14-JUN-2000; 2000WO-US016223.                                             |  |
| PF |                                                                           |  |
| XX | 16-JUN-1999; 99US-00335032.                                               |  |
| PR |                                                                           |  |
| XX | (UYJO ) UNIV JOHNS HOPKINS.                                               |  |
| PA |                                                                           |  |
| XX | Velculescu V, Vogelstein B, Kinzler K;                                    |  |
| PI |                                                                           |  |
| XX | WPI; 2001-061874/07.                                                      |  |
| DR |                                                                           |  |
| XX | Yeast gene coding sequences comprising NORF genes with serial analysis of |  |
| PT | gene expression (SAGE) tags, useful for studying, monitoring and          |  |
| PT | affecting phases of the cell cycle.                                       |  |
| XX |                                                                           |  |
| PS | Example; Page 156; 419pp; English.                                        |  |
| XX |                                                                           |  |
| CC | The present invention describes an isolated DNA molecule comprising a     |  |
| CC | coding sequence of a yeast gene selected from a group of 745 NORF (not    |  |
| CC | previously assigned open reading frame; or nonannotated ORF) genes        |  |
| CC | comprising a SAGE (serial analysis of gene expression) tag. Also          |  |
| CC | described are: (1) a method (M1) of using NORF genes to affect the cell   |  |
| CC | cycle comprising administering a NORF gene whose expression varies by at  |  |
| CC | least 10% between any two phases of the cell cycle selected from log      |  |
| CC | phase, S phase and G2/M; (2) a method (M2) for screening candidate        |  |
| CC | antifungal drugs comprising: (a) contacting a test substance with a yeast |  |
| CC | cell; and (b) monitoring expression of a NORF gene whose expression       |  |
| CC | varies as in M1, where a test substance which modifies the expression of  |  |
| CC | the yeast gene is a candidate antifungal drug; (3) a method (M3) for      |  |
| CC | identifying human genes which are involved in cell cycle progression      |  |
| CC | comprising contacting human DNA with a probe which comprises at least 10  |  |
| CC | contiguous nucleotides of a NORF gene whose expression varies as in M1;   |  |
| CC | and (4) a method (M4) for identifying a candidate drug as a member of a   |  |
| CC | class of drugs having a characteristic effect on gene expression in a     |  |
| CC | yeast cell comprising contacting a yeast cell with a candidate drug and   |  |
| CC | monitoring expression in the yeast cell of at least 1 NORF gene whose     |  |
| CC | expression is affected by the class of drugs. The NORF genes may be used  |  |
| CC | to study, monitor and affect phases of the cell cycle, the differentially |  |
| CC | expressed genes may be used as markers of phases of the cell cycle. The   |  |
| CC | methods may be used to identify candidate drugs which affect the cell     |  |
| CC | cycle and for identification of antifungal drugs. AAF33268 to AAF44064    |  |
| CC | represent SAGE tags used in the exemplification of the present invention. |  |
| CC | AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE   |  |
| CC | method, in the exemplification of the present invention                   |  |
| XX |                                                                           |  |
| SQ | Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;                         |  |
|    |                                                                           |  |
|    | Query Match 31.0%; Score 9; DB 1; Length 10;                              |  |
|    | Best Local Similarity 100.0%; Pred. No. 1.3e+02;                          |  |
|    | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                |  |
|    |                                                                           |  |
| QY | 5 CCACCTGCT 13                                                            |  |
|    |                                                                           |  |
| Db | 10 CCACCTGCT 2                                                            |  |
|    |                                                                           |  |
|    | RESULT 181                                                                |  |
|    | ABL52170/c                                                                |  |
| ID | ABL52170 standard; DNA; 10 BP.                                            |  |
| XX |                                                                           |  |
| AC | ABL52170;                                                                 |  |
| XX |                                                                           |  |
| DT | 12-JUL-2002 (first entry)                                                 |  |
|    |                                                                           |  |
|    | Query Match 31.0%; Score 9; DB 1; Length 10;                              |  |
|    | Best Local Similarity 100.0%; Pred. No. 1.3e+02;                          |  |
|    | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                |  |
|    |                                                                           |  |
| QY | 6 CACCTGCTG 14                                                            |  |
|    |                                                                           |  |
| Db | 10 CACCTGCTG 2                                                            |  |
|    |                                                                           |  |
|    | RESULT 182                                                                |  |
|    | AAS94664                                                                  |  |
| ID | AAS94664 standard; DNA; 10 BP.                                            |  |
| XX |                                                                           |  |
| AC | AAS94664;                                                                 |  |
| XX |                                                                           |  |
| DT | 14-FEB-2002 (first entry)                                                 |  |
| XX |                                                                           |  |
| DE | Human PLTP gene allele-specific oligonucleotide PCR primer #23.           |  |
| XX |                                                                           |  |
| KW | Human; phospholipid transfer protein; PLTP; haplotyping; haplotype pair;  |  |
| KW | single nucleotide polymorphism; genotyping; gene therapy; drug screening; |  |
| KW | binding affinity; atherosclerosis; ss; sequencing primer; PCR primer;     |  |
| KW | probe.                                                                    |  |
| XX |                                                                           |  |
| OS | Homo sapiens.                                                             |  |
|    |                                                                           |  |
|    | Human PER1 preferred oligonucleotide primer SEQ ID NO:95.                 |  |
| XX |                                                                           |  |
| DE |                                                                           |  |
| XX | Human; period (Drosophila) homologue 1; PER1; polymorphic variant;        |  |
| KW | polymorphic site; genotyping; haplotyping; circadian rhythm regulation;   |  |
| KW | single nucleotide polymorphism; SNP; gene; primer; ss.                    |  |
| XX |                                                                           |  |
| OS | Homo sapiens.                                                             |  |
| XX |                                                                           |  |
| PN | WO200222650-A2.                                                           |  |
| XX |                                                                           |  |
| PD | 21-MAR-2002.                                                              |  |
| XX |                                                                           |  |
| PF | 13-SEP-2001; 2001WO-US028780.                                             |  |
| XX |                                                                           |  |
| PR | 13-SEP-2000; 2000US-0232468P.                                             |  |
| XX |                                                                           |  |
| PA | (GENA-) GENAISSANCE PHARM INC.                                            |  |
| XX |                                                                           |  |
| PI | Duda A, Kliem SE, Koshy B;                                                |  |
| XX |                                                                           |  |
| DR | WPI; 2002-393941/42.                                                      |  |
| XX |                                                                           |  |
| PT | Novel isolated human period Drosophila homolog 1 polynucleotide, useful   |  |
| PT | for therapeutic purposes, for studying the expression and function of the |  |
| PT | polynucleotide, and for expressing the homolog.                           |  |
| XX |                                                                           |  |
| PS | Claim 19; Page 15; 162pp; English.                                        |  |
| XX |                                                                           |  |
| CC | The present invention describes an isolated human period (Drosophila)     |  |
| CC | homologue 1, (PER1) polynucleotide (I) comprising a sequence which is a   |  |
| CC | polymorphic variant for a reference sequence (ABL52077) for the PER1 gene |  |
| CC | or its fragment, or a polymorphic variant of a reference sequence         |  |
| CC | (ABL52078) for a PER1 cDNA or its fragment. The present invention also    |  |
| CC | describes methods for genotyping and haplotyping the PER1 gene of an      |  |
| CC | individual. (I) is useful in studying the expression and function of      |  |
| CC | PER1, and in expressing PER1 protein for use in screening for candidate   |  |
| CC | drugs to treat diseases related to PER1 activity. (I) is useful for       |  |
| CC | therapeutic purposes. A recombinant non-human organism transformed or     |  |
| CC | transfected with (I) can be used for studying expression of the PER1      |  |
| CC | isogenes in vivo, for in vivo screening and testing of drugs targeted     |  |
| CC | against PER1 protein, and for testing the efficacy of therapeutic agents  |  |
| CC | and compounds for disorders associated with circadian rhythm regulation.  |  |
| CC | The present sequence represents a preferred oligonucleotide primer for    |  |
| CC | human PER1, which is used in the exemplification of the present invention |  |
| XX |                                                                           |  |
| SQ | Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;                         |  |
|    |                                                                           |  |
|    | Query Match 31.0%; Score 9; DB 1; Length 10;                              |  |
|    | Best Local Similarity 100.0%; Pred. No. 1.3e+02;                          |  |
|    | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                |  |
|    |                                                                           |  |
| QY | 6 CACCTGCTG 14                                                            |  |
|    |                                                                           |  |
| Db | 10 CACCTGCTG 2                                                            |  |
|    |                                                                           |  |
|    | RESULT 182                                                                |  |
|    | AAS94664                                                                  |  |
| ID | AAS94664 standard; DNA; 10 BP.                                            |  |
| XX |                                                                           |  |
| AC | AAS94664;                                                                 |  |
| XX |                                                                           |  |
| DT | 14-FEB-2002 (first entry)                                                 |  |
| XX |                                                                           |  |
| DE | Human PLTP gene allele-specific oligonucleotide PCR primer #23.           |  |
| XX |                                                                           |  |
| KW | Human; phospholipid transfer protein; PLTP; haplotyping; haplotype pair;  |  |
| KW | single nucleotide polymorphism; genotyping; gene therapy; drug screening; |  |
| KW | binding affinity; atherosclerosis; ss; sequencing primer; PCR primer;     |  |
| KW | probe.                                                                    |  |
| XX |                                                                           |  |
| OS | Homo sapiens.                                                             |  |
|    |                                                                           |  |
|    | Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;      |  |
| KW | nor previously assigned open reading frame; nonannotated ORF; SAGE;       |  |
| KW | serial analysis of gene expression; antifungal; tag; identification;      |  |
| KW | linker; PCR primer; ds.                                                   |  |
| XX | Saccharomyces cerevisiae.                                                 |  |
| OS |                                                                           |  |
| XX | WO200077214-A2.                                                           |  |
| PN |                                                                           |  |
| XX | 21-DEC-2000.                                                              |  |
| PD |                                                                           |  |
| XX | 14-JUN-2000; 2000WO-US016223.                                             |  |
| PF |                                                                           |  |
| XX | 16-JUN-1999; 99US-00335032.                                               |  |
| PR |                                                                           |  |
| XX | (UYJO ) UNIV JOHNS HOPKINS.                                               |  |
| PA |                                                                           |  |
| XX | Velculescu V, Vogelstein B, Kinzler K;                                    |  |
| PI |                                                                           |  |
| XX | WPI; 2001-061874/07.                                                      |  |
| DR |                                                                           |  |
| XX | Yeast gene coding sequences comprising NORF genes with serial analysis of |  |
| PT | gene expression (SAGE) tags, useful for studying, monitoring and          |  |
| PT | affecting phases of the cell cycle.                                       |  |
| XX |                                                                           |  |
| PS | Example; Page 156; 419pp; English.                                        |  |
| XX |                                                                           |  |
| CC | The present invention describes an isolated DNA molecule comprising a     |  |
| CC | coding sequence of a yeast gene selected from a group of 745 NORF (not    |  |
| CC | previously assigned open reading frame; or nonannotated ORF) genes        |  |
| CC | comprising a SAGE (serial analysis of gene expression) tag. Also          |  |
| CC | described are: (1) a method (M1) of using NORF genes to affect the cell   |  |
| CC | cycle comprising administering a NORF gene whose expression varies by at  |  |
| CC | least 10% between any two phases of the cell cycle selected from log      |  |
| CC | phase, S phase and G2/M; (2) a method (M2) for screening candidate        |  |
| CC | antifungal drugs comprising: (a) contacting a test substance with a yeast |  |
| CC | cell; and (b) monitoring expression of a NORF gene whose expression       |  |
| CC | varies as in M1, where a test substance which modifies the expression of  |  |
| CC | the yeast gene is a candidate antifungal drug; (3) a method (M3) for      |  |
| CC | identifying human genes which are involved in cell cycle progression      |  |
| CC | comprising contacting human DNA with a probe which comprises at least 10  |  |
| CC | contiguous nucleotides of a NORF gene whose expression varies as in M1;   |  |
| CC | and (4) a method (M4) for identifying a candidate drug as a member of a   |  |
| CC | class of drugs having a characteristic effect on gene expression in a     |  |
| CC | yeast cell comprising contacting a yeast cell with a candidate drug and   |  |
| CC | monitoring expression in the yeast cell of at least 1 NORF gene whose     |  |
| CC | expression is affected by the class of drugs. The NORF genes may be used  |  |
| CC | to study, monitor and affect phases of the cell cycle, the differentially |  |
| CC | expressed genes may be used as markers of phases of the cell cycle. The   |  |
| CC | methods may be used to identify candidate drugs which affect the cell     |  |
| CC | cycle and for identification of antifungal drugs. AAF33268 to AAF44064    |  |
| CC | represent SAGE tags used in the exemplification of the present invention. |  |
| CC | AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE   |  |
| CC | method, in the exemplification of the present invention                   |  |
| XX |                                                                           |  |
| SQ | Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;                         |  |
|    |                                                                           |  |
|    | Query Match 31.0%; Score 9; DB 1; Length 10;                              |  |
|    | Best Local Similarity 100.0%; Pred. No. 1.3e+02;                          |  |
|    | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                |  |
|    |                                                                           |  |
| QY | 5 CCACCTGCT 13                                                            |  |
|    |                                                                           |  |
| Db | 10 CCACCTGCT 2                                                            |  |
|    |                                                                           |  |
|    | RESULT 181                                                                |  |
|    | ABL52170/c                                                                |  |
| ID | ABL52170 standard; DNA; 10 BP.                                            |  |
| XX |                                                                           |  |
| AC | ABL52170;                                                                 |  |
| XX |                                                                           |  |
| DT | 12-JUL-2002 (first entry)                                                 |  |

XX WO200172966-A2.  
PN  
XX  
PD 04-OCT-2001.  
XX  
PF 26-MAR-2001; 2001WO-US009776.  
XX  
PR 24-MAR-2000; 2000US-0192127P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Chew A, Choi JY, Koshy B;  
XX WPI; 2002-010724/01.  
DR  
XX New isolated polynucleotide which is polymorphic variant of phospholipid  
PT transfer protein (PLTP) gene, having any one of polymorphic sites PSL-  
PT PS25, for studying function of PLTP, and expressing PLTP protein.  
XX  
PS Claim 17; Page 85; 99pp; English.  
XX  
CC The invention relates to single nucleotide polymorphisms in the gene  
CC encoding the human phospholipid transfer protein (PLTP). A method for  
CC haplotyping the PLTP gene in an individual comprises identifying the  
CC nucleotide at one or more polymorphic sites and determining whether one  
CC of the copies of the gene is defined by one of the PLTP haplotypes given  
CC in the specification or whether both copies are defined by a haplotype  
CC pair. This method is useful in genotyping, whereby all possible haplotype  
CC pairs can be assigned to specific genotypes. An association between a  
CC trait and a haplotype or haplotype pair of the PLTP gene can be  
CC identified by comparing the frequency of the haplotype or haplotype pair  
CC in a population exhibiting the trait with the frequency of the haplotype  
CC or haplotype pair in a reference population, where a higher haplotype  
CC frequency in the trait population indicates the trait is associated with  
CC the haplotype or haplotype pair. PLTP and its corresponding DNA are used  
CC for studying the expression and function of PLTP, for use in screening  
CC for candidate drugs to treat diseases related to PLTP activity. The  
CC sequences are also useful for studying the effect of variation on the  
CC biological activity of PLTP as well as on the binding affinity of  
CC candidate drugs targeting PLTP for treating atherosclerosis. Sequences  
CC AAS94566-AAS94691 represent allele-specific oligonucleotide probes,  
CC sequencing primers and PCR primers used for detecting PLTP gene  
CC polymorphisms  
XX  
SQ Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 U; 0 Other;  
  
Query Match 31.0%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 11 GCTGTGTGA 19  
Db 1 GCTGTGTGA 9  
  
RESULT 183  
AAL39779  
ID AAL39779 standard; DNA; 10 BP.  
XX  
AC AAL39779;  
XX  
DT 05-SEP-2002 (first entry)  
XX  
DE SMOH polymorphism detecting primer SEQ ID No 94.  
XX  
KW Cytostatic; polymorphic variant; single nucleotide polymorphism; SMOH;  
KW human smoothened Drosophila homologue; basal cell carcinoma; BCC;  
KW gene therapy; antisense gene therapy; PCR; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200229004-A2.  
XX

PD 11-APR-2002.  
XX  
PF 04-OCT-2001; 2001WO-US031304.  
XX  
PR 04-OCT-2000; 2000US-0237871P.  
XX (GENA-) GENAISSANCE PHARM INC.  
XX Bentivegna SC, Choi JY, Koshy B, Lee HH, Sausker EA;  
XX WPI; 2002-519113/55.  
DR  
XX New genetic variants of smoothened Drosophila homolog (SMOH) gene useful  
PT for therapeutic purposes and for expressing SMOH protein useful in  
PT identifying drugs to treat basal cell carcinomas.  
XX  
PS Claim 17; Page 15; 179pp; English.  
XX  
CC The invention relates to an isolated polynucleotide comprising a sequence  
CC which is a polymorphic variant of a reference sequence for the human  
CC smoothened Drosophila homologue (SMOH) gene or its fragment, or a  
CC polymorphic variant of a reference sequence for a SMOH cDNA or its  
CC fragment. A new isolated polypeptide is useful for screening for drugs  
CC targeting the polypeptide. A new method is useful for identifying an  
CC association between a trait such as a clinical response to a drug  
CC targeting SMOH and a haplotype or haplotype pair of SMOH gene. The  
CC methods have applicability in developing diagnostic tests and therapeutic  
CC treatments for basal cell carcinomas (BCCs). The isolated polynucleotide  
CC is useful for studying the expression and function of SMOH and expressing  
CC SMOH protein for use in screening for candidate drugs to treat diseases  
CC related to SMOH activity. The polymorphism and haplotype data are useful  
CC for validating whether SMOH is a suitable target for drugs to treat BCCs,  
CC screening for the drugs and reducing bias in clinical trials of the  
CC drugs. The isolated polynucleotide is useful for therapeutic purposes.  
CC The new method, an oligonucleotide and kit of the invention are useful  
CC for determining whether an individual has one of the haplotypes or the  
CC haplotype pairs. The polynucleotides of the invention can be used to  
CC treat disorders by gene therapy and antisense gene therapy. This  
CC polynucleotide sequence represents a primer used for detecting human  
CC smoothened Drosophila homologue gene polymorphisms of the invention  
XX  
SQ Sequence 10 BP; 0 A; 2 C; 4 G; 4 T; 0 U; 0 Other;  
  
Query Match 31.0%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 10 TGCTGTGTG 18  
Db 1 TGCTGTGTG 9  
  
RESULT 184  
ADE14133  
ID ADE14133 standard; DNA; 10 BP.  
XX  
AC ADE14133;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Optineurin promoter motif, repeat element or regulatory region #242.  
XX  
KW Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;  
KW SNP; glaucoma; progressive ocular hypertensive disorder;  
KW glaucoma related disorder; motif; repeat element; regulatory region.  
XX  
OS Homo sapiens.  
XX US2003190617-A1.  
PN  
XX  
PD 09-OCT-2003.  
XX  
PF 06-MAR-2002; 2002US-00091281.



XX PF 14-JUL-1998; 98WO-US014901.  
XX PR 14-JUL-1997; 97US-0052403P.  
XX PA (GENE-) GENEMEDICINE INC.  
XX PI Schwartz RJ, Eastman EM, Li X, Nordstrom J;  
XX WPI; 1999-120937/10.  
DR XX Identifying transcriptional regulatory regions - by identifying binding  
PT sites for transcription factors and evaluating whether a selective gene  
PT is expressed in cells.  
XX XX Example 1; Page 36; 106pp; English.  
PS XX A method has been developed for identifying transcription factor binding  
XX sites comprising identifying the oligonucleotides (ONs) in ON-protein  
CC complexes formed between one or more proteins of a cellular or nuclear  
CC extract and any double stranded (ds) ON fragments in a mixture of free  
CC fragments and the extract, where the complexes are separated from free  
CC ONs in the mixture using size exclusion chromatography; and where the  
CC presence of the ON in the complex is indicative that the ON comprises a  
CC binding site. The synthetic regulatory regions obtained using the method  
CC can be used in gene delivery or gene therapy to achieve desired gene  
CC expression in targeted cells. They can also be used to achieve the  
CC production of recombinant proteins at high levels. The present sequence  
CC represents a transcription factor binding site given in an example from  
CC the present invention  
XX SQ Sequence 11 BP; 1 A; 5 C; 2 G; 3 T; 0 U; 0 Other;  
  
Query Match 31.0%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 CACCTGCTG 14  
Db 3 CACCTGCTG 11  
  
RESULT 187  
AAA16595/C  
ID AAA16595 standard; DNA; 11 BP.  
XX AC AAA16595;  
XX DT 16-JUN-2000 (first entry)  
XX DE Human MN gene 5' donor consensus splice sequence SEQ ID NO:73.  
XX KW Human; MN protein; MN gene; oncogene; carbonic anhydrase; tumour;  
KW oncogenesis; diagnosis; neoplastic disease; cancer; carcinoma;  
KW MN/CA IX isoenzyme; ds.  
XX OS Homo sapiens.  
XX PN US6027887-A.  
XX PD 22-FEB-2000.  
XX PF 24-JAN-1997; 97US-00787739.  
XX PR 21-OCT-1992; 92US-00964589.  
PR 30-DEC-1993; 93US-00177093.  
PR 15-JUN-1994; 94US-00260190.  
PR 07-JUN-1995; 95US-00477504.  
PR 07-JUN-1995; 95US-00481658.  
PR 07-JUN-1995; 95US-00485049.  
PR 07-JUN-1995; 95US-00485862.  
PR 07-JUN-1995; 95US-00485863.  
PR 07-JUN-1995; 95US-00486756.

PR 07-JUN-1995; 95US-00487077.  
XX (SLSC-) SLOVAK ACAD SCI INST VIROLOGY.  
XX PI Pastorek J, Zavada J, Pastorekova S;  
XX WPI; 2000-194827/17.  
DR XX Nucleic acid based assay for diagnosing a wide variety of  
XX preneoplastic/neoplastic disease comprises screening for the presence of  
PT abnormal MN gene expression in a vertebrate.  
XX PS Disclosure; Col 16; 87pp; English.  
XX CC The present invention describes a method of screening for  
CC preneoplastic/neoplastic disease. The method comprises: (1) determining  
CC whether abnormal MN gene expression is present in a vertebrate; and (2)  
CC if abnormal MN gene expression is determined to be present in the  
CC vertebrate, determining that the vertebrate has a significant risk of  
CC having preneoplastic/neoplastic disease. The MN gene is an oncogene and  
CC encodes an MN protein (also referred to as MN/CA IX isoenzyme). The MN  
CC protein is a tumour associated carbonic anhydrase isoenzyme. The method  
CC is used for detecting a wide variety of preneoplastic/neoplastic diseases  
CC in a vertebrate, preferably a human. The disease detected is mammary,  
CC bladder, renal, urinary tract, ovarian, uterine, cervical, endometrial,  
CC vaginal, vulval, prostate, liver, lung, skin, thyroid, pancreatic,  
CC testicular, brain, head and neck, mesodermal, gallbladder, rectal,  
CC duodenal, jejunal, ileal, gastric, pancreatic duct, liver duct, gastric  
CC mucosa, gallbladder epithelium, small intestinal mucosa, colorectal  
CC mucosa, pancreatic duct epithelium or liver duct epithelium  
CC preneoplastic/neoplastic disease. AAA16540 to AAA16617 and AAY53228 to  
CC AAY53245 represent sequences used in the exemplification of the present  
CC invention  
XX SQ Sequence 11 BP; 2 A; 2 C; 6 G; 1 T; 0 U; 0 Other;  
  
Query Match 31.0%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 CCACCTGCT 13  
Db 9 CCACCTGCT 1  
  
RESULT 188  
AAA52514/c  
ID AAA52514 standard; DNA; 11 BP.  
XX AC AAA52514;  
XX DT 25-SEP-2000 (first entry)  
XX DE Human MN gene intron 7 splice donor sequence.  
XX KW MN protein; tumour associated cell adhesion molecule; oncoprotein;  
KW proteoglycan domain; PG domain; carbonic anhydrase; CA domain;  
KW abnormal expression; neoplastic disease; cancer; gene therapy; ds.  
XX OS Homo sapiens.  
XX PN WO200024913-A2.  
XX PD 04-MAY-2000.  
XX PF 22-OCT-1999; 99WO-US024879.  
XX PR 23-OCT-1998; 98US-00177776.  
PR 23-OCT-1998; 98US-00178115.  
XX PA (FARB ) BAYER CORP.  
PA (VIRO-) INST VIROLOGY.  
XX



PI Zavada J, Pastorekova S, Pastorek J;  
XX WPI; 2000-350752/30.  
DR  
XX  
PT A molecule which specifically binds to a site on MN protein (oncoprotein)  
PT and prevents adhesion of vertebrate cells to the protein, useful for  
PT treating preneoplastic or neoplastic diseases such as cancer.  
XX  
XX  
PS Disclosure; Page 26; 154pp; English.  
XX  
CC The invention relates to the inhibition of cell adhesion mediated by the  
CC MN oncoprotein (also known as the MN/CA IX isoenzyme or the MN/G250  
CC protein). The MN protein is a tumour-associated adhesion molecule which  
CC comprises a proteoglycan-like (PG) domain (AAB03017) which contains the  
CC protein's binding site, and a carbonic anhydrase (CA) domain (AAB03018).  
CC Abnormal expression of the MN protein is associated with tumorigenicity.  
CC The invention encompasses molecules (e.g., proteins and peptides) which  
CC which specifically bind to a site on the MN protein, thereby preventing  
CC adhesion of vertebrate cells to the protein in a cell adhesion assay. It  
CC also encompasses MN proteins or MN protein fragments which can be added  
CC to the extracellular environment to prevent the adhesion of vertebrate  
CC cells to each other. The invention also relates to the identification of  
CC the binding site of the MN protein and to a method of identifying a site  
CC on an MN protein to which cells adhere, comprising testing a series of  
CC overlapping peptides from the protein in a cell adhesion assay. The  
CC invention encompasses a vector comprising an expression control sequence  
CC operatively linked to a nucleic acid encoding the variable domains of a  
CC MN-specific antibody, where the domains are separated by a flexible  
CC linker peptide (AAB03035) and the vector inhibits the growth of a  
CC vertebrate preneoplastic or neoplastic cell that abnormally expresses MN  
CC protein. The invention also encompasses a vector comprising a nucleic  
CC acid encoding a cytotoxic protein or peptide operatively linked to the MN  
CC gene promoter, which inhibits the growth of a vertebrate preneoplastic or  
CC neoplastic cell. Also claimed is a repressor complex that binds to the MN  
CC gene promoter (AAA52473). MN proteins and peptides, MN-binding proteins  
CC and peptides, and expression vectors encoding such proteins and peptides  
CC are useful for treating patients with preneoplastic or neoplastic disease  
CC (e.g., cancers) associated with or characterised by abnormal MN  
CC expression. The present sequence represents a fragment of the human MN  
CC gene (AAA52462) specified in the invention  
XX  
SQ Sequence 11 BP; 2 A; 2 C; 6 G; 1 T; 0 U; 0 Other;  
  
Query Match 31.0%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 CCACCTGCT 13  
Db |||||||||  
9 CCACCTGCT 1  
  
RESULT 189  
ABQ86329/c  
ID ABQ86329 standard; cDNA; 11 BP.  
XX  
AC ABQ86329;  
XX  
DT 10-SEP-2002 (first entry)  
XX  
DE Human skin stress/ageing related EST SEQ ID NO 84.  
XX  
KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253773-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015178.  
XX  
PR 03-JAN-2001; 2001DE-01000121.

XX (HENK ) HENKEL KGAA.  
PA Petersohn D, Conradt M, Hofmann K;  
XX WPI; 2002-528865/56.  
DR  
XX  
PT Identifying genes involved in skin stress and aging, useful e.g. in  
PT screening for cosmetic or therapeutic agents, based on differential gene  
PT expression.  
XX  
XX Claim 8; Page 40; 325pp; German.  
PS  
XX The invention relates to identifying (M1) genes in vitro that, in humans  
CC or animals, are important for skin ageing and/or skin stress by serial  
CC analysis of gene expression between mixtures of transcribed and  
CC optionally translated, genetically encoded factors (A) obtained from  
CC young and aged skin, to identify that genes that show strong differential  
CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is  
CC useful for: identifying markers of skin ageing and/or stress; determining  
CC skin ageing and/or stress; and identifying or determining the effects of  
CC pharmaceutical or cosmetic agents for control of skin ageing. The present  
CC sequence is one of a group of human skin ageing/stress related expressed  
CC sequence tags (ABQ86246-ABQ87680) of the invention  
XX  
SQ Sequence 11 BP; 4 A; 4 C; 1 G; 2 T; 0 U; 0 Other;  
  
Query Match 31.0%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 11 GCTGTGTGA 19  
Db |||||||||  
10 GCTGTGTGA 2  
  
RESULT 190  
ABV62312/c  
ID ABV62312 standard; cDNA; 11 BP.  
XX  
AC ABV62312;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 98.  
XX  
KW Human; skin; dermatological; vulnerrary; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 28; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed



CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 4 A; 4 C; 1 G; 2 T; 0 U; 0 Other;  
  
Query Match 31.0%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 11 GCTGTGTGA 19  
Db 10 GCTGTGTGA 2  
|||||  
  
RESULT 191  
ABV69491  
ID ABV69491 standard; cDNA; 11 BP.  
XX  
AC ABV69491;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 7277.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 228; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 0 A; 2 C; 4 G; 5 T; 0 U; 0 Other;  
  
Query Match 31.0%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 11 GCTGTGTGA 19  
Db 10 GCTGTGTGA 2  
|||||  
  
RESULT 191  
ABV69491  
ID ABV69491 standard; cDNA; 11 BP.  
XX  
AC ABV69491;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 7277.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 228; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 0 A; 2 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 31.0%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 10 TGCTGTGTG 18  
Db 1 TGCTGTGTG 9  
|||||  
  
RESULT 192  
ABV69733/c  
ID ABV69733 standard; cDNA; 11 BP.  
XX  
AC ABV69733;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 7519.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Claim 24; Page 237; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 4 A; 4 C; 1 G; 2 T; 0 U; 0 Other;  
  
Query Match 31.0%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 11 GCTGTGTGA 19  
Db 10 GCTGTGTGA 2  
|||||  
  
RESULT 193  
ABL91944/c  
ID ABL91944 standard; cDNA; 11 BP.

```
XX ABL91944;
AC
XX 30-MAY-2002 (first entry)
DT
XX Human Pan-Endothelial Marker SEQ ID NO 42.
DE
XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
KW normal endothelial marker; pan-endothelial marker; immunostimulant;
KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
KW psoriasis; ss.
XX
XX Homo sapiens.
OS
XX WO200210217-A2.
PN
XX 07-FEB-2002.
PD
XX 01-AUG-2001; 2001WO-US024031.
PF
XX 02-AUG-2000; 2000US-0222599P.
PR
XX 11-AUG-2000; 2000US-0224360P.
PR
XX 11-APR-2001; 2001US-0282850P.
PR
XX (UYJO ) UNIV JOHNS HOPKINS.
PA
XX St Croix B, Kinzler KW, Vogelstein B;
PI
XX WPI; 2002-291856/33.
DR
XX An isolated molecule comprising an antibody variable region which
PT specifically binds to an extracellular domain of a tumor endothelial
PT marker (TEM) protein, useful for inhibiting tumor growth.
XX
PS Example 4; Page 325; 331pp; English.
XX
XX The invention relates to an isolated molecule comprising an antibody
CC variable region which specifically binds to an extracellular domain of a
CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
CC They are useful for inhibiting tumour growth, neoangiogenesis in subjects
CC bearing a vascularised tumour, polycystic kidney disease, diabetic
CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)
CC are disclosed, as are marker oligonucleotide sequences: tumour
CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal
CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
CC (PEM) ABL91903-ABL91995. The present sequence is that of an
CC oligonucleotide marker useful to the invention
XX
SQ Sequence 11 BP; 4 A; 4 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GCTGTGTGA 19
Db 10 GCTGTGTGA 2

RESULT 194
ABX71869/c
ID ABX71869 standard; DNA; 11 BP.
XX
AC ABX71869;
XX
DT 12-MAR-2003 (first entry)
XX
DE DNA tag used to identify human gene encoding PEM 42.
XX
```

```
KW Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;
KW Tumour endothelial marker; normal endothelial marker; PEM;
KW pan-endothelial marker; polycystic kidney disease; psoriasis;
KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
KW neoangiogenesis; immune response; cytostatic; antidiabetic;
KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic; ds.
XX
OS Homo sapiens.
XX WO200283874-A2.
PN
XX 24-OCT-2002.
PD
XX 10-APR-2002; 2002WO-US008253.
PF
XX 11-APR-2001; 2001US-0282850P.
PR
XX 06-FEB-2002; 2002US-0354262P.
PR
XX (UYJO ) UNIV JOHNS HOPKINS.
PA
XX Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;
PI
XX WPI; 2003-093016/08.
DR
XX New purified human transmembrane protein, designated as tumor endothelial
PT marker (TEM) 3, useful for detecting, diagnosing or treating tumors,
PT polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
PT psoriasis.
XX
PS Disclosure; Page 94; 374pp; English.
XX
CC The present invention relates to a novel method for the isolation of
CC endothelial cells (ECs), and the identification of genes expressed in
CC normal and tumour ECs. Tumour endothelial marker (TEM), normal
CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are
CC identified in human ECs. The human EC marker proteins and the
CC polynucleotide sequences encoding them are useful for detecting,
CC diagnosing or treating tumours as well as polycystic kidney disease,
CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also
CC useful for inhibiting neoangiogenesis or tumour angiogenesis, for
CC inducing an immune response to tumour endothelial cells in a patient, or
CC for identifying candidate drugs for treating tumours. ABX71828-ABX71999
CC represent DNA tags for human PEM, TEM or NEM genes
XX
SQ Sequence 11 BP; 4 A; 4 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GCTGTGTGA 19
Db 10 GCTGTGTGA 2

RESULT 195
ADK41823/c
ID ADK41823 standard; DNA; 11 BP.
XX
AC ADK41823;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human MN gene intron-exon boundary sequence SeqID52.
XX
KW carbonic anhydrase IX; CA IX; precancerous cell; MN; cancerous cell;
KW human; vertebrate; cytostatic; vaccine; gene therapy;
KW renal cell carcinoma; breast cancer; colorectal cancer; splice acceptor;
KW ds.
XX
OS Homo sapiens.
XX
XX WO2004005348-A1.
```

XX PD 15-JAN-2004.  
XX PF 22-FEB-2003; 2003WO-US005137.  
XX PR 23-MAY-2002; 2002US-0383068P.  
XX PR 05-DEC-2002; 2002US-0431499P.  
XX PA (FARB ) BAYER CORP.  
XX PA (VIRO-) INST VIROLOGY.  
XX PI Zavada J, Pastorekova S, Pastorek J, Zavadova Z;  
XX DR WPI; 2004-083500/08.  
XX PT New soluble form of the carbonic anhydrase IX (CA IX) protein for  
PT screening, diagnosing or prognosing diseases associated with abnormal  
PT expression of CA IX protein, e.g. renal cell carcinoma, breast cancer or  
PT colorectal cancer.  
XX PS Disclosure; SEQ ID NO 52; 159pp; English.  
XX CC This invention relates to a novel soluble form of the carbonic anhydrase  
CC IX (CA IX) (or MN) protein or CA IX polypeptide which is released from  
CC precancerous and/or cancerous cells of a vertebrate into a body fluid.  
CC The invention may be useful for the development of compounds with a  
CC cytostatic activity or a vaccine whilst the disclosed sequences may be  
CC used for gene therapy. The protein and method are useful for screening,  
CC diagnosing or prognosing diseases associated with abnormal expression of  
CC carbonic anhydrase IX protein, such as precancerous and cancerous  
CC diseases like renal cell carcinoma, breast cancer or colorectal cancer.  
CC The monoclonal antibody may also be used for treating or preventing  
CC precancerous and cancerous diseases. The present sequence is that of a  
CC splice acceptor site from a human MN gene intron-exon boundary which is  
CC related to the invention.  
XX SQ Sequence 11 BP; 2 A; 2 C; 6 G; 1 T; 0 U; 0 Other;  
Query Match 31.0%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 CCACCTGCT 13  
Db 9 CCACCTGCT 1  
RESULT 196  
ABH83073/c  
ID ABH83073 standard; DNA; 12 BP.  
XX AC ABH83073;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 283066 for detecting SNP TSC0011130.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.

XX PD 15-JAN-2004.  
XX PF 22-FEB-2003; 2003WO-US005137.  
XX PR 23-MAY-2002; 2002US-0383068P.  
XX PR 05-DEC-2002; 2002US-0431499P.  
XX PA (FARB ) BAYER CORP.  
XX PA (VIRO-) INST VIROLOGY.  
XX PI Zavada J, Pastorekova S, Pastorek J, Zavadova Z;  
XX DR WPI; 2004-083500/08.  
XX PT New soluble form of the carbonic anhydrase IX (CA IX) protein for  
PT screening, diagnosing or prognosing diseases associated with abnormal  
PT expression of CA IX protein, e.g. renal cell carcinoma, breast cancer or  
PT colorectal cancer.  
XX PS Disclosure; SEQ ID NO 52; 159pp; English.  
XX CC This invention relates to a novel soluble form of the carbonic anhydrase  
CC IX (CA IX) (or MN) protein or CA IX polypeptide which is released from  
CC precancerous and/or cancerous cells of a vertebrate into a body fluid.  
CC The invention may be useful for the development of compounds with a  
CC cytostatic activity or a vaccine whilst the disclosed sequences may be  
CC used for gene therapy. The protein and method are useful for screening,  
CC diagnosing or prognosing diseases associated with abnormal expression of  
CC carbonic anhydrase IX protein, such as precancerous and cancerous  
CC diseases like renal cell carcinoma, breast cancer or colorectal cancer.  
CC The monoclonal antibody may also be used for treating or preventing  
CC precancerous and cancerous diseases. The present sequence is that of a  
CC splice acceptor site from a human MN gene intron-exon boundary which is  
CC related to the invention.  
XX SQ Sequence 11 BP; 2 A; 2 C; 6 G; 1 T; 0 U; 0 Other;  
Query Match 31.0%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 CCACCTGCT 13  
Db 9 CCACCTGCT 1  
RESULT 196  
ABH83073/c  
ID ABH83073 standard; DNA; 12 BP.  
XX AC ABH83073;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 283066 for detecting SNP TSC0011130.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 283066; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;  
Query Match 31.0%; Score 9; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 CATCCACCT 10  
Db 9 CATCCACCT 1  
RESULT 197  
ABI66469/c  
ID ABI66469 standard; DNA; 12 BP.  
XX AC ABI66469;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 366442 for detecting SNP TSC0055762.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 366442; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 2 A; 0 C; 5 G; 5 T; 0 U; 0 Other;  
  
Query Match 31.0%; Score 9; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 CATCCACCT 10  
Db 9 CATCCACCT 1  
|||||  
RESULT 198  
ABI17481  
ID ABI17481 standard; DNA; 12 BP.  
XX  
AC ABI17481;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 317454 for detecting SNP TSC0028024.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 317454; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 2 A; 7 C; 1 G; 2 T; 0 U; 0 Other;  
  
Query Match 31.0%; Score 9; DB 1; Length 12;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CCATCCACC 9  
Db 2 CCATCCACC 10  
|||||  
RESULT 199  
ABI77789/c  
ID ABI77789 standard; DNA; 12 BP.  
XX  
AC ABI77789;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 377762 for detecting SNP TSC0007285.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 377762; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;  
  
Query Match 31.0%; Score 9; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 CATCCACCT 10  
Db 11 CATCCACCT 3  
|||||  
RESULT 200  
ABI74143/c  
ID ABI74143 standard; DNA; 12 BP.  
XX  
AC ABI74143;



XX DT 22-FEB-2002 (first entry)  
XX PF Oligonucleotide primer SEQ ID NO 374116 for detecting SNP TSC0060503.  
DE XX  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 374116; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 12 BP; 1 A; 0 C; 6 G; 5 T; 0 U; 0 Other;  
  
Query Match 31.0%; Score 9; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CCATCCACC 9  
Db 9 CCATCCACC 1  
  
RESULT 201  
ABI17480  
ID ABI17480 standard; DNA; 12 BP.  
XX AC ABI17480;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 317453 for detecting SNP TSC0028024.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PX

PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 317453; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 12 BP; 3 A; 7 C; 0 G; 2 T; 0 U; 0 Other;  
  
Query Match 31.0%; Score 9; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CCATCCACC 9  
Db 2 CCATCCACC 10  
  
RESULT 202  
ABH73202/c  
ID ABH73202 standard; DNA; 12 BP.  
XX AC ABH73202;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 273187 for detecting SNP TSC0003081.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX PX Set of oligonucleotides, useful for diagnosis and cell typing, is



PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 273187; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 5 A; 0 C; 5 G; 2 T; 0 U; 0 Other;  
  
Query Match 31.0%; Score 9; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 CATCCACCT 10  
Db 10 CATCCACCT 2  
  
RESULT 203  
ABI56716  
ID ABI56716 standard; DNA; 12 BP.  
XX  
AC ABI56716;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 356689 for detecting SNP TSC0050259.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
DR  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 356689; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 4 A; 7 C; 0 G; 1 T; 0 U; 0 Other;  
  
Query Match 31.0%; Score 9; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CCATCCACC 9  
Db 4 CCATCCACC 12  
  
RESULT 204  
AAL44624  
ID AAL44624 standard; DNA; 12 BP.  
XX  
AC AAL44624;  
XX  
DT 26-APR-2002 (first entry)  
XX  
DE Muscle creatine kinase MCK-R control element #1.  
XX  
KW Muscle-specific enhancer; gene therapy; regulatory element; haemostatic;  
KW antibacterial; antiviral; antitumour; antiinflammatory; anti-HIV;  
KW cytostatic; antilipemic; antidiabetic; antianaemic; MCK; MCK-R;  
KW muscle creatine kinase control element; ds.  
XX  
OS Unidentified.  
XX  
PN WO200206495-A2.  
XX  
PD 24-JAN-2002.  
XX  
PF 13-JUL-2001; 2001WO-US022092.  
XX  
PR 14-JUL-2000; 2000US-0218436P.  
XX  
PA (UNMI ) UNIV MICHIGAN.  
XX Chamberlain JS, Hauschka SD;  
PI WPI; 2002-171809/22.  
DR  
XX Composition comprising nucleic acid which comprises mutant muscle-  
PT specific enhancer region having two muscle creatine kinase-R control  
PT elements, useful in gene therapy, drug screening, and diagnostic assays.  
XX  
PS Disclosure; Fig 16; 6lpp; English.  
XX  
CC The present invention relates to a composition comprising a nucleic acid,  
CC where the nucleic acid contains a mutant muscle-specific enhancer region  
CC which comprises at least 2 muscle creatine kinase (MCK)-R control  
CC elements. The nucleic acid can be used in gene therapy, particularly  
CC where the therapy is directed at muscle cells and in the treatment of  
CC endocrine, metabolic, haematologic, cardiovascular, neurologic,  
CC musculoskeletal, urologic, pulmonary and immune disorders such as  
CC inflammatory diseases, autoimmune disease, chronic and infectious  
CC diseases such as AIDS, cancer, hypercholesterolaemia, insulin disorders  
CC such as diabetes, growth disorders, various blood disorders including  
CC anaemia, thalassaemia, haemophilia, genetic defects such as cystic  
CC fibrosis, Gaucher's disease, Hurler's disease, adenosine deaminase (ADA)  
CC deficiency, and emphysema. The present sequence is an MCK-R control  
CC element  
XX  
SQ Sequence 12 BP; 3 A; 5 C; 2 G; 2 T; 0 U; 0 Other;  
  
Query Match 31.0%; Score 9; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|                                                            |                                                                           |                |    |                |
|------------------------------------------------------------|---------------------------------------------------------------------------|----------------|----|----------------|
| Qy                                                         | 6                                                                         | CACCTGCTG 14   | 15 | TGTGACCTG 23   |
| Db                                                         | 3                                                                         |                | 11 |                |
|                                                            |                                                                           | 3 CACCTGCTG 11 |    | 11 TGTGACCTG 3 |
| RESULT 205                                                 |                                                                           |                |    |                |
| ADF78489/c                                                 |                                                                           |                |    |                |
| ID                                                         | ADF78489. standard; DNA; 12 BP.                                           |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| AC                                                         | ADF78489;                                                                 |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| DT                                                         | 26-FEB-2004 (first entry)                                                 |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| DE                                                         | Chromosomal abnormality detection-related PCR primer 70.                  |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| KW                                                         | chromosomal abnormality; maternal locus; genetic disorder; foetus;        |                |    |                |
| KW                                                         | mutation; translocation; transversion; monosomy; trisomy; trisomy 21;     |                |    |                |
| KW                                                         | chromosome 21; Down's Syndrome; aneuploidies; chromosome deletion;        |                |    |                |
| KW                                                         | chromosome addition; chromosome amplification; chromosome translocation;  |                |    |                |
| KW                                                         | chromosome rearrangement; single nucleotide polymorphism detection;       |                |    |                |
| KW                                                         | SNP detection; pregnant female; PCR; primer; ss.                          |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| OS                                                         | Homo sapiens.                                                             |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| PN                                                         | WO2003074723-A2.                                                          |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| PD                                                         | 12-SEP-2003.                                                              |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| PF                                                         | 28-FEB-2003; 2003WO-US006198.                                             |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| PR                                                         | 01-MAR-2002; 2002US-0360232P.                                             |                |    |                |
| PR                                                         | 11-MAR-2002; 2002US-00093618.                                             |                |    |                |
| PR                                                         | 08-MAY-2002; 2002US-0378354P.                                             |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| PA                                                         | (DHALL/) DHALLAN R.                                                       |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| PI                                                         | Dhallan R;                                                                |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| DR                                                         | WPI; 2003-845073/78.                                                      |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| PT                                                         | Detection of chromosomal abnormalities e.g. Down's Syndrome, non-         |                |    |                |
| PT                                                         | invasively in a fetus, comprises forming a ratio of amounts of alleles at |                |    |                |
| PT                                                         | a locus of interest and a different heterozygous locus.                   |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| PS                                                         | Example 11; Page 214; 164pp; English.                                     |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| CC                                                         | This invention relates to a novel method of detecting chromosomal         |                |    |                |
| CC                                                         | abnormalities by determining the sequence of alleles of a locus of        |                |    |                |
| CC                                                         | interest from template DNA, determining which alleles are present and     |                |    |                |
| CC                                                         | comparing to amounts of alleles at a different, selected heterozygous     |                |    |                |
| CC                                                         | locus (for example on another chromosome or a maternal locus); relative   |                |    |                |
| CC                                                         | amounts are expressed as a ratio indicating presence or absence of the    |                |    |                |
| CC                                                         | abnormality. The method is useful for the detection of genetic disorders, |                |    |                |
| CC                                                         | especially in a foetus, including chromosomal abnormalities and           |                |    |                |
| CC                                                         | mutations, for example translocations, transversions, monosomies,         |                |    |                |
| CC                                                         | trisomies (for example trisomy 21 in which an additional copy of          |                |    |                |
| CC                                                         | chromosome 21 results in Down's Syndrome) and other aneuploidies,         |                |    |                |
| CC                                                         | deletions, additions, amplifications, translocations and rearrangements.  |                |    |                |
| CC                                                         | It can be used to detect any alterations in a gene sequence, especially   |                |    |                |
| CC                                                         | single nucleotide polymorphisms (SNPs), and may be used to detect         |                |    |                |
| CC                                                         | numerous abnormalities simultaneously, for example if several SNPs are    |                |    |                |
| CC                                                         | associated with a particular disease. The method provides a rapid, non-   |                |    |                |
| CC                                                         | invasive method for determining the sequence of DNA from a foetus using a |                |    |                |
| CC                                                         | sample from a pregnant female, for example to detect genetic disorders as |                |    |                |
| CC                                                         | above or to determine if a foetus is a carrier of a disease or            |                |    |                |
| CC                                                         | predisposed to a disease.                                                 |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| SQ                                                         | Sequence 12 BP; 4 A; 3 C; 3 G; 2 T; 0 U; 0 Other;                         |                |    |                |
| Query Match 31.0%; Score 9; DB 1; Length 12;               |                                                                           |                |    |                |
| Best Local Similarity 100.0%; Pred. No. 1.5e+02;           |                                                                           |                |    |                |
| Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                                                                           |                |    |                |

|                                                            |                                                                           |                |    |                |
|------------------------------------------------------------|---------------------------------------------------------------------------|----------------|----|----------------|
| Qy                                                         | 15                                                                        | TGTGACCTG 23   | 11 | TGTGACCTG 3    |
| Db                                                         | 11                                                                        |                | 3  |                |
|                                                            |                                                                           | 11 TGTGACCTG 3 |    | 3 CACCTGCTG 11 |
| RESULT 206                                                 |                                                                           |                |    |                |
| ADO08498                                                   |                                                                           |                |    |                |
| ID                                                         | ADO08498 standard; DNA; 12 BP.                                            |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| AC                                                         | ADO08498;                                                                 |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| DT                                                         | 12-AUG-2004 (first entry)                                                 |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| DE                                                         | Human papillomavirus (HPV) detection-related PNA probe XII SeqID30.       |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| KW                                                         | detection; typing; Human Papilloma Virus; HPV; infection; PNA probe;      |                |    |                |
| KW                                                         | high-risk; infectious organism; probe; ss.                                |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| OS                                                         | Human papillomavirus.                                                     |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| PN                                                         | WO2004042071-A2.                                                          |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| PD                                                         | 21-MAY-2004.                                                              |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| PF                                                         | 07-OCT-2003; 2003WO-US031841.                                             |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| PR                                                         | 01-NOV-2002; 2002US-00286387.                                             |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| PA                                                         | (CYTY-) CYTYC CORP.                                                       |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| PI                                                         | Cohenford MA, Lentrichia BB;                                              |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| DR                                                         | WPI; 2004-400683/37.                                                      |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| PT                                                         | New peptide-nucleic acids, useful as a probe for detecting and typing     |                |    |                |
| PT                                                         | Human Papilloma Virus infection, or in screening assay toward the         |                |    |                |
| PT                                                         | diagnostically most-relevant strains or species of a disease organism.    |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| PS                                                         | Example 4; SEQ ID NO 30; 26pp; English.                                   |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| CC                                                         | This invention relates to a novel method for detection and typing of a    |                |    |                |
| CC                                                         | Human Papilloma Virus (HPV) infection using PNA primers or probes,        |                |    |                |
| CC                                                         | including methods for detecting high-risk types of HPV infection with     |                |    |                |
| CC                                                         | minimal numbers of PNA probes or using PNA primers to selectively amplify |                |    |                |
| CC                                                         | only high-risk types of HPV. Specifically claimed are novel primer/probe  |                |    |                |
| CC                                                         | sequences which are useful as primers/probes for detecting and typing HPV |                |    |                |
| CC                                                         | infection. The methods are used in a screening assay toward the           |                |    |                |
| CC                                                         | diagnostically most-relevant strains or species of a disease organism or  |                |    |                |
| CC                                                         | to selectively amplify high-risk strains of an infectious organism. The   |                |    |                |
| CC                                                         | present sequence is that of a HPV PNA probe which was used in the         |                |    |                |
| CC                                                         | exemplification of the invention.                                         |                |    |                |
| XX                                                         |                                                                           |                |    |                |
| SQ                                                         | Sequence 12 BP; 2 A; 1 C; 5 G; 4 T; 0 U; 0 Other;                         |                |    |                |
| Query Match 31.0%; Score 9; DB 1; Length 12;               |                                                                           |                |    |                |
| Best Local Similarity 100.0%; Pred. No. 1.5e+02;           |                                                                           |                |    |                |
| Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                                                                           |                |    |                |

|            |                                               |               |    |              |
|------------|-----------------------------------------------|---------------|----|--------------|
| Qy         | 11                                            | GCTGTGTGA 19  | 11 | GCTGTGTGA 19 |
| Db         | 1                                             |               | 1  |              |
|            |                                               | 1 GCTGTGTGA 9 |    |              |
| RESULT 207 |                                               |               |    |              |
| ADR98065/c |                                               |               |    |              |
| ID         | ADR98065 standard; DNA; 12 BP.                |               |    |              |
| XX         |                                               |               |    |              |
| AC         | ADR98065;                                     |               |    |              |
| XX         |                                               |               |    |              |
| DT         | 02-DEC-2004 (first entry)                     |               |    |              |
| XX         |                                               |               |    |              |
| DE         | Human SNP TSC1261039 multiplex PCR primer #1. |               |    |              |

XX ss; chromosomal abnormality; detection; fetus; translocation;  
KW transversion; monosomy; trisomy; aneuploidy; deletion; addition;  
KW amplification; prenatal diagnosis; PCR; primer; SNP;  
KW single nucleotide polymorphism; human; multiplex; TSC1261039.  
XX  
OS Homo sapiens.  
XX  
PN WO2004079011-A1.  
XX  
PD 16-SEP-2004.  
XX  
PF 29-AUG-2003; 2003WO-US027308.  
XX  
PR 28-FEB-2003; 2003WO-US006198.  
XX (RAVG-) RAVGEN INC.  
PA  
XX  
PI Dhallan R;  
XX  
DR WPI; 2004-677127/66.  
XX  
PT Detecting a chromosomal abnormality, e.g. translocations, transversions,  
PT monosomes, trisomies, aneuploidies, deletions, or arrangements, comprises  
PT determining the sequence of alleles of a locus of interest in the sample  
PT from template DNA.  
XX  
PS Example 12; Page 200; 429pp; English.  
XX  
CC This invention describes a novel method for detecting a chromosomal  
CC abnormality in a sample which comprises determining the sequence of  
CC alleles of a locus of interest in a sample from template DNA where  
CC determining the sequence of the alleles comprises amplifying the locus of  
CC interest, hybridising the amplified loci to GeneCHIP array, washing  
CC GeneCHIP array, staining the GeneCHIP array with detectable reagents, and  
CC scanning GeneCHIP array. The amplification method is self-sustained  
CC sequence reaction, ligase chain reaction, rapid amplification of cDNA  
CC ends, PCR and ligase chain reaction, Q-beta phage amplification, strand  
CC displacement amplification, or splice overlap extension PCR, preferably  
CC PCR. The determination of the sequence of the alleles comprises  
CC amplifying the locus of interest, fragmenting the amplicon, hybridising  
CC fragmented amplicons to CodeLink Arrays, extension reaction to  
CC incorporate a nucleotide and detecting incorporated nucleotides. The  
CC amplicon fragmentation is by exonuclease digestion. Detecting a  
CC chromosomal abnormality in a sample comprises determining the sequence of  
CC alleles of a locus of interest from template DNA, where determining the  
CC sequence of the alleles comprises using BeadArray Technology. The  
CC determination of the sequence of the alleles may also be done by  
CC amplifying the locus of interest, dephosphorylation of the unused  
CC reagents, in vitro transcription reaction of the products, RNase A  
CC cleavage of the products, mixing the products with CleanResin,  
CC transferring products to SpectroCHIP, and analysing the SpectroCHIP. The  
CC dephosphorylation reaction is with shrimp alkaline phosphatase.  
CC Alternatively, the determination of the sequence of the alleles comprises  
CC amplifying the locus of interest, dephosphorylation of the unused  
CC reagents, hybridising a primer to the locus of interest, incorporating a  
CC nucleotide, mixing the products with CleanResin, transferring products to  
CC SpectroCHIP, and analysing the SpectroCHIP. The hybridisation of primer  
CC is adjacent to the locus of interest. The determination of the sequence  
CC of the alleles may also comprise amplifying the locus of interest,  
CC treating the products with exonuclease, single stranded DNA is annealed  
CC to an oligonucleotide, incorporating a nucleotide using the annealed  
CC template and primer, and detecting the incorporated nucleotide. The  
CC method is useful for detecting a chromosomal abnormality in a sample.  
CC Specifically, the method is useful for detecting chromosomal  
CC abnormalities in a fetus including translocations, transversions,  
CC monosomes, trisomies, and other aneuploidies, deletions, additions,  
CC amplifications, and arrangements. The method of the invention can also be  
CC used for prenatal diagnosis. This sequence represents a multiplex PCR  
CC primer used to amplify the human SNP TSC1261039.  
XX  
SQ Sequence 12 BP; 4 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 31.0%; Score 9; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 15 TGTGACCTG 23  
| | | | | | | | | |  
Db 11 TGTGACCTG 3  
RESULT 208  
ADS08752/c  
ID ADS08752 standard; DNA; 12 BP.  
XX  
AC ADS08752;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Human DNA PCR primer #89.  
XX  
KW Human; PCR; primer; ss; nucleic acid detection; cell lysis;  
KW chromosomal abnormality; cancer; carcinoma; bladder; breast; bronchus;  
KW colon; kidney; liver; lung; oesophagus; gall bladder; ovary; pancreas;  
KW stomach; cervix; thyroid; prostate; skin; small cell lung cancer;  
KW squamous cell carcinoma; leukaemia; lymphoma; myelodysplastic syndrome;  
KW fibrosarcoma; rhabdomyosarcoma; astrocytoma; neuroblastoma; glioma;  
KW schwannoma; melanoma; seminoma; teratocarcinoma; osteosarcoma.  
XX  
OS Homo sapiens.  
XX  
PN WO2004078994-A2.  
XX  
PD 16-SEP-2004.  
XX  
PF 01-MAR-2004; 2004WO-US006337.  
XX  
PR 28-FEB-2003; 2003WO-US006198.  
XX (RAVG-) RAVGEN INC.  
XX  
PI Dhallan R;  
XX  
DR WPI; 2004-662434/64.  
XX  
PT Detecting presence or absence of nucleic acid, containing mutation,  
PT involves isolating nucleic acid from sample containing cell lysis  
PT inhibitor, and detecting presence or absence of nucleic acid.  
XX  
PS Example 12; Page 209; 440pp; English.  
XX  
CC The invention relates to a method for detecting a nucleic acid, involving  
CC isolating a nucleic acid from a sample, where an agent that impedes cell  
CC lysis was added to the sample, and detecting the presence or absence of  
CC the nucleic acid. The invention also relates to a method for detecting  
CC chromosomal abnormalities in a DNA sample and determining the sequence of  
CC foetal DNA from a sample of a pregnant female. The nucleic acid contains  
CC at least one mutation chosen from a single point mutation, multiple point  
CC mutations, an insertion, a frameshift, a truncation, a deletion, a  
CC duplication and a transversion. The method is useful for detecting  
CC nucleic acid in a sample obtained from a source chosen from bacteria,  
CC viruses, fungi, mycobacteria, protozoa, molds, yeasts, plants, humans,  
CC non-humans, multi-cellular parasites, animals and archaeobacteria. The  
CC method is useful for detecting, diagnosing or monitoring a disease such  
CC as cancer chosen from carcinoma of the bladder, breast, bronchus, colon,  
CC kidney, liver, lung, oesophagus, gall bladder, ovary, pancreas, stomach,  
CC cervix, thyroid, prostate and skin, small cell lung cancer, squamous cell  
CC carcinoma, haematopoietic tumours of lymphoid lineage, leukaemia, acute  
CC lymphocytic leukaemia, acute lymphoblastic leukaemia, B-cell lymphoma, T-  
CC cell-lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma, hairy cell  
CC lymphoma, Burkett's lymphoma, haematopoietic tumours of myeloid lineage,  
CC acute and chronic myelogenous leukaemias, myelodysplastic syndrome and  
CC promyelocytic leukaemia, tumours of mesenchymal origin, fibrosarcoma and  
CC rhabdomyosarcoma, tumours of the central and peripheral nervous system,  
CC astrocytoma, neuroblastoma, glioma and schwannomas, melanoma, seminoma,

CC teratocarcinoma and osteosarcoma. The method is also useful for  
CC monitoring response to treatment chosen from surgery, radiation,  
CC lifestyle change, dietary protocol and supplementation and administration  
CC of a drug. The drug is chosen from chemotherapeutic agents, anti-  
CC bacterial agents, anti-viral agents, anti-fungal agents, targeted-cancer  
CC drugs, cytotoxic agents, cytostatic agents and anti-proliferative agents.  
CC This sequence represents a PCR primer used in the scope of the invention.

XX  
SQ Sequence 12 BP; 4 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 31.0%; Score 9; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TGTGACCTG 23  
| | | | | | | |  
Db 11 TGTGACCTG 3

RESULT 209  
AAQ86030/c  
ID AAQ86030 standard; DNA; 12 BP.  
XX  
AC AAQ86030;  
XX  
DT 25-MAR-2003 (revised)  
DT 05-MAY-1995 (first entry)  
XX  
DE IT10C3 coding region, exon 7-intron border.  
XX  
KW transporter protein; IT10C3; superfamily; tetracycline resistance;  
KW exon amplification; PCR; D4S95; Huntington's disease; dementia;  
KW choreiform movements; cognitive decline; neurodegenerative; ss.  
XX  
OS Homo sapiens.

FH Key Location/Qualifiers  
FT exon 1..6  
FT /\*tag= a  
FT /number= exon 7  
FT intron 7..12  
FT /\*tag= b

XX EP617125-A2.  
XX  
PD 28-SEP-1994.  
XX  
PF 23-MAR-1994; 94EP-00302092.  
XX  
PR 23-MAR-1993; 93US-00035928.  
XX  
PA (GEO ) GEN HOSPITAL CORP.  
XX  
PI Duyao MP, Macdonald ME, Gusella JF;  
XX  
DR WPI; 1994-295776/37.  
XX  
PT New transporter protein IT10C3 and related nucleic acid - vectors and  
PT antibodies, for diagnosis and treatment, of e.g. neuro-degenerative  
PT disorders, derived from the Huntington's disease region of chromosome 4.  
XX  
PS Example 2; Fig 5; 36pp; English.  
XX

CC A series of nucleotide sequences (AAQ86018-35) showing the exon-intron  
CC borders of the gene for the novel transporter protein IT10C3. The  
CC composite DNA sequence presented (AAQ73384) covers 1788 bp including a  
CC 1365 bp open reading frame with a 29-mer poly A-tail. The gene encodes a  
CC protein of 455 amino acids with strong similarity to a superfamily of  
CC transporter protein typified by tetracycline resistance proteins. The  
CC gene was isolated from a human frontal cortex cDNA library with cosmid  
CC Y24 and trapped, uncloned exon PCR products. The products were used to  
CC rescreen the library and pull out a series of clone whose sequence form  
CC the composite of AAQ73384. The gene maps distal to D4S95 in the

CC Huntington's region. Probes to this gene can be used for presymptomatic  
CC (e.g. prenatal) diagnosis of IT10C3-related diseases e.g. choreiform  
CC movements, dementia, cognitive decline and/or neurodegenerative disorders  
CC such as Huntington's disease. (Updated on 25-MAR-2003 to correct PN  
CC field.)

XX  
SQ Sequence 12 BP; 2 A; 1 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATCCACCTGCTG 14  
| | | | | | | |  
Db 12 ACCCACCTACTG 1

RESULT 210  
AAQ88466  
ID AAQ88466 standard; DNA; 12 BP.  
XX  
AC AAQ88466;  
XX  
DT 19-DEC-1995 (first entry)  
XX  
DE Human mitochondrial D-loop region DNA probe 11-2.  
XX  
KW Tiling strategy; immobilised nucleic acid probe array; mitochondrial DNA;  
KW D-loop region; biological chip; hybridisation fingerprint;  
KW interrogation position; ss.  
XX  
OS Synthetic.

FH Key Location/Qualifiers  
FT modified\_base 12  
FT /\*tag= a  
FT /note= "3'-end of probe is covalently attached to chip  
FT surface"

PN WO9511995-A1.  
XX  
PD 04-MAY-1995.  
XX  
PF 26-OCT-1994; 94WO-US012305.  
XX  
PR 26-OCT-1993; 93US-00143312.  
PR 02-AUG-1994; 94US-00284064.  
XX  
PA (AFFY-) AFFYMAX TECHNOLOGIES NV.  
XX  
PI Chee M, Cronin MT, Fodor SP, Gingeras TR, Huang XC, Hubbell EA;  
PI Lipshutz RJ, Lobbann PE, Miyada CG, Morris MS, Shah N, Sheldon EL;  
XX  
DR WPI; 1995-178887/23.  
XX  
PT New arrays of oligo:nucleotide probes - used for comparing known  
PT sequences with variants for detection of mutation(s) and sequencing.

PS Disclosure; Page 107; 223pp; English.  
XX

CC A DNA chip was prepared for analysing sequences contained in a 1.3kb  
CC fragment of human mitochondrial DNA from the D-loop region, the most  
CC polymorphic region of human mitochondrial DNA. The chip comprised a set  
CC of 268 overlapping oligonucleotide probes (see AAQ88421-Q88684) of  
CC varying length (9-14 nucleotides) with varying overlaps arranged in a 1cm  
CC x 1cm array. Each position in the sequence was represented by at least  
CC one probe (usually 2 or more). DNA was amplified from six human donors  
CC and then transcribed to give the 1.3kb RNA transcripts which were  
CC fragmented and hybridised to the chip. For each individual, a unique  
CC hybridisation fingerprint was produced on the chip; all differences could  
CC be correlated with differences in the cloned genomic DNA sequence

XX  
SQ Sequence 12 BP; 0 A; 1 C; 6 G; 5 T; 0 U; 0 Other;



Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 TGTGTGACCTGG 24  
Db 1 TGTGTGTGCTGG 12

RESULT 211  
AAA59759  
ID AAA59759 standard; DNA; 12 BP.  
XX AC  
AC AAA59759;  
XX DT 06-OCT-2000 (first entry)  
XX DE Bacteriophage M13mp18 nucleotide sequence SEQ ID 3.  
XX KW Replaceable matrix formulation; biomacromolecule separation;  
KW capillary electrophoresis; nucleic acid sequencing; differential display;  
KW dideoxyfingerprinting; short tandem repeat analysis; ds.  
XX OS Bacteriophage M13mp18.  
XX PN WO200028314-A1.  
XX PD 18-MAY-2000.  
XX PF 10-NOV-1999; 99WO-US026465.  
XX PR 10-NOV-1998; 98US-0107798P.  
PR 13-AUG-1999; 99US-00374174.  
XX PA (CURA-) CURAGEN CORP.  
XX PI Ruiz-Martinez MC;  
XX WPI; 2000-376654/32.  
DR  
XX Replaceable matrix formulation, used for the separation of biological  
PT macromolecules using capillary electrophoresis, comprises linear  
PT polyacrylamide solution and at least one denaturant.  
XX PS Disclosure; Page 30; 33pp; English.  
XX CC The invention relates to a replaceable matrix formulation, comprising a  
CC linear polyacrylamide solution, at least one denaturant, a buffer, and 6M  
CC urea. Also included in the invention is a method of biomacromolecule  
CC separation using a capillary electrophoresis device, comprising the  
CC replaceable matrix formulation and a buffer. The method is used for  
CC capillary array electrophoresis and biomacromolecule separation. The  
CC biomacromolecule separation method is used in nucleic acid sequencing, to  
CC determine the molecular size of a biomacromolecule, for differential  
CC display of mRNA, in dideoxyfingerprinting, or in short tandem repeat  
CC (STR) analysis. The present sequence represents a fragment of  
CC bacteriophage M13mp18 DNA, and is disclosed in the course of the  
CC invention  
XX SQ Sequence 12 BP; 1 A; 4 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TCCACCTGCTGT 15  
Db 1 TCCACCTGGTTT 12

RESULT 212  
ABI24861/C

ID ABI24861 standard; DNA; 12 BP.  
XX AC ABI24861;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 324834 for detecting SNP TSC0032247.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
DR  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 324834; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 12 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 TGTGTGACCTGG 24  
Db 12 TGTGTGAAGTGG 1

RESULT 213  
ABI11597  
ID ABI11597 standard; DNA; 12 BP.  
XX AC ABI11597;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 311570 for detecting SNP TSC0024559.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.



XX WO200177384-A2.  
PN 18-OCT-2001.  
XX  
PD  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
PI WPI; 2001-657177/75.  
DR  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 311570; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 4 A; 3 C; 1 G; 4 T; 0 U; 0 Other;  
  
Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 18 GACCTGGTAAAT 29  
Db 1 GACCTCTTAAAT 12  
  
RESULT 214  
ABI10363/c  
ID ABI10363 standard; DNA; 12 BP.  
XX  
AC ABI10363;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 310336 for detecting SNP TSC0023922.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 310336 for detecting SNP TSC0023922.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX

DR WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 310336; 29pp + Sequence Listing; German.  
PS  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 0 Other;  
  
Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 14 GTGTGACCTGGT 25  
Db 12 GTGTGAGATGGT 1  
  
RESULT 215  
ABH87537/c  
ID ABH87537 standard; DNA; 12 BP.  
XX  
AC ABH87537;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 287530 for detecting SNP TSC0013133.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
PI WPI; 2001-657177/75.  
DR  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 287530; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATCCACCTGCT 13  
Db 12 CATCCAACACTACT 1  
||||| |||

RESULT 216  
ABI52832/c  
ID ABI52832 standard; DNA; 12 BP.  
XX  
AC ABI52832;  
XX  
DT 22-FEB-2002 (first entry)  
DE Oligonucleotide primer SEQ ID NO 352805 for detecting SNP TSC0048107.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 352805; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 0 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATCCACCTGCT 13  
Db 12 CCTCCACCTCCT 1  
||||| |||

RESULT 217  
ABI39693  
ID ABI39693 standard; DNA; 12 BP.  
XX  
AC ABI39693;  
XX  
DT 22-FEB-2002 (first entry)  
DE Oligonucleotide primer SEQ ID NO 339666 for detecting SNP TSC0041130.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 339666; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 1 A; 8 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCCACCTGC 12  
Db 1 CCATCCTCCCGC 12  
||||| |||

RESULT 218  
ABH80092/c  
ID ABH80092 standard; DNA; 12 BP.  
XX  
AC ABH80092;  
XX  
DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 280085 for detecting SNP TSC0008178.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
OS XX WO200177384-A2.  
PN XX 18-OCT-2001.  
PD XX  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
PT  
XX PS Claim 1; SEQ ID NO 280085; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 12 BP; 1 A; 1 C; 7 G; 3 T; 0 U; 0 Other;  
Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CCATCCACCTGC 12  
Db 12 CAATCCACCCGC 1  
RESULT 219  
ABH77417  
ID ABH77417 standard; DNA; 12 BP.  
XX AC ABH77417;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 277410 for detecting SNP TSC0004463.  
DE KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
OS XX WO200177384-A2.  
PN XX 18-OCT-2001.  
PD XX

PF 06-APR-2001; 2001WO-IB000713.  
XX 07-APR-2000; 2000DE-01019173.  
PR (EPIG-) EPIGENOMICS AG.  
PA Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
PT  
XX PS Claim 1; SEQ ID NO 277410; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 12 BP; 2 A; 5 C; 0 G; 5 T; 0 U; 0 Other;  
Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 CATCCACCTGCT 13  
Db 1 CATCTACCTTCT 12  
RESULT 220  
ABH83668/c  
ID ABH83668 standard; DNA; 12 BP.  
XX AC ABH83668;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 283661 for detecting SNP TSC0011446.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
OS XX WO200177384-A2.  
PN XX 18-OCT-2001.  
PD XX  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
PT

XX PS Claim 1; SEQ ID NO 283661; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 12 BP; 4 A; 0 C; 6 G; 2 T; 0 U; 0 Other;  
  
Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2 CATCCACCTGCT 13  
Db 12 CATCCTCTACT 1  
  
RESULT 221  
ABH87588  
ID ABH87588 standard; DNA; 12 BP.  
XX AC ABH87588;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 287581 for detecting SNP TSC0013161.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 287581 for detecting SNP TSC0013161.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX DR WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 287581; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but

CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 12 BP; 2 A; 9 C; 0 G; 1 T; 0 U; 0 Other;  
  
Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 CCATCCACCTGC 12  
Db 1 CCACCCACCTCC 12  
  
RESULT 222  
ABI40468/c  
ID ABI40468 standard; DNA; 12 BP.  
XX AC ABI40468;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 340441 for detecting SNP TSC0041530.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX DR WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 340441; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 0 Other;  
  
Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2 CATCCACCTGCT 13  
Db 12 CAACCCACCTCT 1



RESULT 223  
ABI60766/c  
ID ABI60766 standard; DNA; 12 BP.  
XX  
AC ABI60766;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 360739 for detecting SNP TSC0052264.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 360739; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 0 C; 7 G; 2 T; 0 U; 0 Other;  
CC  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 0 C; 7 G; 2 T; 0 U; 0 Other;  
Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CCATCCACCTGC 12  
DB 12 CCATCCACCTCC 1  
RESULT 224  
ABI62806  
ID ABI62806 standard; DNA; 12 BP.  
XX  
AC ABI62806;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 362779 for detecting SNP TSC0053443.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 362779; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 7 C; 0 G; 2 T; 0 U; 0 Other;  
Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CCATCCACCTGC 12  
DB 1 CCATCCACATCC 12  
RESULT 225  
ABI17729  
ID ABI17729 standard; DNA; 12 BP.  
XX  
AC ABI17729;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 317702 for detecting SNP TSC0028181.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.



XX Olek A, Piepenbrock C, Berlin K;  
PI WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 317702; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 5 C; 0 G; 4 T; 0 U; 0 Other;  
  
Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2 CATCCACCTGCT 13  
Db 1 CATCTACCTACT 12  
  
RESULT 226  
ABH94984/c  
ID ABH94984 standard; DNA; 12 BP.  
XX  
AC ABH94984;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 294977 for detecting SNP TSC0016386.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
DR WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 294977; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 1 C; 3 G; 5 T; 0 U; 0 Other;  
  
Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 18 GACCTGGTAAAT 29  
Db 12 GACCTACTAAAT 1  
  
RESULT 227  
ABI26645/c  
ID ABI26645 standard; DNA; 12 BP.  
XX  
AC ABI26645;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 326618 for detecting SNP TSC0033177.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
DR WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 326618; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 5 A; 0 C; 6 G; 1 T; 0 U; 0 Other;

```
Query Match      30.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 TCCACCTGCTGT 15
Db      12 TCCACCTCCTTT 1
      ||||| |||
RESULT 228
ABI39600
ID      ABI39600 standard; DNA; 12 BP.
XX
AC      ABI39600;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 339573 for detecting SNP TSC0041077.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
AC      ABI39600;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 339573 for detecting SNP TSC0041077.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.
XX
PR      07-APR-2000; 2000DE-01019173.
XX
PA      (EPIG-) EPIGENOMICS AG.
PI      Olek A, Piepenbrock C, Berlin K;
XX      WPI; 2001-657177/75.
DR
XX      Set of oligonucleotides, useful for diagnosis and cell typing, is
PT      designed to detect single-nucleotide polymorphisms and cytosine
PT      methylation status.
XX
PS      Claim 1; SEQ ID NO 339573; 29pp + Sequence Listing; German.
XX
CC      This invention describes novel oligonucleotide primers or peptide nucleic
CC      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC      and cytosine methylation status in chemically pretreated genomic DNA. The
CC      oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC      range of diseases including immune system, gastrointestinal, respiratory,
CC      central nervous system, cardiovascular and metabolic disorders. The
CC      oligomers are also used for detecting cell type differentiation. ABC00010
CC      -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC      represent the oligomers described in the invention. NOTE: The sequence
CC      data for this patent did not form part of the printed specification, but
CC      was obtained in electronic format from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
SQ      Sequence 12 BP; 2 A; 1 C; 6 G; 3 T; 0 U; 0 Other;

Query Match      30.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      13 TGTGTGACCTGG 24
Db      1 TGTGTGACGAGG 12
      ||||| |||
RESULT 229
ABI59140/c
ID      ABI59140 standard; DNA; 12 BP.
XX
```

```
AC      ABI59140;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 359113 for detecting SNP TSC0009017.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.
XX
PR      07-APR-2000; 2000DE-01019173.
XX
PA      (EPIG-) EPIGENOMICS AG.
PI      Olek A, Piepenbrock C, Berlin K;
XX      WPI; 2001-657177/75.
DR
XX      Set of oligonucleotides, useful for diagnosis and cell typing, is
PT      designed to detect single-nucleotide polymorphisms and cytosine
PT      methylation status.
XX
PS      Claim 1; SEQ ID NO 359113; 29pp + Sequence Listing; German.
XX
CC      This invention describes novel oligonucleotide primers or peptide nucleic
CC      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC      and cytosine methylation status in chemically pretreated genomic DNA. The
CC      oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC      range of diseases including immune system, gastrointestinal, respiratory,
CC      central nervous system, cardiovascular and metabolic disorders. The
CC      oligomers are also used for detecting cell type differentiation. ABC00010
CC      -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC      represent the oligomers described in the invention. NOTE: The sequence
CC      data for this patent did not form part of the printed specification, but
CC      was obtained in electronic format from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
SQ      Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

Query Match      30.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CATCCACCTGCT 13
Db      12 CATTCACCTACT 1
      ||| ||||| ||
RESULT 230
ABI60733
ID      ABI60733 standard; DNA; 12 BP.
XX
AC      ABI60733;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 360706 for detecting SNP TSC0052238.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
```

XX 18-OCT-2001.  
PD 06-APR-2001; 2001WO-IB0000713.  
XX 07-APR-2000; 2000DE-01019173.  
PF (EPIG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
PI WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
DR designed to detect single-nucleotide polymorphisms and cytosine  
XX methylation status.  
PS Claim 1; SEQ ID NO 360706; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;  
  
Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 15 TGTGACCTGGTA 26  
Db 1 TGTGATTGGTA 12  
  
RESULT 231  
ABI26571  
ID ABI26571 standard; DNA; 12 BP.  
XX  
AC ABI26571;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 326544 for detecting SNP TSC0033133.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 326544 for detecting SNP TSC0033133.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB0000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX

PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 326544; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 0 Other;  
  
Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 CCATCCACCTGC 12  
Db 1 CCATCCACATAC 12  
  
RESULT 232  
ABH77044  
ID ABH77044 standard; DNA; 12 BP.  
XX  
AC ABH77044;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 277037 for detecting SNP TSC0004364.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB0000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 277037; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 1 A; 1 C; 5 G; 5 T; 0 U; 0 Other;  
  
Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 7 ACCTGCTGTGTG 18  
DB 1 ACGTGTGTGTG 12  
  
RESULT 233  
ABH84669/c  
ID ABH84669 standard; DNA; 12 BP.  
XX  
AC ABH84669;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 284662 for detecting SNP TSC0011922.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 284662; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 5 A; 6 C; 0 G; 1 T; 0 U; 0 Other;  
  
Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 14 GTGTGACCTGGT 25

Db 12 GTGTGATGTGGT 1  
  
RESULT 234  
ACD28673  
ID ACD28673 standard; DNA; 12 BP.  
XX  
AC ACD28673;  
XX  
DT 06-NOV-2003 (first entry)  
XX  
DE Human acid sphingomyelinase, ASM, proband 2 deletion mutant DNA fragment.  
XX  
KW Human; ds; gene; ASM; acid sphingomyelinase; Ashkenazi Jew; proband 2;  
KW Niemann-Pick disease; NPD; Type B NPD; mutant.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..12  
FT /\*tag= a  
FT /product= "ASM proband 2 deletion mutant fragment"  
XX  
PN US6541218-B1.  
XX  
PD 01-APR-2003.  
XX  
PF 29-JUN-1998; 98US-00106375.  
XX  
PR 29-JUN-1998; 98US-00106375.  
XX  
PA (MOUN ) MOUNT SINAI SCHOOL MEDICINE.  
XX  
PI Schuchman EH, Desnick RJ;  
XX  
DR WPI; 2003-539725/51.  
DR P-PSDB; ABU63676.  
XX  
PT New isolated human acid sphingomyelinase polypeptide, useful for  
PT diagnosing and treating Type B Niemann-Pick Disease, possesses an acid  
PT sphingomyelinase activity.  
XX  
PS Disclosure; Fig 10; 62pp; English.  
XX  
CC The invention relates to an isolated human acid sphingomyelinase (ASM)  
CC polypeptide possessing acid sphingomyelinase (ASM) activity. The invention  
CC also discloses a missense mutation in the ASM gene of Ashkenazi Jewish  
CC Niemann-Pick disease patients. The polypeptide is useful in diagnosing  
CC and treating Type B Niemann-Pick disease. The present sequence represents  
CC human acid sphingomyelinase, ASM, proband 2 deletion mutant DNA fragment  
XX  
SQ Sequence 12 BP; 1 A; 5 C; 3 G; 3 T; 0 U; 0 Other;  
  
Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 12 CTGTGTGACCTG 23  
DB 1 CTGTGCCACCTG 12  
  
RESULT 235  
ADE13943  
ID ADE13943 standard; DNA; 12 BP.  
XX  
AC ADE13943;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Optineurin promoter motif, repeat element or regulatory region #52.  
XX



KW Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;  
KW SNP; glaucoma; progressive ocular hypertensive disorder;  
KW glaucoma related disorder; motif; repeat element; regulatory region.  
XX  
OS Homo sapiens.  
XX  
PN US2003190617-A1.  
XX  
PD 09-OCT-2003.  
XX  
PF 06-MAR-2002; 2002US-00091281.  
XX  
PR 06-MAR-2002; 2002US-00091281.  
XX  
PA (SIEE/) SI E.  
PA (RAYM/) RAYMOND V.  
PA (MORI/) MORISSETTE J.  
XX  
PI Raymond V, Morissette J, Si E;  
XX  
DR WPI; 2003-864168/80.  
XX  
PT New nucleic acid sequences of the optineurin gene are useful to detect  
PT polymorphisms particularly single nucleotide polymorphisms in the  
PT optineurin promoter to diagnose, prognosis and treat glaucoma and related  
PT disorders.  
XX  
PS Claim 11; SEQ ID NO 54; 159pp; English.  
XX  
CC The invention relates to an isolated nucleic acid (N1) comprising at  
CC least 20 but not more than 1500 consecutive nucleotides of the optineurin  
CC promoter appearing as ADE13890. Also included are the optineurin promoter  
CC operably linked to a heterologous nucleic acid, a nucleic acid capable of  
CC detecting a single nucleotide polymorphism (SNP) in the optineurin  
CC promoter, a host cell comprising the promoter operably linked to a  
CC heterologous sequence, diagnosing or prognosing glaucoma in a sample  
CC obtained from a cell or bodily fluid (comprising detecting a polymorphism  
CC in a promoter region of the optineurin gene, associated with a glaucoma  
CC phenotype), detecting a SNP sequence variation in a sample containing  
CC DNA, detecting the presence of an optineurin promoter sequence variation  
CC in a sample containing DNA, determining the presence or increased  
CC susceptibility to glaucoma or to a progressive ocular hypertensive  
CC disorder resulting in loss of visual field in a patient (or the severity  
CC or progression of glaucoma in a patient, comprising providing  
CC amplification reaction primers that direct amplification of a selected  
CC nucleic acid region containing the variation within the optineurin  
CC promoter and amplifying the DNA) and detecting a polymorphism (comprising  
CC obtaining a sample containing human genomic DNA, providing a nucleic acid  
CC capable of detecting a SNP located within an optineurin promoter, and  
CC detecting the polymorphism). The invention is used to diagnose and  
CC prognose glaucoma and also to treat glaucoma related disorders. The  
CC present sequence is an optineurin promoter motif, repeat element or  
CC putative regulatory region.  
XX  
SQ Sequence 12 BP; 2 A; 3 C; 4 G; 3 T; 0 U; 0 Other;  
  
Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 3 ATCCACCTGCTG 14  
||| |||||  
Db 1 ATGCAGCTGCTG 12  
  
RESULT 236  
ABZ77024/c  
ID ABZ77024 standard; DNA; 12 BP.  
XX  
AC ABZ77024;  
XX  
DT 07-MAY-2003 (first entry)  
XX

DE Bovine DGAT exon-intron junction oligonucleotide #14.  
XX  
KW Acyl CoA:diacylglycerol transferase; DGAT; enzyme; chromosome 14; bovine;  
KW milk; meat marbling; low fat; polymorphic; SNP; gene; ds;  
KW single nucleotide polymorphism.  
XX  
OS Bos taurus.  
OS Synthetic.  
XX  
PN WO2003004630-A2.  
XX  
PD 16-JAN-2003.  
XX  
PF 05-JUL-2002; 2002WO-EP007520.  
XX  
PR 06-JUL-2001; 2001EP-00116412.  
PR 13-MAY-2002; 2002US-0379412P.  
XX  
PA (ARBE-) ARBEITSGEMEINSCHAFT DEUT RINDERZUECHTER.  
XX  
PI Fries H, Winter A;  
XX  
DR WPI; 2003-239205/23.  
XX  
PT New nucleic acid molecule comprising a sequence of an allele of a  
PT polymorphic bovine acyl CoA-diacylglycerol transferase gene useful for  
PT testing a mammal for its predisposition for fat content of milk and for  
PT meat marbling.  
XX  
PS Disclosure; Page 40; 91pp; English.  
XX  
CC The present invention describes a nucleic acid molecule (NA) (I) encoding  
CC a bovine acyl CoA-diacylglycerol transferase (DGAT) contributing to or  
CC indicative for low fat content of milk and to low meat marbling  
CC (intramuscular fat content). Human DGAT is located to chromosome 8, and  
CC bovine DGAT is located to chromosome 14. (I) is useful for testing a  
CC mammal for its predisposition for fat content of milk and/or its  
CC predisposition for meat marbling. The method comprises analysing the gene  
CC encoding DGAT for nucleotide polymorphisms (e.g. single nucleotide  
CC polymorphisms (SNPs)) which are connected with the predisposition. The  
CC nucleotide polymorphisms are located in the coding region of the DGAT  
CC gene and result in substitution, deletion and/or addition of an amino  
CC acid sequence of the polypeptide which is encoded by the gene. The  
CC nucleic acid molecule has at the position 10433 and 10434 of the DGAT  
CC gene a guanine and a cytosine residue, at position 3343 a cytosine or  
CC guanine, 11030 a guanine, 11048 a cytosine or thymine and 11093 a  
CC thymine, which correlate with a predisposition for low fat content of  
CC milk and low meat marbling. The nucleic acid molecule has at the position  
CC corresponding to position 10433 and 10434 of the DGAT gene two adenine  
CC residues which correlate with a predisposition for high content of milk  
CC and high meat marbling. The nucleotide polymorphisms are located in a  
CC region which is responsible for the regulation of the expression of the  
CC product of the gene encoding DGAT. ABZ76924 to ABZ77045 and ABP96035 to  
CC ABP96046 represent sequences used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 12 BP; 2 A; 2 C; 5 G; 3 T; 0 U; 0 Other;  
  
Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 3 ATCCACCTGCTG 14  
||| |||||  
Db 12 ACCCACCTGATG 1  
  
RESULT 237  
ADZ24155/c  
ID ADZ24155 standard; DNA; 12 BP.  
XX  
AC ADZ24155;  
XX



DT 16-JUN-2005 (first entry)  
XX  
DE Human SNP detection related oligonucleotide #1122.  
DE  
XX ss; haplotype mapping; SNP detection; tumor; cytostatic; neoplasm;  
KW immune disorder; cardiovascular disease; metabolic disorder;  
KW respiratory disease; musculoskeletal disease; renal disease;  
KW nephrotropic; endocrine disease; genitourinary disease.  
XX  
OS Homo sapiens.  
XX  
XX WO2005030952-A1.  
PN  
XX  
XX 07-APR-2005.  
PD  
XX  
XX 30-SEP-2004; 2004WO-JP014784.  
PF  
XX  
XX 30-SEP-2003; 2003JP-00342519.  
PR  
XX 28-MAY-2004; 2004JP-00158717.  
PR  
XX  
PA (RIKE ) RIKEN KK.  
PA (STAG-) STAGEN CO LTD.  
PA (SEKI/) SEKINE A.  
PA (IIDA/) IIDA A.  
PA (SAIT/) SAITO S.  
XX  
XX Sekine A, Iida A, Saito S, Nakamura Y, Kamatani N;  
PI  
XX WPI; 2005-305936/31.  
DR  
XX  
XX Analyzing haplotype, by detecting polymorphism in drug-related genes,  
PT electing common polymorphism (CP), building haplotype block using CP,  
PT specifying CP within block, specifying tag polymorphism from CP within  
PT block.  
PT  
XX  
PS Disclosure; SEQ ID NO 1122; 1290pp; Japanese.  
PS  
XX  
XX The invention relates to a method of analyzing haplotype, by detecting  
CC gene polymorphism in drug-related genes such as aryl acetylamide  
CC deacetylase, arylalkylamine N-acetyl transferase or ATP-binding cassette,  
CC sub-family A (ABCI), member 1. The method is useful for analyzing  
CC haplotype. The method is useful for estimating the sensitivity or disease  
CC of a medicine or a foreign material, for selecting medicine for  
CC preventing or treating diseases, for determining appropriate dosage of  
CC medicine for preventing or treating a disease, for analyzing a drug  
CC interaction, and for determining the related polymorphism relative to the  
CC sensitivity of the medicine, foreign material or disease. The diseases  
CC include malignant tumor, immune disorder circulatory disease, metabolic  
CC disease, kidney disease, respiratory disease and muscle associated  
CC disease. The method enables analysis of the individual differences  
CC related to the sensitivity of a medicine, using a haplotype, without  
CC using each single nucleotide polymorphism. The present sequence  
CC represents a human SNP detection related oligonucleotide.  
XX  
SQ Sequence 12 BP; 4 A; 5 C; 1 G; 2 T; 0 U; 0 Other;  
  
Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 13 TGTGTGACCTGG 24  
Db |||||  
12 TGTATGAGCTGG 1  
  
RESULT 238  
ADS77727/c  
ID ADS77727 standard; DNA; 11 BP.  
XX  
AC ADS77727;  
XX  
DT 30-DEC-2004 (first entry)  
XX

DE Breast cancer detection oligonucleotide #1509.  
XX  
KW ss; primer; cytostatic; RNA interference; RNAi; gene silencing;  
KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;  
KW cathepsin L inhibitor; cathepsin F inhibitor;  
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;  
KW collagen antagonist; diagnosis; breast tissue; cancer.  
XX  
OS Homo sapiens.  
XX  
XX WO2004085621-A2.  
PN  
XX  
XX 07-OCT-2004.  
PD  
XX  
XX 22-MAR-2004; 2004WO-US008866.  
PF  
XX  
XX 20-MAR-2003; 2003US-0456735P.  
PR  
XX  
PA (DAND ) DANA FARBER CANCER INST INC.  
XX  
XX Polyak K, Porter D, Allinen M;  
PI  
XX WPI; 2004-728732/71.  
DR  
XX  
XX Diagnosing breast cancer comprises determining expression levels of a  
PT gene selected from those differentially expressed in normal or cancerous  
PT cells of a breast tissue sample including interleukin 1, thrombospondin 1  
PT and cystatin C.  
XX  
PS Example 6; SEQ ID NO 1509; 149pp; English.  
PS  
XX The invention relates to a method of diagnosis (M1) comprising: (a)  
CC providing a test sample of breast tissue; (b) determining the level of  
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide  
CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the  
CC specification, and (c) if the gene is expressed in the test sample at a  
CC lower level than in a control normal breast tissue sample, diagnosing the  
CC test sample as containing cancer cells. The method is used for diagnosing  
CC breast cancer. This sequence corresponds to an oligonucleotide primer  
CC used in the method of the invention.  
XX  
SQ Sequence 11 BP; 5 A; 3 C; 2 G; 0 T; 0 U; 1 Other;  
  
Query Match 29.7%; Score 8.6; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 1.7e+02;  
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 7 ACCTGCTGTGT 17  
Db :|||  
11 HCTTGCTGTGT 1  
  
RESULT 239  
ADS77874/c  
ID ADS77874 standard; DNA; 11 BP.  
XX  
AC ADS77874;  
XX  
DT 30-DEC-2004 (first entry)  
XX  
DE Breast cancer detection oligonucleotide #1656.  
XX  
KW ss; primer; cytostatic; RNA interference; RNAi; gene silencing;  
KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;  
KW cathepsin L inhibitor; cathepsin F inhibitor;  
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;  
KW collagen antagonist; diagnosis; breast tissue; cancer.  
XX  
OS Homo sapiens.  
XX  
XX WO2004085621-A2.  
PN  
XX 07-OCT-2004.  
XX

XX 22-MAR-2004; 2004WO-US008866.  
PF  
XX  
PR 20-MAR-2003; 2003US-0456735P.  
XX  
XX (DAND ) DANA FARBER CANCER INST INC.  
PA Polyak K, Porter D, Allinen M;  
XX WPI; 2004-728732/71.  
DR  
XX Diagnosing breast cancer comprises determining expression levels of a  
PT gene selected from those differentially expressed in normal or cancerous  
PT cells of a breast tissue sample including interleukin 1, thrombospondin 1  
PT and cystatin C.  
XX  
PS Example 6; SEQ ID NO 1656; 149pp; English.  
PS  
XX The invention relates to a method of diagnosis (M1) comprising: (a)  
CC providing a test sample of breast tissue; (b) determining the level of  
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide  
CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the  
CC specification, and (c) if the gene is expressed in the test sample at a  
CC lower level than in a control normal breast tissue sample, diagnosing the  
CC test sample as containing cancer cells. The method is used for diagnosing  
CC breast cancer. This sequence corresponds to an oligonucleotide primer  
CC used in the method of the invention.  
XX  
SQ Sequence 11 BP; 5 A; 3 C; 2 G; 0 T; 0 U; 1 Other;  
PS  
XX Query Match 29.7%; Score 8.6; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 1.7e+02;  
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 7 ACCTGCTGTGT 17  
Db 11 HCTTGCTGTGT 1  
RESULT 240  
ADS77394/c  
ID ADS77394 standard; DNA; 11 BP.  
XX  
AC ADS77394;  
XX  
DT 30-DEC-2004 (first entry)  
XX  
DE Breast cancer detection oligonucleotide #1176.  
XX  
KW ss; primer; cytostatic; RNA interference; RNAi; gene silencing;  
KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;  
KW cathepsin L inhibitor; cathepsin F inhibitor;  
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;  
KW collagen antagonist; diagnosis; breast tissue; cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO2004085621-A2.  
XX  
PD 07-OCT-2004.  
XX  
PF 22-MAR-2004; 2004WO-US008866.  
XX  
PR 20-MAR-2003; 2003US-0456735P.  
XX  
PA (DAND ) DANA FARBER CANCER INST INC.  
XX Polyak K, Porter D, Allinen M;  
XX WPI; 2004-728732/71.  
DR  
XX Diagnosing breast cancer comprises determining expression levels of a  
PT gene selected from those differentially expressed in normal or cancerous  
PT cells of a breast tissue sample including interleukin 1, thrombospondin 1  
PT and cystatin C.

PT cells of a breast tissue sample including interleukin 1, thrombospondin 1  
PT and cystatin C.  
XX  
PS Example 6; SEQ ID NO 1176; 149pp; English.  
XX  
CC The invention relates to a method of diagnosis (M1) comprising: (a)  
CC providing a test sample of breast tissue; (b) determining the level of  
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide  
CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the  
CC specification, and (c) if the gene is expressed in the test sample at a  
CC lower level than in a control normal breast tissue sample, diagnosing the  
CC test sample as containing cancer cells. The method is used for diagnosing  
CC breast cancer. This sequence corresponds to an oligonucleotide primer  
CC used in the method of the invention.  
XX  
SQ Sequence 11 BP; 5 A; 3 C; 2 G; 0 T; 0 U; 1 Other;  
PS  
XX Query Match 29.7%; Score 8.6; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 1.7e+02;  
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 7 ACCTGCTGTGT 17  
Db 11 HCTTGCTGTGT 1  
RESULT 241  
AAD44125  
ID AAD44125 standard; DNA; 12 BP.  
XX  
AC AAD44125;  
XX  
DT 13-DEC-2002 (first entry)  
XX  
DE PCR primer #6 designed to bind human MMP SPR region.  
XX  
KW Sequential consensus region-directed amplification; gene expression;  
KW disease diagnosis; gene analysis; human; matrix metalloproteinase; MMP;  
KW signal peptide region; SPR; PCR; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN US6277571-B1.  
XX  
PD 21-AUG-2001.  
XX  
PF 30-SEP-1998; 98US-00163485.  
XX  
PR 03-OCT-1997; 97US-00943162.  
PR 03-OCT-1997; 97US-0108152P.  
XX  
PA (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.  
XX  
PI Fillmore H, Broadus W, Gillies G;  
XX  
DR WPI; 2002-412824/44.  
XX  
PT Sequential consensus region-directed amplification for sorting mixture of  
PT DNAs into 2 or more subsets or distinguishing gene expression patterns in  
PT 2 samples, useful for disease diagnosis and gene analysis.  
XX  
PS Example; Col 12; 19pp; English.  
XX  
CC The invention relates to a method of sequential consensus region-directed  
CC amplification for sorting a mixture of DNAs into 2 or more subsets or  
CC distinguishing gene expression patterns in 2 samples. The methods, kits  
CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or  
CC more subsets or distinguishing gene expression patterns in 2 samples e.g.  
CC for disease diagnosis and gene analysis. The present sequence is a PCR  
CC primer designed to bind to human matrix metalloproteinase (MMP) signal  
CC peptide region (SPR). This primer is used to illustrate the method of the  
CC invention  
XX

SQ Sequence 12 BP; 0 A; 3 C; 4 G; 4 T; 0 U; 1 Other;

Query Match 29.7%; Score 8.6; DB 1; Length 12;  
Best Local Similarity 88.9%; Pred. No. 1.8e+02;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 9 CTGCTGTGT 17  
|||  
Db 4 CTGCTGTGY 12

RESULT 242  
AAQ97150  
ID AAQ97150 standard; DNA; 10 BP.  
XX  
AC AAQ97150;  
XX  
DT 16-OCT-2003 (revised)  
DT 27-MAR-1996 (first entry)  
XX  
DE HIV-1 NL4-3 LTR nucleotide deletion 132.  
XX  
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO9521912-A1.  
XX  
PD 17-AUG-1995.  
XX  
PF 14-FEB-1995; 95WO-AU0000063.  
XX  
PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.  
XX  
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX WPI; 1995-293115/38.  
XX  
PD 17-AUG-1995.  
XX  
PF 14-FEB-1995; 95WO-AU0000063.  
XX  
PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.  
XX  
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX WPI; 1995-293115/38.  
XX  
PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
PT LTR region - can be used in a vaccine to inhibit/reduce productive  
PT infection in an individual by a pathogenic strain.  
XX  
PS Claim 14; Page 198; 301pp; English.  
XX  
CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
CC resulting avirulent HIV strains are still capable of inducing an immune  
CC response in humans, and enable the generation of therapeutic, diagnostic  
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 10 BP; 1 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 10 TGCTGTGTGA 19  
|||  
Db 1 TGTGTGTGA 10

RESULT 243  
AAQ96785/c  
ID AAQ96785 standard; DNA; 10 BP.  
XX

AC AAQ96785;  
XX  
DT 16-OCT-2003 (revised)  
DT 26-MAR-1996 (first entry)  
XX  
DE HIV-1 NL4-3 nef gene nucleotide deletion 380.  
XX  
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO9521912-A1.  
XX  
PD 17-AUG-1995.  
XX  
PF 14-FEB-1995; 95WO-AU0000063.  
XX  
PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.  
XX  
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX WPI; 1995-293115/38.  
XX  
PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
PT LTR region - can be used in a vaccine to inhibit/reduce productive  
PT infection in an individual by a pathogenic strain.  
XX  
PS Claim 13; Page 193; 301pp; English.  
XX  
CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
CC resulting avirulent HIV strains are still capable of inducing an immune  
CC response in humans, and enable the generation of therapeutic, diagnostic  
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 10 BP; 4 A; 4 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 8 CCTGCTGTGT 17  
|||  
Db 10 CCTGCTGTGT 1

RESULT 244  
AAQ97151  
ID AAQ97151 standard; DNA; 10 BP.  
XX  
AC AAQ97151;  
XX  
DT 16-OCT-2003 (revised)  
DT 27-MAR-1996 (first entry)  
XX  
DE HIV-1 NL4-3 LTR nucleotide deletion 133.  
XX  
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO9521912-A1.  
XX  
PD 17-AUG-1995.  
XX

|            |                                                                           |                 |    |                                                                           |
|------------|---------------------------------------------------------------------------|-----------------|----|---------------------------------------------------------------------------|
| PF         | 14-FEB-1995;                                                              | 95WO-AU0000063. | PT | infection in an individual by a pathogenic strain.                        |
| XX         |                                                                           |                 | XX |                                                                           |
| PR         | 14-FEB-1994;                                                              | 94AU-00003864.  | PS | Claim 13; Page 189; 301pp; English.                                       |
| PR         | 21-FEB-1994;                                                              | 94AU-00004002.  | XX |                                                                           |
| PR         | 23-DEC-1994;                                                              | 94AU-00000284.  | CC | Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or    |
| XX         |                                                                           |                 | CC | more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more |
| PA         | (MACF-) MACFARLANE BURNET CENT MEDICAL.                                   |                 | CC | decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of    |
| PA         | (AURE-) AUSTRALIAN RED CROSS SOC.                                         |                 | CC | AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  |
| PI         | Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;                     |                 | CC | resulting avirulent HIV strains are still capable of inducing an immune   |
| XX         |                                                                           |                 | CC | response in humans, and enable the generation of therapeutic, diagnostic  |
| DR         | WPI; 1995-293115/38.                                                      |                 | CC | and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  |
| XX         |                                                                           |                 | CC | standardise OS field)                                                     |
| PT         | New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or    |                 | XX |                                                                           |
| PT         | LTR region - can be used in a vaccine to inhibit/reduce productive        |                 | SQ | Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;                         |
| PT         | infection in an individual by a pathogenic strain.                        |                 |    |                                                                           |
| XX         |                                                                           |                 |    |                                                                           |
| PS         | Claim 14; Page 198; 301pp; English.                                       |                 |    |                                                                           |
| XX         |                                                                           |                 |    |                                                                           |
| CC         | Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or    |                 |    |                                                                           |
| CC         | more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more |                 |    |                                                                           |
| CC         | decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of    |                 |    |                                                                           |
| CC         | AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  |                 |    |                                                                           |
| CC         | resulting avirulent HIV strains are still capable of inducing an immune   |                 |    |                                                                           |
| CC         | response in humans, and enable the generation of therapeutic, diagnostic  |                 |    |                                                                           |
| CC         | and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  |                 |    |                                                                           |
| CC         | standardise OS field)                                                     |                 |    |                                                                           |
| XX         |                                                                           |                 |    |                                                                           |
| SQ         | Sequence 10 BP; 1 A; 1 C; 4 G; 4 T; 0 U; 0 Other;                         |                 |    |                                                                           |
|            |                                                                           |                 |    |                                                                           |
|            | Query Match 29.0%; Score 8.4; DB 1; Length 10;                            |                 |    |                                                                           |
|            | Best Local Similarity 90.0%; Pred. No. 1.6e+02;                           |                 |    |                                                                           |
|            | Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;                |                 |    |                                                                           |
|            |                                                                           |                 |    |                                                                           |
| QY         | 11 GCTGTGTGAC 20                                                          |                 |    |                                                                           |
|            |                                                                           |                 |    |                                                                           |
| Db         | 1 GTTGTGTGAC 10                                                           |                 |    |                                                                           |
|            |                                                                           |                 |    |                                                                           |
|            | RESULT 245                                                                |                 |    |                                                                           |
| AAQ96482/C |                                                                           |                 |    |                                                                           |
| ID         | AAQ96482 standard; DNA; 10 BP.                                            |                 |    |                                                                           |
| XX         |                                                                           |                 |    |                                                                           |
| AC         | AAQ96482;                                                                 |                 |    |                                                                           |
| XX         |                                                                           |                 |    |                                                                           |
| DT         | 16-OCT-2003 (revised)                                                     |                 |    |                                                                           |
| DT         | 20-MAR-1996 (first entry)                                                 |                 |    |                                                                           |
| XX         |                                                                           |                 |    |                                                                           |
| DE         | HIV-1 NL4-3 nef gene nucleotide deletion 77.                              |                 |    |                                                                           |
| XX         |                                                                           |                 |    |                                                                           |
| KW         | HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.              |                 |    |                                                                           |
| XX         |                                                                           |                 |    |                                                                           |
| OS         | Human immunodeficiency virus 1.                                           |                 |    |                                                                           |
| XX         |                                                                           |                 |    |                                                                           |
| PN         | WO9521912-A1.                                                             |                 |    |                                                                           |
| XX         |                                                                           |                 |    |                                                                           |
| PD         | 17-AUG-1995.                                                              |                 |    |                                                                           |
| XX         |                                                                           |                 |    |                                                                           |
| PF         | 14-FEB-1995; 95WO-AU0000063.                                              |                 |    |                                                                           |
| XX         |                                                                           |                 |    |                                                                           |
| PR         | 14-FEB-1994; 94AU-00003864.                                               |                 |    |                                                                           |
| DT         | 20-MAR-1996 (first entry)                                                 |                 |    |                                                                           |
| XX         |                                                                           |                 |    |                                                                           |
| DE         | HIV-1 NL4-3 nef gene nucleotide deletion 77.                              |                 |    |                                                                           |
| XX         |                                                                           |                 |    |                                                                           |
| KW         | HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.              |                 |    |                                                                           |
| XX         |                                                                           |                 |    |                                                                           |
| OS         | Human immunodeficiency virus 1.                                           |                 |    |                                                                           |
| XX         |                                                                           |                 |    |                                                                           |
| PN         | WO9521912-A1.                                                             |                 |    |                                                                           |
| XX         |                                                                           |                 |    |                                                                           |
| PD         | 17-AUG-1995.                                                              |                 |    |                                                                           |
| XX         |                                                                           |                 |    |                                                                           |
| PF         | 14-FEB-1995; 95WO-AU0000063.                                              |                 |    |                                                                           |
| XX         |                                                                           |                 |    |                                                                           |
| PR         | 14-FEB-1994; 94AU-00003864.                                               |                 |    |                                                                           |
| PR         | 21-FEB-1994; 94AU-00004002.                                               |                 |    |                                                                           |
| PR         | 23-DEC-1994; 94AU-00000284.                                               |                 |    |                                                                           |
| XX         |                                                                           |                 |    |                                                                           |
| PA         | (MACF-) MACFARLANE BURNET CENT MEDICAL.                                   |                 |    |                                                                           |
| PA         | (AURE-) AUSTRALIAN RED CROSS SOC.                                         |                 |    |                                                                           |
| XX         |                                                                           |                 |    |                                                                           |
| PI         | Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;                     |                 |    |                                                                           |
| XX         |                                                                           |                 |    |                                                                           |
| DR         | WPI; 1995-293115/38.                                                      |                 |    |                                                                           |
| XX         |                                                                           |                 |    |                                                                           |
| PT         | New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or    |                 |    |                                                                           |
| PT         | LTR region - can be used in a vaccine to inhibit/reduce productive        |                 |    |                                                                           |

Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTGCTGTGTG 18  
Db 1 CTGTTGTGTG 10

RESULT 247  
AAV34960/c  
ID AAV34960 standard; DNA; 10 BP.  
XX  
AC AAV34960;  
XX  
DT 13-OCT-1998 (first entry)  
XX  
DE Synthetic Agaricus bisporus RAPD primer.  
XX  
KW Random amplified polymorphic DNA; primer; mushroom; RAPD; ss.  
XX  
OS Synthetic.  
XX WO9821975-A1.  
PN  
XX 28-MAY-1998.  
PD  
XX 19-NOV-1996; 96WO-US018686.  
PF  
XX 19-NOV-1996; 96WO-US018686.  
PR  
XX (AMYC-) AMYCEL INC.  
PA  
XX Loftus MG, Lodder SC, Legg EJ;  
PI  
XX WPI; 1998-312054/27.  
DR  
XX New strains of Agaricus bisporus with improved cap whiteness - compared with the U1 strain but retaining other desirable features of this strain.  
PT  
XX Disclosure; Page 10; 26pp; English.  
PS  
XX The sequence is that of an RAPD (random amplified DNA) primer which was used in the isolation of an Agaricus bisporus mushroom strain which has whiter caps, less scaling than known strains, particularly for mushrooms produced in the first break, so it is more valuable (suitable for marketing fresh rather than canning). It also retains the desirable characteristics (good cap shape and shelf life, thick stem and veil) of the U1 strain  
CC  
XX Sequence 10 BP; 2 A; 5 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 GTGACCTGGT 25  
Db 10 GTGACCGGGT 1

RESULT 248  
AAV03254  
ID AAV03254 standard; DNA; 10 BP.  
XX  
AC AAV03254;  
XX  
DT 25-MAR-2003 (revised)  
DT 08-JUN-1998 (first entry)  
XX  
DE Homo sapiens mutant melanocortin 4 receptor Ile137Thr PCR primer.  
XX Melanocortin 4 receptor; MC4-R gene; body weight disorder; treatment;

KW obesity; anorexia; cachexia; Ile137Thr; mutant; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9747316-A1.  
XX  
PD 18-DEC-1997.  
XX  
XX  
PF 09-JUN-1997; 97WO-US009969.  
XX  
PR 10-JUN-1996; 96US-00662560.  
PR 08-JAN-1997; 97US-00780749.  
PR 06-JUN-1997; 97US-00870511.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
XX Lee F, Huszar D, Gu W;  
PI  
XX WPI; 1998-052026/05.  
DR  
XX Drug screening assays to identify compounds for body weight disorder treatment - e.g. obesity, anorexia and cachexia, using melanocortin 4 receptor as target.  
PT  
XX  
PT  
XX Disclosure; Page 57; 111pp; English.  
PS  
XX The sequence is that of a PCR primer which may be used in the identification of the mutant melanocortin 4 receptor (MC4-R) Ile137Thr. This may be of use in the treatment of body weight disorders e.g. obesity, anorexia and cachexia. (Updated on 25-MAR-2003 to correct PR field.)  
CC  
XX Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATCCACCTGC 12  
Db 1 ATCCACTTGC 10

RESULT 249  
AAV18637/c  
ID AAX18637 standard; DNA; 10 BP.  
XX  
AC AAX18637;  
XX  
DT 06-MAY-1999 (first entry)  
XX  
DE p53 serial analysis of gene expression tag #38.  
XX  
KW p53; serial analysis of gene expression; SAGE tag; cancer; neoplastic; rat embryo fibroblast; REF; tumour suppressor; cell cycle control;  
KW tumourigenesis; diagnosis; ss.  
XX  
OS Synthetic.  
OS Rattus sp.  
XX  
XX WO9901581-A1.  
PN  
XX  
PD 14-JAN-1999.  
XX  
PF 02-JUL-1998; 98WO-US013903.  
XX  
PR 02-JUL-1997; 97US-0051573P.  
XX  
PA (GENZ ) GENZYME CORP.  
XX  
PI Madden SL, Galella EA, Bertelsen AH, Beaudry GA;  
XX



DR WPI; 1999-106079/09.

XX

PT Diagnosis of cancer in potentially neoplastic samples - by comparing the

PT level of transcription between RNA transcripts in two tissue samples,

PT useful for providing an extensive profile of gene expression in rat

PT embryo fibroblast (REF) cells.

XX

PS Example 2; Page 16; 32pp; English.

XX

CC A method has been developed for the diagnosis of cancer in potentially

CC neoplastic samples. The method comprises comparing the level of

CC transcription between RNA transcripts in two tissue samples (which are of

CC the same type), where the first sample is potentially neoplastic, and the

CC second sample is normal human tissue. The first sample is categorized as

CC neoplastic if its level of transcription is lower than that of the second

CC sample. The transcript is selected from Alu, RAS, U6 snRNA, 16S RNA, EGR-

CC 1, ribosomal protein S27, ETS-1, 28S RNA, CGR11, and LIMK-2, and it is

CC identified by a tag selected from ribosomal protein Li3a, alpha-tubulin

CC (T1) and (T2), thymosin beta-4, and gamma- actin. The present sequence

CC represents a serial analysis of gene expression (SAGE) tag from the

CC present invention. The use of SAGE tags provides an extensive profile of

CC gene expression in rat embryo fibroblast (REF) cells containing the (non)

CC -functional p53 tumour suppression gene. The discovery of new SAGE tags,

CC which are regulated by p53, enables the diagnosis of genes that are

CC related to cell cycle control and tumourigenesis

XX

SQ Sequence 10 BP; 1 A; 1 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 1.6e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATCCACCTG 11

Db || |||||

10 CACCCACCTG 1

RESULT 250

AAZ11274/C

ID AAZ11274 standard; DNA; 10 BP.

XX

AC AAZ11274;

XX

DT 15-NOV-1999 (first entry)

XX

DE Splice donor site #1 for VP16 gene trap vector.

XX

KW Splice donor; VP16 gene trap vector; protein-cell interaction; detection;

KW protein-protein interaction; transcriptional activator domain; ds.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT misc\_feature 1..5

FT /\*tag= a

FT /label= sticky end

FT /note= "the 5'-end of the complementary strand overhangs

FT the 3' end of this strand by the sequence 5'-GATC-3'"

XX

PN WO9943848-A1.

XX

PD 02-SEP-1999.

XX

PF 25-FEB-1999; 99WO-CA000173.

XX

PR 25-FEB-1998; 98CA-02224475.

XX

PA (UYBR-) UNIV BRITISH COLUMBIA.

XX

PI Ong CJ, Jirik FR;

XX

DR WPI; 1999-540605/45.

XX

PT New protein interaction and transcription factor trap used for

PT identification of unknown genes encoding transcriptional activator

PT domains.

XX

PS Example 1; Page 26; 40pp; English.

XX

CC This sequence represents a splice donor site that can be used in a VP16

CC gene trap vector used in the method of the invention. The method is for

CC detecting interaction between an endogenous protein of a cell and a test

CC protein. The cell contains a first DNA sequence encoding a reporter under

CC transcriptional control of a transcriptional regulatory element, and a

CC second DNA sequence that is expressed by the cell and which encodes a

CC first hybrid protein comprising a first transcriptional regulatory

CC protein moiety (TRP) selected from a DNA-binding domain that recognises a

CC binding site on the transcriptional regulatory element controlling

CC transcriptional of the first DNA sequence and, a transcriptional

CC activator functional in the cell; and a test protein. The method

CC comprises: (a) placing into the cell a DNA construct comprising one or

CC more mRNA splice sites, and a third DNA sequence encoding a second TRP

CC which, when combined with the first TRP, will reconstitute a TRP capable

CC of binding to and activating the transcriptional regulatory element

CC controlling transcription of the first DNA sequence; and (b) determining

CC whether the reporter is expressed by the cell, as an indicator of

CC expression of a second hybrid protein comprising the second TRP and an

CC endogenous protein of the cell capable of interaction with the test

CC protein. The method is used for the identification and characterisation

CC of unknown genes according to protein-protein interactions or for

CC identification of genes encoding transcriptional activator domains

XX

SQ Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 1.6e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 TGTGACCTGG 24

Db || |||||

10 TCGACCTGG 1

RESULT 251

AAZ78697

ID AAZ78697 standard; DNA; 10 BP.

XX

AC AAZ78697;

XX

DT 10-APR-2000 (first entry)

XX

DE Human dendritic cell SAGE tag, SEQ ID NO:1125.

XX

KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;

KW APC; monocyte-derived dendritic cell; differential gene expression;

KW immunostimulatory cofactor; costimulatory factor; CTL;

KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

XX

OS Homo sapiens.

XX

PN WO9965924-A2.

XX

PD 23-DEC-1999.

XX

PF 18-JUN-1999; 99WO-US013800.

XX

PR 19-JUN-1998; 98US-0089833P.

PR 19-JUN-1998; 98US-0089844P.

PR 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-0089878P.

PR 19-JUN-1998; 98US-0089991P.

PR 19-JUN-1998; 98US-0089992P.

PR 19-JUN-1998; 98US-0089993P.

PR 19-JUN-1998; 98US-0089994P.

PR 19-JUN-1998; 98US-0089997P.

PR 19-JUN-1998; 98US-0089999P.

PR 19-JUN-1998; 98US-00900000P.  
PR 19-JUN-1998; 98US-00900035P.  
PR 19-JUN-1998; 98US-00900036P.  
PR 19-JUN-1998; 98US-00900039P.  
PR 19-JUN-1998; 98US-00900040P.  
PR 19-JUN-1998; 98US-00900041P.  
PR 19-JUN-1998; 98US-00900042P.  
PR 19-JUN-1998; 98US-00900043P.  
PR 19-JUN-1998; 98US-00900044P.  
PR 19-JUN-1998; 98US-00900045P.  
PR 19-JUN-1998; 98US-00900047P.  
PR 19-JUN-1998; 98US-00900048P.  
PR 19-JUN-1998; 98US-00900072P.  
PR 19-JUN-1998; 98US-00900076P.  
PR 19-JUN-1998; 98US-00900077P.  
PR 19-JUN-1998; 98US-00900078P.  
PR 19-JUN-1998; 98US-00900079P.  
PR 19-JUN-1998; 98US-00900080P.  
PR 08-DEC-1998; 98US-0111715P.

XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.

XX  
PI Roberts BL, Shankara S;

XX  
DR WPI; 2000-106077/09.

XX  
PT Isolated polynucleotides differentially expressed in antigen-presenting  
PT cells, useful in gene vaccines against cancer.

PS Claim 1; Page 97; 130pp; English.

XX  
CC Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene  
CC expression) tags used to identify mRNA transcripts encoding  
CC immunostimulatory cofactor proteins which are preferentially or  
CC differentially expressed in monocyte-derived dendritic cells compared  
CC with monocytes. Some of the transcripts correspond to known genes or ESTs  
CC (expressed sequence tags) which were previously unknown to be  
CC preferentially or differentially expressed in dendritic cells, while  
CC other transcripts correspond to novel genes. Antigen-presenting cell  
CC (APC)-associated costimulatory factors play an important role in the  
CC activation of the cytotoxic immune response, particularly against tumour  
CC cells. Tumour antigen presentation via the MHC (major histocompatibility  
CC complex) and subsequent recognition by T-cell receptors is alone  
CC insufficient to activate a robust cytotoxic immune response that can lyse  
CC the tumour cells, immunostimulatory cofactors also being required for  
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid  
CC sequences identified using the SAGE tags have several potential uses.  
CC They may be used in vaccines to induce an immune response, particularly  
CC against a tumour antigen; to modulate the genotype of an APC; to screen  
CC for agents that modulate expression of differentially expressed genes in  
CC an APC; and as hybridisation probes/amplification primers for the  
CC diagnosis, prognosis and monitoring of diseases related to abnormal  
CC expression of these genes. Detection of the dendritic cell differentially  
CC expressed genes, or of their encoded proteins, can be used to identify  
CC cells as belonging to the monocyte lineage. Cells containing these genes  
CC can be used in active immunotherapy (or to stimulate production of a  
CC population of antigen-specific effector cells) and vectors containing  
CC them are used in gene therapy. Co-administration of tumour antigens and  
CC APC-associated costimulatory factors ensures adequate antigen  
CC presentation to endogenous APCs and upregulates the APCs for the  
CC presentation of co-stimulatory signals, migration to T cell-rich sites,  
CC secretion of T cell growth factors and secretion of chemokines for  
CC recruitment of immune effector cells

XX  
SQ Sequence 10 BP; 1 A; 5 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ATCCACCTGC 12

Db  
1 ATCCGCCTGC 10

RESULT 252  
AAZ77846/c  
ID AAZ77846 standard; DNA; 10 BP.

XX AC AAZ77846;  
XX DT 10-APR-2000 (first entry)  
XX DE Human dendritic cell SAGE tag, SEQ ID NO:274.

XX KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;  
KW APC; monocyte-derived dendritic cell; differential gene expression;  
KW immunostimulatory cofactor; costimulatory factor; CTL; anticancer; ss.  
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

XX OS Homo sapiens.

XX PN WO9965924-A2.

XX PD 23-DEC-1999.

XX PF 18-JUN-1999; 99WO-US013800.

XX PR 19-JUN-1998; 98US-0089833P.

XX PR 19-JUN-1998; 98US-0089844P.

XX PR 19-JUN-1998; 98US-0089853P.

XX PR 19-JUN-1998; 98US-0089878P.

XX PR 19-JUN-1998; 98US-0089991P.

XX PR 19-JUN-1998; 98US-0089992P.

XX PR 19-JUN-1998; 98US-0089993P.

XX PR 19-JUN-1998; 98US-0089994P.

XX PR 19-JUN-1998; 98US-0089997P.

XX PR 19-JUN-1998; 98US-0089999P.

XX PR 19-JUN-1998; 98US-0090000P.

XX PR 19-JUN-1998; 98US-00900035P.

XX PR 19-JUN-1998; 98US-00900036P.

XX PR 19-JUN-1998; 98US-00900039P.

XX PR 19-JUN-1998; 98US-00900040P.

XX PR 19-JUN-1998; 98US-00900041P.

XX PR 19-JUN-1998; 98US-00900042P.

XX PR 19-JUN-1998; 98US-00900043P.

XX PR 19-JUN-1998; 98US-00900044P.

XX PR 19-JUN-1998; 98US-00900045P.

XX PR 19-JUN-1998; 98US-00900047P.

XX PR 19-JUN-1998; 98US-00900048P.

XX PR 19-JUN-1998; 98US-00900072P.

XX PR 19-JUN-1998; 98US-00900076P.

XX PR 19-JUN-1998; 98US-00900077P.

XX PR 19-JUN-1998; 98US-00900078P.

|||||

1 ATCCGCCTGC 10

(GENZ ) GENZYME CORP.  
(ROBE/) ROBERTS B L.  
(SHAN/) SHANKARA S.

Roberts BL, Shankara S;

WPI; 2000-106077/09.

Isolated polynucleotides differentially expressed in antigen-presenting  
cells, useful in gene vaccines against cancer.

Claim 1; Page 72; 130pp; English.

Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene  
expression) tags used to identify mRNA transcripts encoding  
immunostimulatory cofactor proteins which are preferentially or

CC differentially expressed in monocyte-derived dendritic cells compared  
CC with monocytes. Some of the transcripts correspond to known genes or ESTs  
CC (expressed sequence tags) which were previously unknown to be  
CC preferentially or differentially expressed in dendritic cells, while  
CC other transcripts correspond to novel genes. Antigen-presenting cell  
CC (APC)-associated costimulatory factors play an important role in the  
CC activation of the cytotoxic immune response, particularly against tumour  
CC cells. Tumour antigen presentation via the MHC (major histocompatibility  
CC complex) and subsequent recognition by T-cell receptors is alone  
CC insufficient to activate a robust cytotoxic immune response that can lyse  
CC the tumour cells, immunostimulatory cofactors also being required for  
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid  
CC sequences identified using the SAGE tags have several potential uses.  
CC They may be used in vaccines to induce an immune response, particularly  
CC against a tumour antigen; to modulate the genotype of an APC; to screen  
CC for agents that modulate expression of differentially expressed genes in  
CC an APC; and as hybridisation probes/amplification primers for the  
CC diagnosis, prognosis and monitoring of diseases related to abnormal  
CC expression of these genes. Detection of the dendritic cell differentially  
CC expressed genes, or of their encoded proteins, can be used to identify  
CC cells as belonging to the monocyte lineage. Cells containing these genes  
CC can be used in active immunotherapy (or to stimulate production of a  
CC population of antigen-specific effector cells) and vectors containing  
CC them are used in gene therapy. Co-administration of tumour antigens and  
CC APC-associated costimulatory factors ensures adequate antigen  
CC presentation to endogenous APCs and upregulates the APCs for the  
CC presentation of co-stimulatory signals, migration to T cell-rich sites,  
CC secretion of T cell growth factors and secretion of chemokines for  
CC recruitment of immune effector cells  
XX  
SQ Sequence 10 BP; 5 A; 3 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGT 17  
Db 10 CTGTCTGTGT 1

RESULT 253  
AAZ79150  
ID AAZ79150 standard; DNA; 10 BP.

XX AC AAZ79150;

XX DT 10-APR-2000 (first entry)

XX DE Human dendritic cell SAGE tag, SEQ ID NO:1578.

XX KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;  
KW APC; monocyte-derived dendritic cell; differential gene expression;  
KW immunostimulatory cofactor; costimulatory factor; CTL;  
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

XX OS Homo sapiens.

XX PN WO9965924-A2.

XX PD 23-DEC-1999.

XX PF 18-JUN-1999; 99WO-US013800.

XX PR 19-JUN-1998; 98US-0089833P.  
PR 19-JUN-1998; 98US-0089844P.  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089878P.  
PR 19-JUN-1998; 98US-0089991P.  
PR 19-JUN-1998; 98US-0089992P.  
PR 19-JUN-1998; 98US-0089993P.  
PR 19-JUN-1998; 98US-0089994P.  
PR 19-JUN-1998; 98US-0089997P.

PR 19-JUN-1998; 98US-0089999P.  
PR 19-JUN-1998; 98US-0090000P.  
PR 19-JUN-1998; 98US-0090035P.  
PR 19-JUN-1998; 98US-0090036P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
PR 19-JUN-1998; 98US-0090042P.  
PR 19-JUN-1998; 98US-0090043P.  
PR 19-JUN-1998; 98US-0090044P.  
PR 19-JUN-1998; 98US-0090045P.  
PR 19-JUN-1998; 98US-0090047P.  
PR 19-JUN-1998; 98US-0090048P.  
PR 19-JUN-1998; 98US-0090072P.  
PR 19-JUN-1998; 98US-0090076P.  
PR 19-JUN-1998; 98US-0090077P.  
PR 19-JUN-1998; 98US-0090078P.  
PR 19-JUN-1998; 98US-0090079P.  
PR 19-JUN-1998; 98US-0090080P.  
PR 08-DEC-1998; 98US-0111715P.

XX (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

PI  
XX WPI; 2000-106077/09.

PT Isolated polynucleotides differentially expressed in antigen-presenting  
PT cells, useful in gene vaccines against cancer.

XX Claim 1; Page 110; 130pp; English.

PS Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene  
XX expression) tags used to identify mRNA transcripts encoding  
CC immunostimulatory cofactor proteins which are preferentially or  
CC differentially expressed in monocyte-derived dendritic cells compared  
CC with monocytes. Some of the transcripts correspond to known genes or ESTs  
CC (expressed sequence tags) which were previously unknown to be  
CC preferentially or differentially expressed in dendritic cells, while  
CC other transcripts correspond to novel genes. Antigen-presenting cell  
CC (APC)-associated costimulatory factors play an important role in the  
CC activation of the cytotoxic immune response, particularly against tumour  
CC cells. Tumour antigen presentation via the MHC (major histocompatibility  
CC complex) and subsequent recognition by T-cell receptors is alone  
CC insufficient to activate a robust cytotoxic immune response that can lyse  
CC the tumour cells, immunostimulatory cofactors also being required for  
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid  
CC sequences identified using the SAGE tags have several potential uses.  
CC They may be used in vaccines to induce an immune response, particularly  
CC against a tumour antigen; to modulate the genotype of an APC; to screen  
CC for agents that modulate expression of differentially expressed genes in  
CC an APC; and as hybridisation probes/amplification primers for the  
CC diagnosis, prognosis and monitoring of diseases related to abnormal  
CC expression of these genes. Detection of the dendritic cell differentially  
CC expressed genes, or of their encoded proteins, can be used to identify  
CC cells as belonging to the monocyte lineage. Cells containing these genes  
CC can be used in active immunotherapy (or to stimulate production of a  
CC population of antigen-specific effector cells) and vectors containing  
CC them are used in gene therapy. Co-administration of tumour antigens and  
CC APC-associated costimulatory factors ensures adequate antigen  
CC presentation to endogenous APCs and upregulates the APCs for the  
CC presentation of co-stimulatory signals, migration to T cell-rich sites,  
CC secretion of T cell growth factors and secretion of chemokines for  
CC recruitment of immune effector cells  
XX  
SQ Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;





Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 TGTGTGACCT 22  
| | | | | | | | | |  
Db 1 TCTGTGACCT 10

RESULT 256  
AAZ83343/c  
ID AAZ83343 standard; DNA; 10 BP.  
XX  
AC AAZ83343;  
XX  
DT 07-APR-2000 (first entry)  
XX  
DE Metastatic breast tumour cell upregulated transcript tag #2577.  
XX  
DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX Homo sapiens.  
OS  
XX WO9965928-A2.  
PN  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013647.  
XX  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX  
XX (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106079/09.  
XX  
PT Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX  
PS Claim 1; Page 128; 219pp; English.  
XX  
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC vaccines; for diagnosing breast cancer and for raising specific  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
XX immunotherapy

SQ Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 GTGTGACCTG 23  
| | | | | | | | | |  
Db 10 GTATGACCTG 1

RESULT 257  
AAZ83792/c  
ID AAZ83792 standard; DNA; 10 BP.  
XX  
AC AAZ83792;  
XX  
DT 07-APR-2000 (first entry)  
XX  
DE Metastatic breast tumour cell upregulated transcript tag #3026.  
XX  
DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX Homo sapiens.  
OS  
XX WO9965928-A2.  
PN  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013647.  
XX  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX  
XX (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106079/09.  
XX  
PT Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX  
PS Claim 1; Page 140; 219pp; English.  
XX  
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC vaccines; for diagnosing breast cancer and for raising specific  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
XX immunotherapy



CC immunotherapy  
XX Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;  
SQ Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 4 TCCACCTGCT 13  
Db 10 TCCACCTGGT 1  
RESULT 258  
AAZ86544  
ID AAZ86544 standard; DNA; 10 BP.  
XX AAZ86544;  
AC AAZ86544;  
XX 07-APR-2000 (first entry)  
DT Metastatic breast tumour cell downregulated transcript tag #5778.  
DE  
XX  
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX Homo sapiens.  
OS  
XX WO9965928-A2.  
PN  
XX 23-DEC-1999.  
PD  
XX 18-JUN-1999; 99WO-US013647.  
PF  
XX 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX Roberts BL, Shankara S;  
PI  
XX WPI; 2000-106079/09.  
DR  
XX Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX Claim 1; Page 211; 219pp; English.  
PS  
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC vaccines; for diagnosing breast cancer and for raising specific  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand

CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy  
XX Sequence 10 BP; 1 A; 1 C; 4 G; 4 T; 0 U; 0 Other;  
SQ Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 13 TGTGTGACCT 22  
Db 1 TGTGTGAGCT 10  
RESULT 259  
AAZ81303  
ID AAZ81303 standard; DNA; 10 BP.  
XX AAZ81303;  
AC AAZ81303;  
XX 07-APR-2000 (first entry)  
DT Metastatic breast tumour cell upregulated transcript tag #537.  
DE  
XX  
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX Homo sapiens.  
OS  
XX WO9965928-A2.  
PN  
XX 23-DEC-1999.  
PD  
XX 18-JUN-1999; 99WO-US013647.  
PF  
XX 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX Roberts BL, Shankara S;  
PI  
XX WPI; 2000-106079/09.  
DR  
XX Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX Claim 1; Page 72; 219pp; English.  
PS  
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC vaccines; for diagnosing breast cancer and for raising specific  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand



XX DE Human macrophage gene Tag oligonucleotide sequence SEQ ID NO:258.  
XX KW Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag;  
KW granulocyte-macrophage colony-stimulating factor; characterisation;  
KW GM-CSF; identification; diagnosis; gene specificity; oncogenesis;  
KW disease onset mechanism; genetic disease; drug development; ss.  
XX OS Homo sapiens.  
XX PN WO200024892-A1.  
XX PD 04-MAY-2000.  
XX PF 28-OCT-1999; 99WO-JP005982.  
XX PR 28-OCT-1998; 98JP-00307532.  
XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
XX PI Hashimoto S, Matsushima K, Suzuki T;  
XX WPI; 2000-350734/30.  
XX CC Genes most frequently expressed in human monocytes and GM-macrophages and  
PT M-macrophages studied and with cDNAs characterized, for study of gene  
PT specificity, disease onset mechanism, drug development and diagnosis.  
XX PS Claim 13; Page 90; 138pp; Japanese.  
XX CC The present invention describes 100 human genes, which are expressed most  
CC frequently in human monocytes. The cDNA of each gene has a sequence fully  
CC defined in the specification, and lacking the CATG sequence located  
CC adjacent to polyA region. Also described are: (1) an antibody  
CC specifically for the protein encoded by any of the genes; (2)  
CC oligonucleotides obtained from the cDNA sequences; (3) 380 human genes  
CC which are expressed most frequently in human macrophages, differentiated  
CC from human monocytes by granulocyte-macrophage colony-stimulating factor,  
CC the cDNA of each gene has a fully defined sequence, given in the  
CC specification, lacking the base sequence CATG located most closely to the  
CC poly A region; (4) an antibody specifically for the protein encoded by  
CC any of the genes of (3); and (5) oligonucleotides obtained from the cDNA  
CC sequences of (3). The genes and cDNAs, are used for the study of gene  
CC specificity and disease onset mechanism e.g. oncogenesis, genetic  
CC diseases, drug development and diagnosis. AAA56107 to AAA56586 represent  
CC specifically claimed oligonucleotide tag sequences for human genes  
CC expressed in monocytes and macrophages  
XX SQ Sequence 10 BP; 5 A; 3 C; 2 G; 0 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 8 CCTGCTGTGT 17  
Db 10 CTTGCTGTGT 1  
  
RESULT 263  
AAZ91928/c  
ID AAZ91928 standard; DNA; 10 BP.  
XX AC AAZ91928;  
XX DT 08-JUN-2000 (first entry)  
XX DE PCR primer for murine mahogany protein genomic sequence.  
XX KW Mahogany gene; mouse; mg gene; regulatory defect; gene therapy; obesity;  
KW weight regulation; cell therapy; body weight disorder; cachexia;  
KW anorexia; hyperpigmentation; increased metabolic rate disorder;  
KW hyperphagia; Antiobesity; antianorexic; anticachexic; PCR primer; ss.

XX OS Mus sp.  
XX PN WO200005373-A2.  
XX PD 03-FEB-2000.  
XX PF 21-JUL-1999; 99WO-US016484.  
XX PR 21-JUL-1998; 98US-0093630P.  
XX PR 20-OCT-1998; 98US-0104978P.  
XX PR 05-FEB-1999; 99US-00245041.  
XX PA (MILL-) MILLENIUM PHARM INC.  
XX PI Moore K, Nagle DL;  
XX WPI; 2000-195103/17.  
XX PT New human and murine mahogany genes, useful, e.g. for diagnosis and  
PT treatment of body weight disorders.  
XX PS Example; Page 83; 188pp; English.  
XX CC This sequence represents a PCR primer for a murine mahogany gene of the  
CC invention. The mahogany genes are used: (i) to produce recombinant  
CC mahogany (mg) proteins (II); (ii) as a source of antisense, ribozyme or  
CC triplex-forming therapeutics; (iii) as a source of diagnostic probes and  
CC primers for detecting expression of mg genes or mutations, regulatory  
CC defects, in this gene, or for isolation of related sequences; and (iv) in  
CC (cell-based) gene therapy. (II) are used to raise specific antibodies  
CC (Ab); to identify other (extra)cellular products involved in weight  
CC regulation, and to screen for agents that disrupt interaction between  
CC (II) and other macromolecules. The Ab are used to detect abnormal levels  
CC (or function) of (II) (for diagnosis, prognosis or monitoring of  
CC treatment); to evaluate (II)-expressing cells intended for cell therapy,  
CC and as therapeutic mg inhibitors. Cells that express the mg gene (or  
CC contain the mg polypeptide) are used to identify agents (A) that modulate  
CC mg activity. (A) are potentially useful for the treatment of body weight  
CC disorders, particularly obesity, cachexia or anorexia, or other  
CC conditions associated with the mg gene such as hyperpigmentation,  
CC hyperphagia and disorders that result in increased metabolic rate  
XX SQ Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 12 CTGTGTGACC 21  
Db 10 CTGTGTGTCC 1  
  
RESULT 264  
AAH18978  
ID AAH18978 standard; DNA; 10 BP.  
XX AC AAH18978;  
XX DT 21-JUN-2001 (first entry)  
XX DE UCP3 polymorphism detection allele specific primer #91.  
XX KW UCP3; uncoupling protein 3; polymorphism; obesity; diabetes mellitus; ss.  
XX OS Homo sapiens.  
XX PN WO200118232-A2.  
XX PD 15-MAR-2001.  
XX PF 08-SEP-2000; 2000WO-US024784.

XX PR 08-SEP-1999; 99US-0152789P.  
XX PA (GENA-) GENAISSANCE PHARM INC.  
PA (STEP/) STEPHENS J C.  
XX PI Chew A, Choi JY, Denton RR, Nandabalan K;  
XX WPI; 2001-218562/22.  
XX Nucleic acids encoding uncoupling protein 3 (mitochondrial, proton carrier) (UCP3) proteins comprising single nucleotide polymorphisms, useful for the design of drugs for treating obesity.  
PS Disclosure; Page 23; 94pp; English.  
XX The present invention relates to the human uncoupling protein 3 (mitochondrial, proton carrier) (UCP3) gene and polymorphisms. The polymorphisms are associated with obesity, especially diabetes mellitus associated obesity. They polymorphisms may be identified and analysed to determine whether an individual is susceptible to obesity and may be used as the basis for targeted design of drugs to treat obesity. The present sequence was used in the identification and amplification of UCP3 polymorphisms  
XX Sequence 10 BP; 1 A; 6 C; 1 G; 2 T; 0 U; 0 Other;  
SQ Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 5 CCACCTGCTG 14  
Db 1 CCACCTCCTG 10  
RESULT 265  
AAH19943  
ID AAH19943 standard; DNA; 10 BP.  
XX AAH19943;  
XX 07-AUG-2001 (first entry)  
XX Mouse Treg immunoregulatory network related tag #14.  
DE Mouse; EST; expressed sequence tag; contig; immunoregulation;  
XX immunosuppression; Treg immunoregulatory network; inflammatory;  
KW immune disorder; T regulatory lymphocyte; T helper cell; dermatological;  
KW antiinflammatory; immunosuppressive; antiarteriosclerotic; antiallergic;  
KW antidiabetic; neuroprotective; osteopathic; antiarthritic; anti-ulcer;  
KW rheumatoid arthritis; osteoarthritis; glomerular nephritis; diabetes;  
KW inflammatory bowel disease; vascular disease; atherosclerosis; psoriasis;  
KW vasculitis; skin disease; dermatitis; Crohn's disease; lung disease;  
KW ulcerative colitis; lupus erythematosus; autoimmune disorder; emphysema;  
KW hypersensitivity; multiple sclerosis; chronic bronchitis; asthma;  
KW idiopathic pulmonary fibrosis; primer; probe; tag; ss.  
XX Mus musculus.  
OS Synthetic.  
XX WO200127267-A2.  
PN 19-APR-2001.  
XX 06-OCT-2000; 2000WO-GB003821.  
PF 08-OCT-1999; 99GB-00023790.  
XX (ISIS-) ISIS INNOVATION LTD.  
XX Adams E, Waldmann H, Cobbold S, Zelenika D;  
PI

DR WPI; 2001-300216/31.  
XX Isolated genes differentially expressed in T helper 1 (Th1) and 2 (Th2) and T regulatory (Treg) lymphocytes useful in prophylaxis, diagnosis and therapy of inflammatory and immune diseases.  
XX Example 4; Page 4; 29pp; English.  
PS The present invention describes an isolated gene (I) obtainable by: (a) comparing the expression of one or more genes in populations of T helper 1 lymphocytes (Th1)-, Th2- and T regulatory cells (Treg)-enriched cell populations to identify a gene which is differentially expressed in the populations; and (b) isolating the gene. (I) can have dermatological, antiinflammatory, immunosuppressive, antiarteriosclerotic, antiallergic, antidiabetic, neuroprotective, osteopathic, antiarthritic and anti-ulcer activities. (I) can be used in anti-inflammatory and immunoregulatory compositions for use in therapy, prophylaxis, or diagnosis and/or in a pharmaceutical excipient, a unit dosage form or in a form suitable for local or systemic administration. Methods from the present invention can be used for detecting Th1 and/or Th2 and/or Treg cells in a biological sample, for cell typing or for determining the number of Th1 and/or Th2 and/or Treg cells in a biological sample. Diseases which may be treated by compositions of the invention include rheumatoid and osteoarthritis, glomerular nephritis, diabetes, inflammatory bowel disease, vascular diseases e.g. atherosclerosis and vasculitis, skin diseases such as psoriasis and dermatitis, Crohn's disease, ulcerative colitis, lupus erythematosus, autoimmune disorders, hypersensitivity, multiple sclerosis, and lung diseases e.g. chronic bronchitis, emphysema, idiopathic pulmonary fibrosis and asthma. (I) can also be used as markers for analysis of serum, urine and biopsy, particularly during and after therapy for multiple sclerosis. AAH19930 to AAH20034 and AAH75133 represent sequence used in the exemplification of the present invention  
XX Sequence 10 BP; 0 A; 2 C; 3 G; 5 T; 0 U; 0 Other;  
SQ Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 9 CTGCTGTGTG 18  
Db 1 CTGCTTGTG 10  
RESULT 266  
AAI67394  
ID AAI67394 standard; DNA; 10 BP.  
XX AAI67394;  
AC AAI67394;  
XX 11-FEB-2002 (first entry)  
DT Human FKBP8 gene polymorphism detecting primer.  
XX FK506-binding protein 8; FKBP8; haplotyping; polymorphism; cancer;  
DE immunosuppression; human; primer; ss.  
KW Homo sapiens.  
XX WO200172965-A2.  
PN 04-OCT-2001.  
XX 26-MAR-2001; 2001WO-US009718.  
PF 24-MAR-2000; 2000US-0192125P.  
PR (GENA-) GENAISSANCE PHARM INC.  
XX Anastasio AE, Bentivegna SC, Choi JY, Kliem SE, Koshy B;  
PI Stephens JC;  
XX WPI; 2001-626261/72.  
DR



XX New haplotypes of the FK506-binding protein 8 gene, useful for genotyping  
PT that gene in individual and to design new therapy for associated disease  
PT such as immunosuppression and cancer.  
XX  
PS Claim 16; Page 15; 98pp; English.  
XX  
CC The invention relates to haplotyping the FK506-binding protein 8 (38kD)  
CC (FKBP8) gene in an individual. The method involves determining the  
CC identity of the nucleotide pair at one or more polymorphic sites selected  
CC from P1 to P26 ( described in the specification). The invention is useful  
CC to improve the efficiency and reliability of several steps in the  
CC discovery and development of drugs for treating diseases associated with  
CC FKBP8 activity, for example immunosuppression and cancer. Sequences  
CC AAI67352-403 represent oligonucleotide primers for detecting FKBP8 gene  
CC polymorphisms by primer extension techniques  
XX  
SQ Sequence 10 BP; 0 A; 2 C; 5 G; 3 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 15 TGTGACCTGG 24  
Db 1 TGTGGCCTGG 10  
  
RESULT 267  
AAH63201  
ID AAH63201 standard; cDNA; 10 BP.  
XX  
AC AAH63201;  
XX  
DT 20-SEP-2001 (first entry)  
XX  
DE Human colon epithelium specific transcriptome sequence SEQ ID NO: 41.  
XX  
KW Human; transcriptome; gene expression pattern; cancer; drug screening;  
KW cancer diagnosis; cell specific gene expression; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200138577-A2.  
XX  
PD 31-MAY-2001.  
XX  
PF 21-NOV-2000; 2000WO-US031922.  
XX  
PR 24-NOV-1999; 99US-00448480.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu VE, Vogelstein B, Kinzler KW;  
XX  
DR WPI; 2001-367706/38.  
XX  
PD 31-MAY-2001.  
XX  
PF 21-NOV-2000; 2000WO-US031922.  
XX  
PR 24-NOV-1999; 99US-00448480.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu VE, Vogelstein B, Kinzler KW;  
XX  
DR WPI; 2001-367706/38.  
XX  
PT New isolated polynucleotides, useful for identifying specific cell type,  
PT such as cancer cell, comprises transcriptomes expressed in particular  
PT cell types.  
XX  
PS Claim 1; Page 39; 94pp; English.  
XX  
CC The present invention describes a method of identifying the type of cell  
CC in a sample, involving determining which of the sequences AAH63161-  
CC AAH64724 is expressed by the cell. The transcriptomes described in the  
CC invention are cell-type specific, cancer specific or ubiquitously  
CC expressed in humans. They can also be used to screen for drugs, reduce  
CC cancer specific gene expression, standardise expression and restore the  
CC function of a diseased cell or tissue. The present sequence is one of the  
CC transcriptomes described in the exemplification of the invention  
XX  
SQ Sequence 10 BP; 0 A; 4 C; 3 G; 3 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 15 TGTGACCTGG 24  
Db 1 TGTGGCCTGG 10  
  
RESULT 267  
AAH63201  
ID AAH63201 standard; cDNA; 10 BP.  
XX  
AC AAH63201;  
XX  
DT 20-SEP-2001 (first entry)  
XX  
DE Human colon epithelium specific transcriptome sequence SEQ ID NO: 41.  
XX  
KW Human; transcriptome; gene expression pattern; cancer; drug screening;  
KW cancer diagnosis; cell specific gene expression; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200138577-A2.  
XX  
PD 31-MAY-2001.  
XX  
PF 21-NOV-2000; 2000WO-US031922.  
XX  
PR 24-NOV-1999; 99US-00448480.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu VE, Vogelstein B, Kinzler KW;  
XX  
DR WPI; 2001-367706/38.  
XX  
PT New isolated polynucleotides, useful for identifying specific cell type,  
PT such as cancer cell, comprises transcriptomes expressed in particular  
PT cell types.  
XX  
PS Claim 1; Page 39; 94pp; English.  
XX  
CC The present invention describes a method of identifying the type of cell  
CC in a sample, involving determining which of the sequences AAH63161-  
CC AAH64724 is expressed by the cell. The transcriptomes described in the  
CC invention are cell-type specific, cancer specific or ubiquitously  
CC expressed in humans. They can also be used to screen for drugs, reduce  
CC cancer specific gene expression, standardise expression and restore the  
CC function of a diseased cell or tissue. The present sequence is one of the  
CC transcriptomes described in the exemplification of the invention  
XX  
SQ Sequence 10 BP; 0 A; 4 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 12 CTGTGTGACC 21  
Db 1 CTGTGTGCCC 10  
  
RESULT 268  
AAH63192  
ID AAH63192 standard; cDNA; 10 BP.  
XX  
AC AAH63192;  
XX  
DT 20-SEP-2001 (first entry)  
XX  
DE Human colon epithelium specific transcriptome sequence SEQ ID NO: 32.  
XX  
KW Human; transcriptome; gene expression pattern; cancer; drug screening;  
KW cancer diagnosis; cell specific gene expression; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200138577-A2.  
XX  
PD 31-MAY-2001.  
XX  
PF 21-NOV-2000; 2000WO-US031922.  
XX  
PR 24-NOV-1999; 99US-00448480.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu VE, Vogelstein B, Kinzler KW;  
XX  
DR WPI; 2001-367706/38.  
XX  
PT New isolated polynucleotides, useful for identifying specific cell type,  
PT such as cancer cell, comprises transcriptomes expressed in particular  
PT cell types.  
XX  
PS Claim 1; Page 39; 94pp; English.  
XX  
CC The present invention describes a method of identifying the type of cell  
CC in a sample, involving determining which of the sequences AAH63161-  
CC AAH64724 is expressed by the cell. The transcriptomes described in the  
CC invention are cell-type specific, cancer specific or ubiquitously  
CC expressed in humans. They can also be used to screen for drugs, reduce  
CC cancer specific gene expression, standardise expression and restore the  
CC function of a diseased cell or tissue. The present sequence is one of the  
CC transcriptomes described in the exemplification of the invention  
XX  
SQ Sequence 10 BP; 0 A; 4 C; 3 G; 3 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 12 CTGTGTGACC 21  
Db 1 CTGTGTGCCC 10  
  
RESULT 269  
AAH63266  
ID AAH63266 standard; cDNA; 10 BP.  
XX  
AC AAH63266;  
XX  
DT 20-SEP-2001 (first entry)  
XX



DE Human colon epithelium specific transcriptome sequence SEQ ID NO: 106.  
XX  
KW Human; transcriptome; gene expression pattern; cancer; drug screening;  
KW cancer diagnosis; cell specific gene expression; ss.  
OS Homo sapiens.  
XX  
PN WO200138577-A2.  
XX  
PD 31-MAY-2001.  
XX  
PF 21-NOV-2000; 2000WO-US031922.  
XX  
PR 24-NOV-1999; 99US-00448480.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu VE, Vogelstein B, Kinzler KW;  
DR WPI; 2001-367706/38.  
XX  
PT New isolated polynucleotides, useful for identifying specific cell type,  
PT such as cancer cell, comprises transcriptomes expressed in particular  
PT cell types.  
XX  
PS Claim 13; Page 41; 94pp; English.  
XX  
CC The present invention describes a method of identifying the type of cell  
CC in a sample, involving determining which of the sequences AAH63161-  
CC AAH64724 is expressed by the cell. The transcriptomes described in the  
CC invention are cell-type specific, cancer specific or ubiquitously  
CC expressed in humans. They can also be used to screen for drugs, reduce  
CC cancer specific gene expression, standardise expression and restore the  
CC function of a diseased cell or tissue. The present sequence is one of the  
CC transcriptomes described in the exemplification of the invention  
XX  
SQ Sequence 10 BP; 0 A; 3 C; 3 G; 4 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 12 CTGTGTGACC 21  
Db 1 CTGTGTGTCC 10  
  
RESULT 270  
AAH63751  
ID AAH63751 standard; cDNA; 10 BP.  
XX  
AC AAH63751;  
XX  
DT 20-SEP-2001 (first entry)  
XX  
DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 591.  
XX  
KW Human; transcriptome; gene expression pattern; cancer; drug screening;  
KW cancer diagnosis; cell specific gene expression; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200138577-A2.  
XX  
PD 31-MAY-2001.  
XX  
PF 21-NOV-2000; 2000WO-US031922.  
XX  
PR 24-NOV-1999; 99US-00448480.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu VE, Vogelstein B, Kinzler KW;

XX WPI; 2001-367706/38.  
DR  
XX New isolated polynucleotides, useful for identifying specific cell type,  
PT such as cancer cell, comprises transcriptomes expressed in particular  
PT cell types.  
XX  
PS Claim 13; Page 52; 94pp; English.  
XX  
CC The present invention describes a method of identifying the type of cell  
CC in a sample, involving determining which of the sequences AAH63161-  
CC AAH64724 is expressed by the cell. The transcriptomes described in the  
CC invention are cell-type specific, cancer specific or ubiquitously  
CC expressed in humans. They can also be used to screen for drugs, reduce  
CC cancer specific gene expression, standardise expression and restore the  
CC function of a diseased cell or tissue. The present sequence is one of the  
CC transcriptomes described in the exemplification of the invention  
XX  
SQ Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 9 CTGCTGTGTG 18  
Db 1 CTGCTGAGTG 10  
  
RESULT 271  
AAH32787  
ID AAH32787 standard; cDNA; 10 BP.  
XX  
AC AAH32787;  
XX  
DT 13-AUG-2001 (first entry)  
XX  
DE LPS activated human monocyte expression gene cDNA tag SEQ:160.  
XX  
KW Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;  
KW expressed sequence tag; diagnosis; human disease; treatment; ss.  
XX  
OS Homo sapiens.  
XX  
PN JP2001069993-A.  
XX  
PD 21-MAR-2001.  
XX  
PF 28-APR-2000; 2000JP-00131079.  
XX  
PR 08-JUL-1999; 99JP-00195103.  
XX  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX  
DR WPI; 2001-304369/32.  
XX  
PT LPS activated human monocyte expression gene group.  
XX  
PS Claim 10; Page 31; 52pp; Japanese.  
XX  
CC The present invention describes an lipopolysaccharide (LPS) activated  
CC human monocyte expression gene group consisting of the high-ranking 50  
CC genes of the highest expression among the genes expressed by human  
CC monocyte stimulated by LPS in which the cDNA of each gene has the base  
CC sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-  
CC CATG-3' nearest to the polyA region. The gene group is useful for the  
CC development of new means for the diagnosis and the treatment of various  
CC human diseases in which human monocyte plays an important role. AAH32628  
CC to AAH32943 represent specifically claimed LPS activated human monocyte  
CC expression gene cDNA tags from the present invention. AAH32944 represents  
CC an LPS activated human monocyte expression gene cDNA sequence encoding  
CC AAB98009, which are given in the exemplification of the present invention  
XX

SQ Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTGCTGTGTG 18  
|||||  
Db 1 CTGCTATGTG 10

RESULT 272  
AAH41694

ID AAH41694 standard; DNA; 10 BP.  
XX  
AC AAH41694;  
XX  
DT 28-AUG-2001 (first entry)  
XX  
DE Anti-PEP gene construction related oligonucleotide S3.  
XX  
KW Phosphoenopyruvate carboxylase; PEPCase; seed; acetyl-CoA carboxylase;  
KW oilseed; PEP; plant breeding; soya bean; sunflower; rapeseed; peanut;  
KW sesame; crop plant; protein content; fatty acid content; anti-PEP; ss.  
XX  
OS Synthetic.  
XX  
PN WO200134812-A1.  
XX  
PD 17-MAY-2001.  
XX  
PF 06-NOV-2000; 2000WO-CN000418.  
XX  
PR 09-NOV-1999; 99CN-00124511.  
XX  
PA (ZHEJ-) ZHEJIANG AGRIC SCI ACAD.  
XX  
PI Chen J, Lang C, Huang R, Hu Z, Liu Z;  
XX  
DR WPI; 2001-335934/35.  
XX  
PT Altering protein/fatty acid composition of seeds, useful for producing  
PT e.g. soya bean or sesame seed with high protein/fatty acid content,  
PT comprises introducing antisense gene.  
XX  
PS Example 8; Page 8; 25pp; Chinese.  
XX  
CC The present invention describes a method for altering the protein/fatty  
CC acid composition of seeds. The method comprises: (1) cloning  
CC phosphoenopyruvate carboxylase (PEP) or acetyl-CoA carboxylase (ACC)  
CC genes or their fragments; (2) constructing the corresponding antisense  
CC gene of anti-PEP or anti-ACC; and (3) introducing the antisense gene into  
CC the plant cell of a crop. The method is applicable in plant breeding to  
CC give oilseed crops with high oil or protein content like soya bean,  
CC sunflower, rapeseed, peanut and sesame. The produced crop plants have  
CC high yield of oil or protein. The present sequence represents an  
CC oligonucleotide which is used in the construction of an anti-PEP gene in  
CC an example from the present invention  
XX  
SQ Sequence 10 BP; 1 A; 6 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATCCACCTG 11  
|||||  
Db 1 CATCCCCCTG 10

RESULT 273  
ABA06109/c

ID ABA06109 standard; cDNA; 10 BP.

XX ABA06109;  
AC  
XX 10-JAN-2002 (first entry)  
DT  
XX Human normal hepatocyte expression gene cDNA, SEQ ID NO: 86.  
DE  
XX Human; hepatocyte; gene expression; hepatopathy; ss.  
KW  
XX Homo sapiens.  
OS  
XX JP2001211883-A.  
PN  
PD 07-AUG-2001.  
XX  
PF 31-JAN-2000; 2000JP-00023170.  
XX  
PR 31-JAN-2000; 2000JP-00023170.  
XX  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX  
DR WPI; 2001-629566/73.  
XX  
PT Human normal hepatocyte expression gene group.  
XX  
PS Claim 1; Page 7; 26pp; Japanese.  
XX  
CC The invention relates to a human normal hepatocyte expression gene group  
CC comprising 200 genes in the human normal hepatocyte. The cDNA of each  
CC gene comprises one of 200 fully defined nucleotide sequences as given in  
CC the specification. The gene group and the cDNAs corresponding to each of  
CC the genes in the group are useful in the diagnosis and treatment of human  
CC hepatopathy. The present sequence is a cDNA corresponding to a gene  
CC expressed by normal human hepatocytes  
XX  
SQ Sequence 10 BP; 5 A; 3 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGT 17  
| | | | | | | |  
Db 10 CTTGCTGTGT 1

RESULT 274  
AAF69625

ID AAF69625 standard; DNA; 10 BP.  
XX  
AC AAF69625;  
XX  
DT 18-APR-2001 (first entry)  
XX  
DE Human IL4Ralpha gene probe #265.  
XX  
KW Polymorphism; human; interleukin 4 receptor-alpha; IL4R-alpha;  
KW allergic disease; probe; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200104270-A1.  
XX  
PD 18-JAN-2001.  
XX  
PF 13-JUL-2000; 2000WO-US019094.  
XX  
PR 13-JUL-1999; 99US-0143435P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;  
PI Windemuth AK;

XX WPI; 2001-103078/11.  
DR  
XX  
PT New isolated polynucleotide useful for the identification of therapeutics  
in allergic diseases is new.  
XX  
PS Disclosure; Page 46; 188pp; English.  
XX  
CC The present invention relates to polymorphisms of the human interleukin 4  
receptor-alpha gene (IL4R-alpha; see AAF57718 for the reference  
sequence). Polynucleotides comprising polymorphic gene variants are  
useful for therapeutic purposes. For example, where a patient may benefit  
from expression of a particular IL4Ralpha protein isoform, an expression  
vector encoding the isoform may be administered to the patient. It may  
be desirable to decrease or block expression of a particular IL4Ralpha  
isogene, which may be done by turning off by transforming a targeted  
organ, tissue or cell population with an expression vector that expresses  
high levels of untranslatable mRNA for the isogene. Specific therapeutics  
identified by these methods may be useful for allergic diseases. The  
present sequence is a probe for human IL4R-alpha  
XX  
SQ Sequence 10 BP; 3 A; 4 C; 1 G; 2 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 ATCCACCTGC 12  
Db 1 ATACACCTGC 10  
  
RESULT 275  
AAF34164/c  
ID AAF34164 standard; DNA; 10 BP.  
XX  
AC AAF34164;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:903.  
XX  
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN WO200077214-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016223.  
XX  
PR 16-JUN-1999; 99US-00335032.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu V, Vogelstein B, Kinzler K;  
XX WPI; 2001-061874/07.  
DR  
XX  
PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
PS Example; Page 32; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC described are: (1) a method (M1) of using NORF genes to affect the cell  
cycle comprising administering a NORF gene whose expression varies by at  
least 10% between any two phases of the cell cycle selected from log  
phase, S phase and G2/M; (2) a method (M2) for screening candidate  
antifungal drugs comprising: (a) contacting a test substance with a yeast  
cell; and (b) monitoring expression of a NORF gene whose expression  
varies as in M1, where a test substance which modifies the expression of  
the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
identifying human genes which are involved in cell cycle progression  
comprising contacting human DNA with a probe which comprises at least 10  
contiguous nucleotides of a NORF gene whose expression varies as in M1;  
and (4) a method (M4) for identifying a candidate drug as a member of a  
class of drugs having a characteristic effect on gene expression in a  
yeast cell comprising contacting a yeast cell with a candidate drug and  
monitoring expression in the yeast cell of at least 1 NORF gene whose  
expression is affected by the class of drugs. The NORF genes may be used  
to study, monitor and affect phases of the cell cycle, the differentially  
expressed genes may be used as markers of phases of the cell cycle. The  
methods may be used to identify candidate drugs which affect the cell  
cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 2 A; 2 C; 1 G; 5 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 19 ACCTGGTAAA 28  
Db 10 AACTGGTAAA 1  
  
RESULT 276  
AAF35667  
ID AAF35667 standard; DNA; 10 BP.  
XX  
AC AAF35667;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2406.  
XX  
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN WO200077214-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016223.  
XX  
PR 16-JUN-1999; 99US-00335032.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu V, Vogelstein B, Kinzler K;  
XX WPI; 2001-061874/07.  
DR  
XX  
PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
PS Example; Page 85; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising nucleotides of a NORF gene whose expression varies at least 10  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 2 A; 5 C; 0 G; 3 T; 0 U; 0 Other;  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 4 TCCACCTGCT 13  
Db 1 TCCACCTACT 10  
RESULT 277  
AAF35804/c  
ID AAF35804 standard; DNA; 10 BP.  
XX  
AC AAF35804;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2543.  
XX  
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN WO200077214-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016223.  
XX  
PR 16-JUN-1999; 99US-00335032.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu V, Vogelstein B, Kinzler K;  
XX  
DR WPI; 2001-061874/07.  
XX  
XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX

PS Example; Page 90; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 13 TGTGTGACCT 22  
Db 10 TGTCTGACCT 1  
RESULT 278  
AAF44017/c  
ID AAF44017 standard; DNA; 10 BP.  
XX  
AC AAF44017;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:12156.  
XX  
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN WO200077214-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016223.  
XX  
PR 16-JUN-1999; 99US-00335032.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu V, Vogelstein B, Kinzler K;  
XX  
DR WPI; 2001-061874/07.  
XX  
XX Yeast gene coding sequences comprising NORF genes with serial analysis of



PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
PS Example; Page 384; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 1 A; 2 C; 2 G; 5 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 19 ACCTGGTAAA 28  
Db 10 ACCTGGAAAA 1  
  
RESULT 279  
AAF43467/c  
ID AAF43467 standard; DNA; 10 BP.  
XX  
AC AAF43467;  
XX  
XX 23-MAR-2001 (first entry)  
XX  
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11606.  
XX  
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN WO200077214-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016223.  
XX  
PR 16-JUN-1999; 99US-00335032.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu V, Vogelstein B, Kinzler K;

DR WPI; 2001-061874/07.  
XX  
PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
PS Example; Page 364; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 3 A; 3 C; 1 G; 3 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 18 GACCTGGTAA 27  
Db 10 GACTTGGTAA 1  
  
RESULT 280  
AAF34829  
ID AAF34829 standard; DNA; 10 BP.  
XX  
AC AAF34829;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1568.  
XX  
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN WO200077214-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016223.  
XX  
PR 16-JUN-1999; 99US-00335032.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.



XX PI Velculescu V, Vogelstein B, Kinzler K;  
XX DR WPI; 2001-061874/07.  
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX PS Example; Page 56; 419pp; English.  
XX CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX SQ Sequence 10 BP; 1 A; 1 C; 3 G; 5 T; 0 U; 0 Other;  
SQ Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 10 TGCTGTGTGA 19  
Db 1 TTCTGTGTGA 10  
RESULT 281  
AAF35820  
ID AAF35820 standard; DNA; 10 BP.  
XX AC AAF35820;  
XX DT 23-MAR-2001 (first entry)  
XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2559.  
XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX OS Saccharomyces cerevisiae.  
XX PN WO200077214-A2.  
XX PD 21-DEC-2000.  
XX PF 14-JUN-2000; 2000WO-US016223.  
XX

PR 16-JUN-1999; 99US-00335032.  
XX PA (UYJO ) UNIV JOHNS HOPKINS.  
XX PI Velculescu V, Vogelstein B, Kinzler K;  
XX DR WPI; 2001-061874/07.  
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX PS Example; Page 91; 419pp; English.  
XX CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX SQ Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;  
SQ Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 ATCCACCTGC 12  
Db 1 ATCCACTTGC 10  
RESULT 282  
AAF35485/c  
ID AAF35485 standard; DNA; 10 BP.  
XX AC AAF35485;  
XX DT 23-MAR-2001 (first entry)  
XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2224.  
XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX OS Saccharomyces cerevisiae.  
XX PN WO200077214-A2.  
XX PD 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.  
PF 16-JUN-1999; 99US-00335032.  
XX (UYJO ) UNIV JOHNS HOPKINS.  
XX Velculescu V, Vogelstein B, Kinzler K;  
PI WPI; 2001-061874/07.  
XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX Example; Page 79; 419pp; English.  
XX The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 CCATCCACCT 10  
Db 10 CCATCAACCT 1  
  
RESULT 283  
ABL42879  
ID ABL42879 standard; cDNA; 10 BP.  
XX ABL42879;  
AC  
XX 12-APR-2002 (first entry)  
DT Human maturation/activation dendritic cell expression gene tag #253.  
DE  
XX Human; maturation/activation dendritic cell expression gene; tag;  
KW maturation; activation; dendritic cell; ss.  
XX Homo sapiens.  
OS  
XX JP2001327293-A.  
PN  
XX

PD 27-NOV-2001.  
XX 22-MAY-2000; 2000JP-00150562.  
PF 22-MAY-2000; 2000JP-00150562.  
PR 22-MAY-2000; 2000JP-00150562.  
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
PA WPI; 2002-127070/17.  
XX Human maturation/activation dendritic cell expression gene group.  
PT Claim 19; Page 16; 41pp; Japanese.  
XX The present invention describes a human maturation/activation dendritic  
CC cell (DC) expression gene group consisting of 100 genes which show the  
CC highest expression among the genes expressed in human maturation/  
CC activation DC. Also described are: (1) a protein expressed by the above  
CC human maturation/activation DC expression gene; (2) an antibody against  
CC the protein; and (3) an antagonist against the expression of each gene  
CC belonging to the above gene group. The gene group is useful for the  
CC treatment and the diagnosis of various human diseases related to human  
CC DC. ABL42627 to ABL42926 represent specifically claimed human  
CC maturation/activation DC expression gene tags from the present invention  
XX  
SQ Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 12 CTGTGTGACC 21  
Db 1 CTGTGAGACC 10  
  
RESULT 284  
ABL42726  
ID ABL42726 standard; cDNA; 10 BP.  
XX ABL42726;  
AC  
XX 12-APR-2002 (first entry)  
DT Human maturation/activation dendritic cell expression gene tag #100.  
DE  
XX Human; maturation/activation dendritic cell expression gene; tag;  
KW maturation; activation; dendritic cell; ss.  
XX Homo sapiens.  
OS  
XX JP2001327293-A.  
PN  
XX 27-NOV-2001.  
PD  
XX 22-MAY-2000; 2000JP-00150562.  
PF  
XX 22-MAY-2000; 2000JP-00150562.  
PR (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX WPI; 2002-127070/17.  
DR Human maturation/activation dendritic cell expression gene group.  
XX Claim 1; Page 10; 41pp; Japanese.  
XX The present invention describes a human maturation/activation dendritic  
CC cell (DC) expression gene group consisting of 100 genes which show the  
CC highest expression among the genes expressed in human maturation/  
CC activation DC. Also described are: (1) a protein expressed by the above  
CC human maturation/activation DC expression gene; (2) an antibody against  
CC the protein; and (3) an antagonist against the expression of each gene  
CC

CC belonging to the above gene group. The gene group is useful for the  
CC treatment and the diagnosis of various human diseases related to human  
CC DC. ABL42627 to ABL42926 represent specifically claimed human  
CC maturation/activation DC expression gene tags from the present invention  
XX  
SQ Sequence 10 BP; 4 A; 3 C; 2 G; 1 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 19 ACCTGGTAAA 28  
|||||  
Db 1 ACCTGGCAAA 10  
  
RESULT 285  
ABL42777  
ID ABL42777 standard; cDNA; 10 BP.  
XX  
AC ABL42777;  
XX  
DT 12-APR-2002 (first entry)  
XX Human maturation/activation dendritic cell expression gene tag #151.  
DE  
DE Human; maturation/activation dendritic cell expression gene; tag;  
KW maturation; activation; dendritic cell; ss.  
KW Homo sapiens.  
XX  
XX JP2001327293-A.  
XX 27-NOV-2001.  
XX  
XX 22-MAY-2000; 2000JP-00150562.  
XX  
XX 22-MAY-2000; 2000JP-00150562.  
XX  
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX  
DR WPI; 2002-127070/17.  
XX Human maturation/activation dendritic cell expression gene group.  
PS Claim 10; Page 13; 4lpp; Japanese.  
XX  
XX The present invention describes a human maturation/activation dendritic  
CC cell (DC) expression gene group consisting of 100 genes which show the  
CC highest expression among the genes expressed in human maturation/  
CC activation DC. Also described are: (1) a protein expressed by the above  
CC human maturation/activation DC expression gene; (2) an antibody against  
CC the protein; and (3) an antagonist against the expression of each gene  
CC belonging to the above gene group. The gene group is useful for the  
CC treatment and the diagnosis of various human diseases related to human  
CC DC. ABL42627 to ABL42926 represent specifically claimed human  
CC maturation/activation DC expression gene tags from the present invention  
XX  
SQ Sequence 10 BP; 4 A; 3 C; 2 G; 1 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 19 ACCTGGTAAA 28  
|||||  
Db 1 ACCTGGCAAA 10  
  
RESULT 286  
ABL42899  
ID ABL42899 standard; cDNA; 10 BP.  
XX

AC ABL42899;  
XX  
DT 12-APR-2002 (first entry)  
XX Human maturation/activation dendritic cell expression gene tag #273.  
DE  
XX Human; maturation/activation dendritic cell expression gene; tag;  
KW maturation; activation; dendritic cell; ss.  
XX  
OS Homo sapiens.  
XX  
XX JP2001327293-A.  
XX 27-NOV-2001.  
XX  
XX 22-MAY-2000; 2000JP-00150562.  
XX  
XX 22-MAY-2000; 2000JP-00150562.  
XX  
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX  
DR WPI; 2002-127070/17.  
XX Human maturation/activation dendritic cell expression gene group.  
PT Claim 19; Page 17; 4lpp; Japanese.  
XX  
XX The present invention describes a human maturation/activation dendritic  
CC cell (DC) expression gene group consisting of 100 genes which show the  
CC highest expression among the genes expressed in human maturation/  
CC activation DC. Also described are: (1) a protein expressed by the above  
CC human maturation/activation DC expression gene; (2) an antibody against  
CC the protein; and (3) an antagonist against the expression of each gene  
CC belonging to the above gene group. The gene group is useful for the  
CC treatment and the diagnosis of various human diseases related to human  
CC DC. ABL42627 to ABL42926 represent specifically claimed human  
CC maturation/activation DC expression gene tags from the present invention  
XX  
SQ Sequence 10 BP; 1 A; 1 C; 4 G; 4 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 13 TGTGTGACCT 22  
|||||  
Db 1 TGTGTGAGCT 10  
  
RESULT 287  
ABL39528/c  
ID ABL39528 standard; DNA; 10 BP.  
XX  
AC ABL39528;  
XX  
DT 22-APR-2002 (first entry)  
XX  
DE Human ETFB primer-extension oligonucleotide 34.  
XX  
KW Human; electron-transfer flavoprotein beta polypeptide; ETFB;  
KW electron acceptor; mitochondrial matrix; glutaric acidaemia type II;  
KW novel polymorphic site; novel polymorphism; ETFB genotype; ss; GAIL;  
KW ETFB haplotype; transgenic animal; primer; probe; chromosome 19q13;  
KW primer-extension oligonucleotide; single nucleotide polymorphism; SNP.  
XX  
OS Homo sapiens.  
XX  
XX WO200202580-A2.  
XX  
PD 10-JAN-2002.  
XX  
PF 05-JUL-2001; 2001WO-US021306.  
XX





XX PS Claim 17; Page 15; 96pp; English.

CC The invention relates to single nucleotide polymorphisms in the gene

CC encoding the human natriuretic peptide receptor A/guanylate cyclase A

CC (atriuretic peptide receptor A) or NPR1 polypeptide. A method for

CC haplotyping the NPR1 gene in an individual comprises identifying the

CC nucleotide at one or more polymorphic sites and determining whether one

CC of the copies of the gene is defined by one of the NPR1 haplotypes given

CC in the specification or whether both copies are defined by a haplotype

CC pair. This method is useful in genotyping, whereby all possible haplotype

CC pairs can be assigned to specific genotypes. An association between a

CC trait and a haplotype or haplotype pair of the NPR1 gene can be

CC identified by comparing the frequency of the haplotype or haplotype pair

CC in a population exhibiting the trait with the frequency of the haplotype

CC or haplotype pair in a reference population, where a higher haplotype

CC frequency in the trait population indicates the trait is associated with

CC the haplotype or haplotype pair. NPR1 and its corresponding DNA are used

CC for studying the expression and function of NPR1, for use in screening

CC for candidate drugs to treat diseases related to NPR1 activity, such as

CC hypertension. The sequences are also useful for studying the effect of

CC variation on the biological activity of NPR1 as well as on the binding

CC affinity of candidate drugs targeting NPR1. Sequences AAS9959-AAS9990

CC and ABK09390-ABK09462 represent probes, sequencing primers and PCR

XX primers used to detect NPR1 gene polymorphisms

SQ Sequence 10 BP; 4 A; 3 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 1.6e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 TGTGACCTGG 24

Db 10 TGTGACCTG 1

|||||

RESULT 290

ABK09921/c

ID ABK09921 standard; DNA; 10 BP.

XX AC ABK09921;

XX DT 14-MAR-2002 (first entry)

XX DE P2RY1 gene allele-specific oligonucleotide #72.

XX KW Purinergic receptor P2Y, G-protein coupled 1; P2RY1; anticoagulant;

KW coagulant; platelet aggregation; haplotyping; drug screening;

KW transgenic animal; human; allele-specific oligonucleotide; ss.

XX OS Homo sapiens.

XX PN WO200190117-A2.

XX PD 29-NOV-2001.

XX PF 21-MAY-2001; 2001WO-US016432.

XX PR 19-MAY-2000; 2000US-0205996P.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Kazemi A, Koshy B, Tanguay DA;

XX DR WPI; 2002-083074/11.

XX PT New purinergic receptor P2Y G-protein coupled 1 (P2RY1) gene polymorphic

PT variants, useful e.g. in studying the expression and function of P2RY1

PT and screening candidate drugs for treating diseases related to P2RY1

PT activity.

XX PS Claim 18; Page 14; 79pp; English.

XX CC The invention relates to a novel isolated polypeptide comprising a

CC sequence which is a polymorphic variant of a reference sequence for the

CC purinergic receptor P2Y, G-protein coupled, 1 (P2RY1) protein or its

CC fragment. The polymorphic variant comprises one or more variant amino

CC acids selected from valine at a position 34 and glycine at a position

CC 262. The polymorphic variants are useful in studying the expression and

CC function of P2RY1, in expressing P2RY1 protein for use in screening for

CC candidate drugs to treat diseases related to P2RY1 activity, in studying

CC the effect of the variation on the biological activity of P2RY1, and the

CC binding affinity of candidate drugs targeting P2RY1 for the treatment of

CC disorders related to platelet aggregation. The haplotyping methods are

CC useful in validating P2RY1 as a candidate target for treating a specific

CC condition or disease predicted to be associated with P2RY1 activity, or

CC in the design of clinical trials of candidate drugs for treating a

CC specific condition or disease associated with P2RY1 activity. The

CC transgenic animals are useful for studying expression of the P2RY1

CC isogenes in vivo, for in vivo screening and testing of drugs targeted

CC against P2RY1 protein, and for testing the efficacy of therapeutic agents

CC and compounds for disorders related to platelet aggregation in a

CC biological system. ABK09950-ABK09924 represent human purinergic receptor

CC P2Y, G-coupled protein 1 (P2RY1) gene allele-specific oligonucleotides of

CC the invention

XX SQ Sequence 10 BP; 1 A; 2 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 1.6e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 ACCTGGTAAA 28

Db 10 ACCAGGTAAA 1

|||||

RESULT 291

ABK09919/c

ID ABK09919 standard; DNA; 10 BP.

XX AC ABK09919;

XX DT 14-MAR-2002 (first entry)

XX DE P2RY1 gene allele-specific oligonucleotide #70.

XX KW Purinergic receptor P2Y, G-protein coupled 1; P2RY1; anticoagulant;

KW coagulant; platelet aggregation; haplotyping; drug screening;

KW transgenic animal; human; allele-specific oligonucleotide; ss.

XX OS Homo sapiens.

XX PN WO200190117-A2.

XX PD 29-NOV-2001.

XX PF 21-MAY-2001; 2001WO-US016432.

XX PR 19-MAY-2000; 2000US-0205996P.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Kazemi A, Koshy B, Tanguay DA;

XX DR WPI; 2002-083074/11.

XX PT New purinergic receptor P2Y G-protein coupled 1 (P2RY1) gene polymorphic

PT variants, useful e.g. in studying the expression and function of P2RY1

PT and screening candidate drugs for treating diseases related to P2RY1

PT activity.

XX PS Claim 18; Page 14; 79pp; English.

XX CC The invention relates to a novel isolated polypeptide comprising a



CC sequence which is a polymorphic variant of a reference sequence for the  
CC purinergic receptor P2Y, G-protein coupled, 1 (P2RY1) protein or its  
CC fragment. The polymorphic variant comprises one or more variant amino  
CC acids selected from valine at a position 34 and glycine at a position  
CC 262. The polymorphic variants are useful in studying the expression and  
CC function of P2RY1, in expressing P2RY1 protein for use in screening for  
CC candidate drugs to treat diseases related to P2RY1 activity, in studying  
CC the effect of the variation on the biological activity of P2RY1, and the  
CC binding affinity of candidate drugs targeting P2RY1 for the treatment of  
CC disorders related to platelet aggregation. The haplotyping methods are  
CC useful in validating P2RY1 as a candidate target for treating a specific  
CC condition or disease predicted to be associated with P2RY1 activity, or  
CC in the design of clinical trials of candidate drugs for treating a  
CC specific condition or disease associated with P2RY1 activity. The  
CC transgenic animals are useful for studying expression of the P2RY1  
CC isogenes in vivo, for in vivo screening and testing of drugs targeted  
CC against P2RY1 protein, and for testing the efficacy of therapeutic agents  
CC and compounds for disorders related to platelet aggregation in a  
CC biological system. ABK09950-ABK09924 represent human purinergic receptor  
CC P2Y, G-coupled protein 1 (P2RY1) gene allele-specific oligonucleotides of  
CC the invention  
XX  
SQ Sequence 10 BP; 2 A; 2 C; 2 G; 4 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 20 CCTGGTAAAT 29  
Db 10 CCAGGTAAT 1  
  
RESULT 292  
ABS64264  
ID ABS64264 standard; DNA; 10 BP.  
XX  
AC ABS64264;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Tachykinin receptor gene TACR2, primer extension oligo #18.  
XX  
KW Human; single nucleotide polymorphism; SNP; TACR2; primer; probe; ss;  
KW tachykinin receptor.  
XX  
OS Homo sapiens.  
XX  
PN WO200263046-A1.  
XX  
PD 15-AUG-2002.  
XX  
PF 09-NOV-2001; 2001WO-US047394.  
XX  
PR 09-NOV-2000; 2000US-0247649P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Cappola G, Chew A, Gilson CR, Koshy B;  
XX  
DR WPI; 2002-636600/68.  
XX  
PT New genetic variants having polymorphisms in the Tachykinin receptor  
PT (TACR2) protein, useful for studying the function of TACR2, and for  
PT treating disorders associated with abnormal expression or function of  
PT TACR2 isogene.  
XX  
PS Claim 16; Page 15; 139pp; English.  
XX  
CC The invention relates to an isolated polypeptide comprising a polymeric  
CC variant of a reference sequence for the Tachykinin receptor (TACR2)  
CC protein. Also described is a method for: (1) haplotyping or genotyping  
CC the TACR2 gene of an individual; (2) predicting a haplotype pair for the

CC TACR2 gene of an individual; (3) identifying an association between a  
CC trait and at least one haplotype or haplotype pair of the TACR2 gene; and  
CC (4) isolated oligonucleotide for detecting a single nucleotide  
CC polymorphism in the TACR2 gene. Polymorphic variants of the TACR2 gene  
CC are useful in studying the expression and biological function of TACR2,  
CC and in identifying drugs targeting TACR2 protein for treating disorders  
CC associated with abnormal expression or function of TACR2, e.g. asthma or  
CC breast cancer. Polynucleotides comprising a polymorphic gene variant or  
CC fragment may be used for therapeutic purposes, where a patient could  
CC benefit from expression or increased expression of a particular TACR2  
CC protein isoform, or an expression vector encoding the isoform may be  
CC administered to the patient. Haplotype information is useful in improving  
CC the efficiency and output of several steps in drug discovery and  
CC development process, including target validation, identifying lead  
CC compounds, and early phase clinical trials. Information on polymorphisms  
CC may be applied in studying biological functions of TACR2 as well as in  
CC identifying drugs targeting this protein for the treatment of disorders  
CC related to its abnormal expression or function. ABS64163-ABS64302  
CC represent human TACR2 gene allele-specific oligonucleotide probes and  
CC primers used to detect haplotypes of the TACR2 gene of the invention  
XX  
SQ Sequence 10 BP; 2 A; 1 C; 3 G; 4 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 10 TGCTGTGTGA 19  
Db 1 TGCTGTGTAA 10  
  
RESULT 293  
ABS64271/c  
ID ABS64271 standard; DNA; 10 BP.  
XX  
AC ABS64271;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Tachykinin receptor gene TACR2, primer extension oligo #25.  
XX  
KW Human; single nucleotide polymorphism; SNP; TACR2; primer; probe; ss;  
KW tachykinin receptor.  
XX  
OS Homo sapiens.  
XX  
PN WO200263046-A1.  
XX  
PD 15-AUG-2002.  
XX  
PF 09-NOV-2001; 2001WO-US047394.  
XX  
PR 09-NOV-2000; 2000US-0247649P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Cappola G, Chew A, Gilson CR, Koshy B;  
XX  
DR WPI; 2002-636600/68.  
XX  
PT New genetic variants having polymorphisms in the Tachykinin receptor  
PT (TACR2) protein, useful for studying the function of TACR2, and for  
PT treating disorders associated with abnormal expression or function of  
PT TACR2 isogene.  
XX  
PS Claim 16; Page 15; 139pp; English.  
XX  
CC The invention relates to an isolated polypeptide comprising a polymeric  
CC variant of a reference sequence for the Tachykinin receptor (TACR2)  
CC protein. Also described is a method for: (1) haplotyping or genotyping  
CC the TACR2 gene of an individual; (2) predicting a haplotype pair for the  
CC TACR2 gene of an individual; (3) identifying an association between a

|          |                                                                           |          |                                                                           |
|----------|---------------------------------------------------------------------------|----------|---------------------------------------------------------------------------|
| CC       | trait and at least one haplotype or haplotype pair of the TACR2 gene; and | CC       | the ALDH5A1 polymorphic variant with a candidate agent and assaying for   |
| CC       | (4) isolated oligonucleotide for detecting a single nucleotide            | CC       | binding activity. The polypeptide and haplotypes are useful for           |
| CC       | polymorphism in the TACR2 gene. Polymorphic variants of the TACR2 gene    | CC       | identifying an association between a trait such as a clinical response to |
| CC       | are useful in studying the expression and biological function of TACR2,   | CC       | a drug targeting ALDH5A1 and a haplotype ALDH5A1 gene. Transgenic animals |
| CC       | and in identifying drugs targeting TACR2 protein for treating disorders   | CC       | are also useful for studying expression of the ALDH5A1 isogenes in vivo,  |
| CC       | associated with abnormal expression or function of TACR2, e.g. asthma or  | CC       | for in vivo screening and testing of drugs against ALDH5A1 protein and    |
| CC       | breast cancer. Polynucleotides comprising a polymorphic gene variant or   | CC       | for testing the efficacy of therapeutic agents and compounds for 4-       |
| CC       | fragment may be used for therapeutic purposes, where a patient could      | CC       | hydroxybutyric aciduria and metabolic diseases in a biological system.    |
| CC       | benefit from expression or increased expression of a particular TACR2     | CC       | Antibodies are useful for diagnostic and prognostic formats and           |
| CC       | protein isoform, or an expression vector encoding the isoform may be      | CC       | therapeutic methods, for immunoprecipitating the polypeptide from         |
| CC       | administered to the patient. Haplotype information is useful in improving | CC       | solution, for detecting ALDH5A1 protein isoforms in biological samples,   |
| CC       | the efficiency and output of several steps in drug discovery and          | CC       | frozen tissue sections, for use in immunocytochemical,                    |
| CC       | development process, including target validation, identifying lead        | CC       | immunohistochemical and immunofluorescence techniques. The polynucleotide |
| CC       | compounds, and early phase clinical trials. Information on polymorphisms  | CC       | is useful for gene therapy and antisense gene therapy. This sequence is a |
| CC       | may be applied in studying biological functions of TACR2 as well as in    | CC       | primer extension oligonucleotide used to detect polymorphisms in the      |
| CC       | identifying drugs targeting this protein for the treatment of disorders   | CC       | ALDH5A1 gene described in the method of the invention                     |
| CC       | related to its abnormal expression or function. ABS64163-ABS64302         | XX       |                                                                           |
| CC       | represent human TACR2 gene allele-specific oligonucleotide probes and     | SQ       | Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;                         |
| CC       | primers used to detect haplotypes of the TACR2 gene of the invention      |          |                                                                           |
| XX       |                                                                           |          |                                                                           |
| SQ       | Sequence 10 BP; 1 A; 1 C; 6 G; 2 T; 0 U; 0 Other;                         |          |                                                                           |
|          |                                                                           |          |                                                                           |
|          | Query Match 29.0%; Score 8.4; DB 1; Length 10;                            |          | Query Match 29.0%; Score 8.4; DB 1; Length 10;                            |
|          | Best Local Similarity 90.0%; Pred. No. 1.6e+02;                           |          | Best Local Similarity 90.0%; Pred. No. 1.6e+02;                           |
|          | Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;                |          | Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;                |
| QY       | 2 CATCCACCTG 11                                                           | QY       | 3 ATCCACCTGC 12                                                           |
| Db       | 10 CACCCACCTG 1                                                           | Db       | 1 ATGCACCTGC 10                                                           |
|          |                                                                           |          |                                                                           |
|          | RESULT 294                                                                |          | RESULT 295                                                                |
| AAS99384 |                                                                           | AAD47793 |                                                                           |
| ID       | AAS99384 standard; DNA; 10 BP.                                            | ID       | AAD47793 standard; DNA; 10 BP.                                            |
| XX       |                                                                           | XX       |                                                                           |
| AC       | AAS99384;                                                                 | AC       | AAD47793;                                                                 |
| XX       |                                                                           | XX       |                                                                           |
| DT       | 12-MAR-2002 (first entry)                                                 | DT       | 24-FEB-2003 (first entry)                                                 |
| XX       |                                                                           | XX       |                                                                           |
| DE       | Aldehyde dehydrogenase 5 family, member A1, oligonucleotide #77.          | DE       | Human GNB3 gene polymorphisms detecting primer #13.                       |
| XX       |                                                                           | XX       |                                                                           |
| KW       | Aldehyde dehydrogenase 5 family member A1; ALDH5A1;                       | KW       | Human; guanine nucleotide binding protein beta polypeptide 3; G protein;  |
| KW       | succinate-semialdehyde dehydrogenase; gene therapy; primer;               | KW       | GNB3; polymorphism; obesity; left ventricular hypertrophy; hypertension;  |
| KW       | antisense technology; primer extension oligonucleotide;                   | KW       | drug discovery; cardiovascular; development process; asthma; anorectic;   |
| KW       | 4-hydroxybutyric aciduria; metabolic disease; transgenic animal; ss.      | KW       | gene therapy; primer; ss.                                                 |
| XX       |                                                                           | XX       |                                                                           |
| OS       | Synthetic.                                                                | OS       | Homo sapiens.                                                             |
| XX       |                                                                           | XX       |                                                                           |
| PN       | WO200190119-A2.                                                           | PN       | WO200277284-A1.                                                           |
| XX       |                                                                           | XX       |                                                                           |
| PD       | 29-NOV-2001.                                                              | PD       | 03-OCT-2002.                                                              |
| XX       |                                                                           | XX       |                                                                           |
| PF       | 21-MAY-2001; 2001WO-US016558.                                             | PF       | 21-MAR-2001; 2001WO-US008961.                                             |
| XX       |                                                                           | XX       |                                                                           |
| PR       | 19-MAY-2000; 2000US-0205849P.                                             | PR       | 21-MAR-2001; 2001WO-US008961.                                             |
| XX       |                                                                           | XX       |                                                                           |
| PA       | (GENA-) GENAISSANCE PHARM INC.                                            | XX       | (GENA-) GENAISSANCE PHARM INC.                                            |
| XX       |                                                                           | XX       |                                                                           |
| PI       | Kliem SE, Koshy B, Tanguay DA;                                            | PI       | Bentivegna SC, Choi JY, Kliem SE, Koshy B;                                |
| XX       |                                                                           | XX       |                                                                           |
| DR       | WPI; 2002-089912/12.                                                      | XX       | WPI; 2003-018947/01.                                                      |
| XX       |                                                                           | XX       |                                                                           |
| PT       | New genetic variants of human aldehyde dehydrogenase 5 family, member A1, | PT       | New genetic variants having polymorphisms in the G protein, GNB3 gene,    |
| PT       | ALDH5A1 gene for treating metabolic diseases and for expressing ALDH5A1   | PT       | useful for treating disorders with abnormal expression or function of the |
| PT       | protein useful in identifying drugs to treat 4-hydroxybutyric aciduria.   | PT       | GNB3 gene, such as asthma, obesity, hypertension and left ventricular     |
| XX       |                                                                           | PT       | hypertrophy.                                                              |
| PS       | Claim 18; Page 14; 151pp; English.                                        | XX       |                                                                           |
| XX       |                                                                           | PS       | Claim 18; Page 15; 88pp; English.                                         |
| CC       | The invention describes an isolated polynucleotide comprising a           | XX       |                                                                           |
| CC       | nucleotide sequence which is a polymorphic variant of a reference         | CC       | The invention relates to an isolated polypeptide which comprises a first  |
| CC       | sequence for the aldehyde dehydrogenase 5 family, member A1 (succinate-   | CC       | nucleotide sequence which is a polymorphic variant of a reference         |
| CC       | semialdehyde dehydrogenase) (ALDH5A1) gene or its fragment. The           | CC       | sequence for the guanine nucleotide binding protein (G protein), beta     |
| CC       | polypeptide is useful for screening for drugs targeting it by contacting  | CC       | polypeptide 3 (GNB3) gene or fragment. Polymorphic variants of the GNB3   |

CC hypertension, obesity, asthma and left ventricular hypertrophy.  
CC Polynucleotides comprising a polymorphic gene variant or fragment may be  
CC used for therapeutic purposes, where a patient could benefit from  
CC expression or increased expression of a particular GNB3 gene isoform or  
CC an expression vector encoding the isoform may be administered to the  
CC patient. Haplotype information is useful in improving the efficiency and  
CC output of several steps in drug discovery and development process,  
CC including target validation, identifying lead compounds and early phase  
CC clinical trials. The invention is used in gene therapy. The present  
CC sequence is human GNB3 gene polymorphisms detecting primer  
XX  
SQ Sequence 10 BP; 1 A; 6 C; 1 G; 2 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 CCACCTGCTG 14  
Db 1 CCACCTCCTG 10  
  
RESULT 296  
ACC69006/c  
ID ACC69006 standard; DNA; 10 BP.  
XX  
AC ACC69006;  
XX  
DT 10-JUL-2003 (first entry)  
XX  
DE AMP protocol HpaII oligonucleotide PCR primer SEQ ID NO:3.  
XX  
KW Amplified DNA methylation polymorphism protocol; AMP protocol;  
KW methylation profile; functional genomics; identification; mapping;  
KW diagnosis; forensic; genomic; PCR primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO2003025215-A1.  
XX  
PD 27-MAR-2003.  
XX  
PF 13-SEP-2002; 2002WO-AU001262.  
XX  
PR 14-SEP-2001; 2001AU-00007685.  
XX  
PA (UYQU ) UNIV QUEENSLAND.  
XX  
PI Carroll BJ, Harrison DK, Aung HT;  
XX  
DR WPI; 2003-371826/35.  
XX  
PT Determining DNA methylation profile within the genome of a eukaryotic  
PT cell comprises the exposure of genomic or transgenic DNA to a methylation  
PT -sensitive enzyme, e.g. HpaII, and subjecting the DNA to an amplification  
PT reaction.  
XX  
PS Example 1; Page 40; 88pp; English.  
XX  
CC The present invention describes a method for determining the methylation  
CC profile of one or more nucleotides at one or more sites within the genome  
CC of a eukaryotic cell or group of cell comprising the exposure of genomic  
CC or transgenic DNA to a methylation-sensitive enzyme and subjecting the  
CC DNA to an amplification reaction. The method is useful in detecting DNA  
CC methylation, in functional genomics, and in the design of therapeutic and  
CC trait-modifying protocols for animals and plants. The method may also be  
CC used in identifying and mapping junctions between methylated and  
CC unmethylated DNA, in identifying DNA methylation polymorphisms that can  
CC be used in diagnosis and forensics, and in monitoring the aging process  
CC of particular cells of an animal, including humans, or plants. The  
CC present sequence represents a PCR primer which is used in an example from  
CC the present invention for an amplified DNA methylation polymorphism (AMP)  
CC protocol

XX  
SQ Sequence 10 BP; 2 A; 5 C; 2 G; 1 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 16 GTGACCTGGT 25  
Db 10 GTGACCGGGT 1  
  
RESULT 297  
ABT14241  
ID ABT14241 standard; DNA; 10 BP.  
XX  
AC ABT14241;  
XX  
DT 20-FEB-2003 (first entry)  
XX  
DE Nucleic acid PCR amplification method-related RAPD PCR primer #11.  
XX  
KW Nucleic acid amplification; nucleic acid analysis; DNA analysis; ss;  
KW RNA analysis; RAPD; PCR; primer; random amplified polymorphic DNA.  
XX  
OS Unidentified.  
XX  
PN WO200281743-A2.  
XX  
PD 17-OCT-2002.  
XX  
PF 28-MAR-2002; 2002WO-GB001489.  
XX  
PR 02-APR-2001; 2001GB-00008182.  
XX  
PA (HAMI/) HAMILL B.  
XX  
PI Hamill B;  
XX  
DR WPI; 2003-075484/07.  
XX  
PT Amplification of nucleotide sequences from polynucleotides by chain  
PT extension of oligonucleotide primers, comprises 2 oligonucleotides in  
PT solution, 2 attached to supports and both share complementary sequences.  
XX  
PS Disclosure; Fig 17; 60pp; English.  
XX  
CC The invention comprises a method for the PCR amplification of nucleic  
CC acids. The method involves a set of primers, where two of the primers are  
CC in solution and at least two other primers are attached to a solid  
CC support. The method of the invention can be used for the analysis of a  
CC nucleic acid or a mixture of nucleic acids, including: single-stranded  
CC DNA molecules, double-stranded DNA molecules and mRNA molecules. The  
CC present DNA sequence represents a random amplified polymorphic DNA (RAPD)  
CC PCR primer of the invention  
XX  
SQ Sequence 10 BP; 1 A; 6 C; 1 G; 2 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 CATCCACCTG 11  
Db 1 CATCCCCCTG 10  
  
RESULT 298  
ADE14194/c  
ID ADE14194 standard; DNA; 10 BP.  
XX  
AC ADE14194;  
XX

DT 29-JAN-2004 (first entry)  
XX Optineurin promoter motif, repeat element or regulatory region #303.  
DE  
XX Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;  
KW SNP; glaucoma; progressive ocular hypertensive disorder;  
KW glaucoma related disorder; motif; repeat element; regulatory region.  
XX Homo sapiens.  
OS US2003190617-A1.  
XX  
PN 09-OCT-2003.  
XX  
PD 06-MAR-2002; 2002US-00091281.  
XX  
PF 06-MAR-2002; 2002US-00091281.  
XX  
PR 06-MAR-2002; 2002US-00091281.  
XX  
XX (SIEE/) SI E.  
PA (RAYM/) RAYMOND V.  
PA (MORI/) MORISSETTE J.  
XX  
PI Raymond V, Morissette J, Si E;  
XX  
XX WPI; 2003-864168/80.  
DR  
XX New nucleic acid sequences of the optineurin gene are useful to detect  
XX polymorphisms particularly single nucleotide polymorphisms in the  
PT optineurin promoter to diagnose, prognose and treat glaucoma and related  
PT disorders.  
XX  
PS Claim 11; SEQ ID NO 305; 159pp; English.  
XX  
CC The invention relates to an isolated nucleic acid (NI) comprising at  
CC least 20 but not more than 1500 consecutive nucleotides of the optineurin  
CC promoter appearing as ADE13890. Also included are the optineurin promoter  
CC operably linked to a heterologous nucleic acid, a nucleic acid capable of  
CC detecting a single nucleotide polymorphism (SNP) in the optineurin  
CC promoter, a host cell comprising the promoter operably linked to a  
CC heterologous sequence, diagnosing or prognosing glaucoma in a sample  
CC obtained from a cell or bodily fluid (comprising detecting a polymorphism  
CC in a promoter region of the optineurin gene, associated with a glaucoma  
CC phenotype), detecting a SNP sequence variation in a sample containing  
CC DNA, detecting the presence of an optineurin promoter sequence variation  
CC in a sample containing DNA, determining the presence or increased  
CC susceptibility to glaucoma or to a progressive ocular hypertensive  
CC disorder resulting in loss of visual field in a patient (or the severity  
CC or progression of glaucoma in a patient, comprising providing  
CC amplification reaction primers that direct amplification of a selected  
CC nucleic acid region containing the variation within the optineurin  
CC promoter and amplifying the DNA) and detecting a polymorphism (comprising  
CC obtaining a sample containing human genomic DNA, providing a nucleic acid  
CC capable of detecting a SNP located within an optineurin promoter, and  
CC detecting the polymorphism). The invention is used to diagnose and  
CC prognose glaucoma and also to treat glaucoma related disorders. The  
CC present sequence is an optineurin promoter motif, repeat element or  
CC putative regulatory region.  
XX  
SQ Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 13 TGTGTGACCT 22  
Db |||||||  
10 TGGGTGACCT 1  
  
RESULT 299  
AAL51289/c  
ID AAL51289 standard; DNA; 10 BP.  
XX

AC AAL51289;  
XX 20-MAR-2003 (first entry)  
DT  
XX SAGE transcript tag SEQ ID No 16.  
DE  
XX SAGE transcription tag; gene therapy; neoplastic cell modulation; OOM;  
KW oncogenic osteomalacia; phosphate homeostasis; hypophosphataemia; PHEX;  
KW fibroblast growth factor 23; FGF-23; phosphaturia; osteomalacia; FRP-4;  
KW ss; low 1,25-dihydroxyvitamin D; phosphate homeostasis-related disease;  
KW X-linked hypophosphataemia rickets; rhabdomyolysis; cardiomyopathy;  
KW tumoural calcinosis; renal failure; bone mineralisation.  
XX  
XX Unidentified.  
OS  
XX WO200292128-A1.  
PN  
XX 21-NOV-2002.  
PD  
XX 13-MAY-2002; 2002WO-US018609.  
XX  
PF 11-MAY-2001; 2001US-0290483P.  
XX  
PR 06-JUN-2001; 2001US-0296298P.  
PR  
XX (GENZ ) GENZYME CORP.  
PA  
XX Schiavi SC, Finnegan R;  
PI  
XX WPI; 2003-129238/12.  
DR  
XX Modulating the phenotype of a neoplastic cell associated with oncogenic  
PT osteomalacia or with phosphate homeostasis, or treating a related disease  
PT (e.g. rickets), by administering modulators of FRP 4 and/or FGF 23, or  
PT PHEX activity.  
XX  
XX Example; Page 47; 64pp; English.  
PS  
XX The invention comprises a method for modulating the phenotype of a  
CC neoplastic cell associated with oncogenic osteomalacia (OOM) or a cell  
CC associated with phosphate homeostasis. The method involves delivering an  
CC agent that alters the activity of FRP-4 and/or fibroblast growth factor  
CC 23 (FGF-23), or PHEX protein. The method of the invention is useful for  
CC modulating the phenotype of a neoplastic cell associated with OOM or a  
CC cell associated with phosphate homeostasis. The method is particularly  
CC useful for alleviating an OOM-associated symptom (e.g. hypophosphataemia,  
CC phosphaturia, low serum concentrations of 1,25-dihydroxyvitamin D, or  
CC osteomalacia). The method is also useful for treating a phosphate  
CC homeostasis-related disease (e.g. X-linked hypophosphataemia rickets,  
CC OOM, rhabdomyolysis, cardiomyopathy, tumoural calcinosis, renal failure  
CC or bone mineralisation). The present DNA sequence represents a SAGE  
CC transcription tag used in an example of the invention  
XX  
SQ Sequence 10 BP; 4 A; 2 C; 2 G; 2 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 20 CCTGGTAAAT 29  
Db |||||||  
10 CCTGGTATAT 1  
  
RESULT 300  
ADL96345/c  
ID ADL96345 standard; DNA; 10 BP.  
XX  
XX AC ADL96345;  
AC  
XX 20-MAY-2004 (first entry)  
DT  
XX CD15+ myeloid cell associated probe seqid 244.  
DE  
XX



KW cytostatic; gene therapy; microarray; gene expression characteristic;  
KW haematopoietic cell; haematopoiesis; myeloid leukaemia; probe;  
KW CD15+ myeloid cell; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2003165949-A1.  
XX  
XX PD 04-SEP-2003.  
XX  
PF 23-DEC-2002; 2002US-00329465.  
XX  
PR 27-DEC-2001; 2001US-0343826P.  
XX  
PA (WANG/) WANG S M.  
PA (LEES/) LEE S.  
PA (CHEN/) CHEN J.  
PA (ZHOU/) ZHOU G.  
PA (ROWL/) ROWLEY J D.  
XX  
PI Wang SM, Lee S, Chen J, Zhou G, Rowley JD;  
XX  
XX WPI; 2003-863699/80.  
XX  
PT New microarray for measuring gene expression characteristics of  
PT hematopoietic cells, useful for preparing a composition for diagnosing or  
PT treating myeloid leukemia.  
XX  
PS Claim 1; SEQ ID NO 244; 32pp; English.  
XX  
CC The invention describes a microarray for measuring gene expression  
CC characteristics of haematopoietic cells comprising at least 5  
CC polynucleotides having distinct sequences. Also described are: a method  
CC of diagnosing or treating an abnormality associated with haematopoiesis;  
CC and diagnosing myeloid leukaemia in a patient. The microarray is useful  
CC for preparing a composition for diagnosing or treating myeloid leukaemia.  
CC This sequence represents a polynucleotide probe comprising a portion of  
CC an expressed gene isolated from a population of CD15+ myeloid cells and  
CC suitable for use in the microarray of the invention.  
XX  
SQ Sequence 10 BP; 5 A; 3 C; 2 G; 0 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 8 CCTGCTGTGT 17  
Db 10 CTTGCTGTGT 1  
  
RESULT 301  
ADG13687/c  
ID ADG13687 standard; RNA; 10 BP.  
XX  
AC ADG13687;  
XX  
DT 26-FEB-2004 (first entry)  
XX  
DE Human EGFR Amberzyme target sequence #19.  
XX  
KW Human; ss; EGFR; epidermal growth factor receptor; HER1; HER2; HER3;  
KW HER4; hammerhead ribozyme; inozyme; zinzyme; DNazyme; amberzyme; cancer;  
KW brain tumour; cytostatic; short interfering RNA; siRNA; RNA interference;  
KW prostate cancer; colorectal cancer; brain cancer; oesophageal cancer;  
KW stomach cancer; bladder cancer; pancreatic cancer; cervical cancer;  
KW head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma;  
KW multidrug resistant cancer.  
XX  
OS Homo sapiens.  
XX  
PN US2003186909-A1.  
XX

PD 02-OCT-2003.  
XX  
PF 21-OCT-2002; 2002US-00277494.  
XX  
PR 27-JAN-1997; 97US-0036749P.  
PR 04-DEC-1997; 97US-00985162.  
PR 22-SEP-1999; 99US-00401063.  
PR 03-MAY-2001; 2001US-00848754.  
PR 25-JUL-2001; 2001US-00916466.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Mcswiggen J;  
XX  
DR WPI; 2004-032029/03.  
XX  
PT New double stranded short interfering ribonucleic acid molecule for  
PT inhibiting expression of epidermal growth factor receptor gene.  
XX  
PS Claim 7; SEQ ID NO 114; 113pp; English.  
XX  
CC The invention relates to a double stranded short interfering RNA (siRNA)  
CC molecule that inhibits expression of epidermal growth factor receptor  
CC (EGFR) gene (e.g. HER1-4) by RNA interference is new. Also included is an  
CC expression vector comprising a nucleic acid sequence encoding siRNA  
CC molecule(s) in a manner that allows expression of the nucleic acid  
CC molecule. The siRNA molecules comprise hammerhead ribozymes, inozymes,  
CC amberzymes zinzymes and DNazymes. The invention is used for inhibiting  
CC expression of EGFR. It can be used for treatment of cancer, prostate  
CC cancer, colorectal cancer, brain cancer, oesophageal cancer, stomach  
CC cancer, bladder cancer, pancreatic cancer, cervical cancer, head and neck  
CC cancer, ovarian cancer, melanoma, lymphoma, glioma, multidrug resistant  
CC cancer or a brain tumour. The invention has enhanced shelf-life, half-  
CC life in vitro , stability, and ease of introduction of oligonucleotide to  
CC target site. The present sequence is an EGFR/HER1-4 target sequence for  
CC an siRNA of the invention.  
XX  
SQ Sequence 10 BP; 3 A; 0 C; 5 G; 0 T; 2 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 CCATCCACCT 10  
Db 10 CCATCCACTT 1  
  
RESULT 302  
ADH14437  
ID ADH14437 standard; DNA; 10 BP.  
XX  
AC ADH14437;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Human retinoblastoma 1 (RB1CC1) genomic DNA 3' border of intron 19.  
XX  
KW cell nucleus; transcription; gene expression; retinoblastoma-1; RB1CC1;  
KW diagnosis; cancer; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2003102028-A1.  
XX  
PD 11-DEC-2003.  
XX  
PF 30-JAN-2003; 2003WO-JP000882.  
XX  
PR 03-JUN-2002; 2002JP-00161400.  
PR 24-JUL-2002; 2002JP-00214978.  
XX  
PA (OKAB/) OKABE H.



PA (IKEG/) IKEGAWA S.  
PA (CHAN/) CHANO T.  
XX Chano T;  
XX WPI; 2004-081932/08.  
DR Protein in the nuclei of human and animal cells associated with  
XX expression of retinoblastoma-1 gene for diagnosis of cancer.  
PT Disclosure; Page 11; 113pp; Japanese.  
XX The invention relates to a protein or polypeptide found in the nuclei of  
CC human and animal cells that are associated with transcription and/or  
CC induction of expression of retinoblastoma-1 gene (RB1CC1). The detection  
CC of RB1CC1 gene and its protein is useful for the diagnosis of cancer. The  
CC human RB1CC1 cDNA is 6.6 kb containing a 4782 bp ORF, encoding a 180 kD  
CC 1594 amino acid protein. This sequence corresponds to the sequence at the  
CC junction between an intron and an exon in the human RB1CC1 genomic  
CC sequence.  
XX Sequence 10 BP; 2 A; 5 C; 2 G; 1 T; 0 U; 0 Other;  
SQ Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 5 CCACCTGCTG 14  
Db 1 CCACCTGCAG 10  
RESULT 303  
ADK12825/c  
ID ADK12825 standard; DNA; 10 BP.  
XX  
AC ADK12825;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human glioma endothelial marker (GEM) standard tag SEQ ID NO:3.  
XX  
KW glioma; brain tissue; neoplastic; glioma endothelial marker; GEM;  
KW anticancer; antiglioma; immune response; cytostatic;  
KW multi-drug sensitive glioma; human; standard tag; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO2004016758-A2.  
XX  
PD 26-FEB-2004.  
XX  
PF 15-AUG-2003; 2003WO-US025614.  
XX  
PR 15-AUG-2002; 2002US-0403390P.  
PR 01-APR-2003; 2003US-0458978P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Madden SI, Wang CJ, Cook BP, Lattera J, Walter K;  
XX WPI; 2004-247973/23.  
DR  
XX Diagnosing glioma by detecting expression product of any one of 255  
PT genes, glioma endothelial markers, in brain tissue sample suspected of  
PT being neoplastic, and comparing the expression with expression in normal  
PT brain tissue sample.  
XX  
PS Claim 36; SEQ ID NO 3; 114pp; English.  
XX  
CC The present invention describes a method (M1) for aiding in the diagnosis

CC of glioma. (M1) involves detecting an expression product of at least one  
CC gene (I) in a first brain tissue sample (T) suspected of being  
CC neoplastic, where (I) is chosen from any one of 255 genes (glioma  
CC endothelial markers (GEMs)) as given in specification, and comparing the  
CC expression of (I) in (T) with expression of (I) in a second normal brain  
CC tissue sample (R), where increased expression of (I) in (T) relative to  
CC (R), identifies (T) as likely to be neoplastic. Also described: (1)  
CC treating (M2) glioma involves contacting cells of the glioma with an  
CC antibody that specifically binds to a extracellular epitope; (2)  
CC identifying (M3) a test compound as potential anticancer or antiglioma  
CC drug involves contacting a test compound with the cell which expresses  
CC (I), monitoring an expression product of the at least one gene and  
CC identifying test compound as a potential anticancer drug if it decreases  
CC the expression of at least one gene; (3) identifying (M4) a test compound  
CC as potential anticancer or antiglioma drug involves contacting a test  
CC compound with the cell which expresses mRNA of at least one gene  
CC identified by a tag as described above, monitoring mRNA of the gene, and  
CC identifying the test compound as a potential anticancer drug if it  
CC decreases the expression of at least one gene; and (4) inducing (M5) an  
CC immune response to glioma involves administering to a mammal, a protein  
CC or (I). (I) have cytostatic activities, and can be used to trigger immune  
CC destruction of glioma cells, and as immune response inducers. (M1) is  
CC useful for aiding in diagnosing glioma. (M2) is useful for treating multi  
CC -drug sensitive glioma in a human. (M5) is useful for inducing an immune  
CC response to a glioma in a mammal having glioma or in a mammal who has had  
CC a glioma surgically removed. The present sequence represents a human GEM  
CC standard tag oligonucleotide, which is used in the exemplification of the  
CC present invention.  
XX  
SQ Sequence 10 BP; 5 A; 3 C; 2 G; 0 T; 0 U; 0 Other;  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 8 CCTGCTGTGT 17  
Db 10 CTTGCTGTGT 1  
RESULT 304  
ADR27959/c  
ID ADR27959 standard; DNA; 10 BP.  
XX  
AC ADR27959;  
XX  
DT 04-NOV-2004 (first entry)  
XX  
DE Murine VE-statin exon 7 3' oligonucleotide.  
XX  
KW Cytostatic; Ophthalmological; Vasotropic; Antiarteriosclerotic;  
KW VE-statin; endothelium; perivascular smooth muscle cell; angiogenesis;  
KW cancer; retinopathy; atherosclerosis; restenosis; gene therapy; mouse;  
KW ds.  
XX  
OS Mus musculus.  
XX  
PN FR2851249-A1.  
PD  
PD 20-AUG-2004.  
XX  
PF 17-FEB-2003; 2003FR-00001875.  
XX  
PR 17-FEB-2003; 2003FR-00001875.  
XX (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.  
PA Soncin F, Mattot V;  
PI  
XX WPI; 2004-618122/60.  
DR  
XX Using VE-statins to inhibit recruitment of perivascular smooth muscle  
PT cells, for treating e.g. cancer and retinopathy, also new VE-statins,

PT related nucleic acids and antibodies.  
XX  
PS Example 3; Page 11; 63pp; French.  
XX  
CC The present invention relates to a method for preparing a composition for  
CC inhibiting recruitment of perivascular cells of smooth muscle type using  
CC a VE-statin protein (I; ADR27861-ADR27863 and ADR27902). VE-statins,  
CC soluble factors secreted by endothelial cells of the blood vessels, block  
CC recruitment of perivascular smooth muscle cells (but do not affect their  
CC proliferation), so inhibit angiogenesis. VE-statins, also their peptide  
CC fragments, nucleic acids encoding them and vectors containing this  
CC nucleic acid, are used for treating cancer, retinopathy, atherosclerosis  
CC and restenosis, including in gene therapy. The VE-statin nucleic acids  
CC can also be used to produce transgenic animals (for studying the VE-  
CC statin proteins and genes); the VE-statins are used to screen for  
CC specific (ant)agonists, and antibodies specific for VE-statins can be  
CC used to determine expression profiles, particularly for diagnosis of  
CC diseases associated with VE-statins. The present sequence was used to  
CC illustrate the structure of the murine VE-statin gene.  
XX  
SQ Sequence 10 BP; 3 A; 5 C; 2 G; 0 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 9 CTGCTGTGTG 18  
| | | | | | | |  
Db 10 CTGCTGTGGG 1  
  
RESULT 305  
ADS78008/c  
ID ADS78008 standard; DNA; 10 BP.  
XX  
AC ADS78008;  
XX  
DT 30-DEC-2004 (first entry)  
XX  
DE Breast cancer detection oligonucleotide #1790.  
XX  
KW ss; primer; cytostatic; RNA interference; RNAi; gene silencing;  
KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;  
KW cathepsin L inhibitor; cathepsin F inhibitor;  
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;  
KW collagen antagonist; diagnosis; breast tissue; cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO2004085621-A2.  
XX  
PD 07-OCT-2004.  
XX  
PF 22-MAR-2004; 2004WO-US008866.  
XX  
PR 20-MAR-2003; 2003US-0456735P.  
XX  
PA (DAND ) DANA FARBER CANCER INST INC.  
PI Polyak K, Porter D, Allinen M;  
XX WPI; 2004-728732/71.  
XX  
PT Diagnosing breast cancer comprises determining expression levels of a  
PT gene selected from those differentially expressed in normal or cancerous  
PT cells of a breast tissue sample including interleukin 1, thrombospondin 1  
PT and cystatin C.  
XX  
PS Example 6; SEQ ID NO 1790; 149pp; English.  
XX  
CC The invention relates to a method of diagnosis (M1) comprising: (a)  
CC providing a test sample of breast tissue; (b) determining the level of  
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide  
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide

CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the  
CC specification, and (c) if the gene is expressed in the test sample at a  
CC lower level than in a control normal breast tissue sample, diagnosing the  
CC test sample as containing cancer cells. The method is used for diagnosing  
CC breast cancer. This sequence corresponds to an oligonucleotide primer  
CC used in the method of the invention.  
XX  
SQ Sequence 10 BP; 5 A; 3 C; 2 G; 0 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 8 CCTGCTGTGT 17  
| | | | | | | |  
Db 10 CTGCTGTGT 1  
  
RESULT 306  
ADS76235/c  
ID ADS76235 standard; DNA; 10 BP.  
XX  
AC ADS76235;  
XX  
DT 30-DEC-2004 (first entry)  
XX  
DE Breast cancer detection oligonucleotide #17.  
XX  
KW ss; primer; cytostatic; RNA interference; RNAi; gene silencing;  
KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;  
KW cathepsin L inhibitor; cathepsin F inhibitor;  
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;  
KW collagen antagonist; diagnosis; breast tissue; cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO2004085621-A2.  
XX  
PD 07-OCT-2004.  
XX  
PF 22-MAR-2004; 2004WO-US008866.  
XX  
PR 20-MAR-2003; 2003US-0456735P.  
XX  
PA (DAND ) DANA FARBER CANCER INST INC.  
PI Polyak K, Porter D, Allinen M;  
XX WPI; 2004-728732/71.  
XX  
PT Diagnosing breast cancer comprises determining expression levels of a  
PT gene selected from those differentially expressed in normal or cancerous  
PT cells of a breast tissue sample including interleukin 1, thrombospondin 1  
PT and cystatin C.  
XX  
PS Example 2; SEQ ID NO 17; 149pp; English.  
XX  
CC The invention relates to a method of diagnosis (M1) comprising: (a)  
CC providing a test sample of breast tissue; (b) determining the level of  
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide  
CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the  
CC specification, and (c) if the gene is expressed in the test sample at a  
CC lower level than in a control normal breast tissue sample, diagnosing the  
CC test sample as containing cancer cells. The method is used for diagnosing  
CC breast cancer. This sequence corresponds to an oligonucleotide primer  
CC used in the method of the invention.  
XX  
SQ Sequence 10 BP; 3 A; 5 C; 2 G; 0 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
expression in the test sample of a gene (e.g. interleukin-8, superoxide



XX 22-MAR-2004; 2004WO-US008866.  
XX 20-MAR-2003; 2003US-0456735P.  
XX (DAND ) DANA FARBER CANCER INST INC.  
XX Polyak K, Porter D, Allinen M;  
PI WPI; 2004-728732/71.  
XX Diagnosing breast cancer comprises determining expression levels of a  
PT gene selected from those differentially expressed in normal or cancerous  
PT cells of a breast tissue sample including interleukin 1, thrombospondin 1  
PT and cystatin C.  
XX Example 2; SEQ ID NO 769; 149pp; English.  
PS The invention relates to a method of diagnosis (M1) comprising: (a)  
XX providing a test sample of breast tissue; (b) determining the level of  
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide  
CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the  
CC specification, and (c) if the gene is expressed in the test sample at a  
CC lower level than in a control normal breast tissue sample, diagnosing the  
CC test sample as containing cancer cells. The method is used for diagnosing  
CC breast cancer. This sequence corresponds to an oligonucleotide primer  
CC used in the method of the invention.  
XX Sequence 10 BP; 2 A; 6 C; 1 G; 1 T; 0 U; 0 Other;  
SQ Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 ATCCACCTGC 12  
Db |||||||  
1 ATCCACCCGC 10  
RESULT 310  
ADU19159  
ID ADU19159 standard; DNA; 10 BP.  
XX AC ADU19159;  
XX 13-JAN-2005 (first entry)  
XX Hypoxia-related tumorigenesis-related SAGE tag #950.  
DE screening; hypoxia-related tumorigenesis;  
XX hypoxia-induced gene regulation; tumour; SAGE tag; ds.  
OS Unidentified.  
XX WO2004092198-A2.  
XX 28-OCT-2004.  
XX 09-APR-2004; 2004WO-US011087.  
XX 09-APR-2003; 2003US-0461712P.  
XX (GENZ ) GENZYME CORP.  
XX Nacht M;  
XX WPI; 2004-758333/74.  
XX Identifying agents that alter biological activity of a polypeptide  
PT encoded by a polynucleotide involved in hypoxia-related tumorigenesis  
PT comprises contacting an agent with a target cell and monitoring activity  
PT of expressed product.  
XX Sequence 10 BP; 1 A; 1 C; 5 G; 3 T; 0 U; 0 Other;  
XX

PS Disclosure; Page 74; 100pp; English.  
XX The invention comprises a method of screening for candidate agents  
CC capable of altering the biological activity of a protein encoded by a  
CC nucleotide involved in hypoxia-related tumorigenesis. The method of the  
CC invention involves: contacting a test agent with a target cell expressing  
CC the nucleotide, and monitoring the activity of the expressed protein  
CC product; if the test agent modifies the activity of the expressed protein  
CC then this is a candidate agent. The method of the invention is useful for  
CC modifying hypoxia-induced gene regulation and for diagnosing, prognosing  
CC or treating tumours. The present DNA sequence represents a SAGE tag that  
CC was used in the exemplification of the invention.  
XX Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;  
SQ Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 16 GTGACCTGGT 25  
Db |||||||  
1 GTGACCAGGT 10  
RESULT 311  
ADU19427/c  
ID ADU19427 standard; DNA; 10 BP.  
XX AC ADU19427;  
XX 13-JAN-2005 (first entry)  
XX Hypoxia-related tumorigenesis-related SAGE tag #1218.  
DE screening; hypoxia-related tumorigenesis;  
XX hypoxia-induced gene regulation; tumour; SAGE tag; ds.  
OS Unidentified.  
XX WO2004092198-A2.  
XX 28-OCT-2004.  
XX 09-APR-2004; 2004WO-US011087.  
XX 09-APR-2003; 2003US-0461712P.  
XX (GENZ ) GENZYME CORP.  
XX Nacht M;  
XX WPI; 2004-758333/74.  
XX Identifying agents that alter biological activity of a polypeptide  
PT encoded by a polynucleotide involved in hypoxia-related tumorigenesis  
PT comprises contacting an agent with a target cell and monitoring activity  
PT of expressed product.  
XX Disclosure; Page 79; 100pp; English.  
XX The invention comprises a method of screening for candidate agents  
CC capable of altering the biological activity of a protein encoded by a  
CC nucleotide involved in hypoxia-related tumorigenesis. The method of the  
CC invention involves: contacting a test agent with a target cell expressing  
CC the nucleotide, and monitoring the activity of the expressed protein  
CC product; if the test agent modifies the activity of the expressed protein  
CC then this is a candidate agent. The method of the invention is useful for  
CC modifying hypoxia-induced gene regulation and for diagnosing, prognosing  
CC or treating tumours. The present DNA sequence represents a SAGE tag that  
CC was used in the exemplification of the invention.  
XX Sequence 10 BP; 1 A; 1 C; 5 G; 3 T; 0 U; 0 Other;  
SQ



```
Query Match      29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 ATCCACCTGC 12
Db      10 AACCCACCTGC 1

RESULT 312
AAV55915
ID AAV55915 standard; DNA; 11 BP.
XX
AC AAV55915;
XX
DT 02-DEC-1998 (first entry)
XX
DE CYP1B1 gene exon II 5' splice donor sequence.
XX
KW CYP1B1; human; cytochrome P4501B1; glaucoma; mutation; 8q24 gene;
KW 10p1 gene; glaucoma-associated gene; primary open-angle glaucoma;
KW primary congenital glaucoma; PCG; gene therapy; optical nerve; ss.
XX
OS Homo sapiens.
XX
PN WO9836098-A1.
XX
PD 20-AUG-1998.
XX
PF 12-FEB-1998; 98WO-US002851.
XX
PR 13-FEB-1997; 97US-00800036.
PR 10-SEP-1997; 97US-00926492.
XX
PA (UYCO-) UNIV CONNECTICUT.
XX
PI Sarfarazi M;
XX
DR WPI; 1998-506317/43.
XX
PT Diagnosis of glaucoma by detecting mutations in, or altered expression
PT from, specific genes - also treatment with non-mutant nucleic acid or
PT proteins, or antibodies against mutant protein.
XX
PS Example; Page 30; 61pp; English.
XX
CC Sequences shown in AAV55913 to AAV55916 represent splice donor and
CC acceptor sequences of the exons of the human cytochrome P4501B1 (CYP1B1)
CC gene. The invention provides a method for the diagnosis of glaucoma which
CC comprises detecting a mutation in a glaucoma-associated gene or by
CC detecting altered expression of the protein encoded by the gene. The
CC method is specifically used to diagnose primary open-angle glaucoma,
CC associated with genes at 8q24 or 10p1 and primary congenital glaucoma
CC (PCG), associated with gene CYP1B1, but more generally for any form of
CC the disease having a genetic cause. Glaucoma can be treated with non-
CC mutant forms of the glaucoma-associated protein (or its mimics) and the
CC encoding gene, or antibodies or correction of a mutation by heterologous
CC recombination. Gene therapy methods can be applied in vivo or cells are
CC transfected ex vivo and then returned to the patient. The method allows
CC diagnosis, and treatment, at an early stage, before significant damage to
CC the optical nerve has occurred. Identification of particular mutations
CC allows optimisation of treatment
XX
SQ Sequence 11 BP; 5 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      19 ACCTGGTAAA 28
Db      1 ACCAGGTAAA 10

Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9 CTGCTGTGTG 18
Db      1 CTGCTTTGTG 10

RESULT 314
AAZ18803
ID AAZ18803 standard; DNA; 11 BP.
XX
AC AAZ18803;
```

```
RESULT 313
AAZ18975
ID AAZ18975 standard; DNA; 11 BP.
XX
AC AAZ18975;
XX
DT 22-OCT-1999 (first entry)
XX
DE Murine MRL SAGE tag 1998778.
XX
KW Wound healing; non-MRL healer mouse; quantitative trait locus; QTL;
KW healing response; microsatellite marker; treatment; central nerve;
KW peripheral nerve; nerve injury; SAGE tag; murine; ss.
XX
OS Mus sp.
XX
PN WO9941364-A2.
XX
PD 19-AUG-1999.
XX
PF 12-FEB-1999; 99WO-US002962.
XX
PR 13-FEB-1998; 98US-0074737P.
PR 26-AUG-1998; 98US-0097937P.
PR 28-SEP-1998; 98US-0102051P.
XX
PA (WIST-) WISTAR INST.
XX
PI Heber-Katz E;
XX
DR WPI; 1999-494533/41.
XX
PT New mammalian model for enhanced wound healing - useful for identifying
PT enhanced wound healing genes.
XX
PS Claim 13; Page 73; 136pp; English.
XX
CC This invention describes a novel non-MRL healer mouse (M) having at least
CC one quantitative trait locus selected from those given in the
CC specification, exhibiting an enhanced healing response to a wound
CC compared to mice (m) without the locus. The invention describes a novel
CC method of identifying a gene involved in enhanced wound healing by
CC identifying DNA microsatellite markers which can distinguish healer mice
CC from non-healer mice and identifying microsatellite markers which
CC segregate with enhanced wound healing in progeny of the mice, where a
CC chromosomal locus containing at least one enhanced wound healing gene is
CC identified. A method of treating a wound in a mammal is also disclosed.
CC The new methods are useful for treating wounds, especially central and
CC peripheral nerve wound. The methods of the invention are useful for
CC restoring function after nerve injury in a mammal. (M) is useful as a
CC mammalian model of enhanced wound healing, useful for identifying genes
CC and gene products involved in enhanced wound healing, and to provide
CC methods for wound healing. AAZ18691-219036 represent murine SAGE tags
CC from C57BL/6 and MRL mice which are used to illustrate the method of the
CC invention
XX
SQ Sequence 11 BP; 0 A; 3 C; 3 G; 5 T; 0 U; 0 Other;

Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9 CTGCTGTGTG 18
Db      1 CTGCTTTGTG 10

RESULT 314
AAZ18803
ID AAZ18803 standard; DNA; 11 BP.
XX
AC AAZ18803;
```



XX 22-OCT-1999 (first entry)  
XX  
DE Murine C57BL/6 SAGE tag 1998778.  
XX  
KW Wound healing; non-MRL healer mouse; quantitative trait locus; QTL;  
KW healing response; microsatellite marker; treatment; central nerve;  
KW peripheral nerve; nerve injury; SAGE tag; murine; ss.  
XX  
OS Mus sp.  
XX  
PN WO9941364-A2.  
XX  
PD 19-AUG-1999.  
XX  
PF 12-FEB-1999; 99WO-US002962.  
XX  
PR 13-FEB-1998; 98US-0074737P.  
PR 26-AUG-1998; 98US-0097937P.  
PR 28-SEP-1998; 98US-0102051P.  
XX  
PA (WIST-) WISTAR INST.  
XX  
PI Heber-Katz E;  
XX  
DR WPI; 1999-494533/41.  
XX  
PT New mammalian model for enhanced wound healing - useful for identifying  
PT enhanced wound healing genes.  
XX  
PS Claim 13; Page 57; 136pp; English.  
XX  
CC This invention describes a novel non-MRL healer mouse (M) having at least  
CC one quantitative trait locus selected from those given in the  
CC specification, exhibiting an enhanced healing response to a wound  
CC compared to mice (m) without the locus. The invention describes a novel  
CC method of identifying a gene involved in enhanced wound healing by  
CC identifying DNA microsatellite markers which can distinguish healer mice  
CC from non-healer mice and identifying microsatellite markers which  
CC segregate with enhanced wound healing in progeny of the mice, where a  
CC chromosomal locus containing at least one enhanced wound healing gene is  
CC identified. A method of treating a wound in a mammal is also disclosed.  
CC The new methods are useful for treating wounds, especially central and  
CC peripheral nerve wound. The methods of the invention are useful for  
CC restoring function after nerve injury in a mammal. (M) is useful as a  
CC mammalian model of enhanced wound healing, useful for identifying genes  
CC and gene products involved in enhanced wound healing, and to provide  
CC methods for wound healing. AAZ18691-Z19036 represent murine SAGE tags  
CC from C57BL/6 and MRL mice which are used to illustrate the method of the  
CC invention  
XX  
SQ Sequence 11 BP; 0 A; 3 C; 3 G; 5 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 9 CTGCTGTGTG 18  
|||||  
Db 1 CTGCTTTGTG 10  
  
RESULT 315  
AAA16608/c  
ID AAA16608 standard; DNA; 11 BP.  
XX  
AC AAA16608;  
XX  
DT 16-JUN-2000 (first entry)  
XX  
DE Human MN gene 3' acceptor consensus splice sequence SEQ ID NO:86.  
XX Human; MN protein; MN gene; oncogene; carbonic anhydrase; tumour;

KW oncogenesis; diagnosis; neoplastic disease; cancer; carcinoma;  
KW MN/CA IX isoenzyme; ds.  
XX  
OS Homo sapiens.  
XX  
PN US6027887-A.  
XX  
PD 22-FEB-2000.  
XX  
PF 24-JAN-1997; 97US-00787739.  
XX  
PR 21-OCT-1992; 92US-00964589.  
PR 30-DEC-1993; 93US-00177093.  
PR 15-JUN-1994; 94US-00260190.  
PR 07-JUN-1995; 95US-00477504.  
PR 07-JUN-1995; 95US-00481658.  
PR 07-JUN-1995; 95US-00485049.  
PR 07-JUN-1995; 95US-00485862.  
PR 07-JUN-1995; 95US-00485863.  
PR 07-JUN-1995; 95US-00486756.  
PR 07-JUN-1995; 95US-00487077.  
XX  
PA (SLSC-) SLOVAK ACAD SCI INST VIROLOGY.  
XX  
PI Pastorek J, Zavada J, Pastorekova S;  
XX  
DR WPI; 2000-194827/17.  
XX  
XX Nucleic acid based assay for diagnosing a wide variety of  
PT preneoplastic/neoplastic disease comprises screening for the presence of  
PT abnormal MN gene expression in a vertebrate.  
XX  
PS Disclosure; Col 16; 87pp; English.  
XX  
CC The present invention describes a method of screening for  
CC preneoplastic/neoplastic disease. The method comprises: (1) determining  
CC whether abnormal MN gene expression is present in a vertebrate; and (2)  
CC if abnormal MN gene expression is determined to be present in the  
CC vertebrate, determining that the vertebrate has a significant risk of  
CC having preneoplastic/neoplastic disease. The MN gene is an oncogene and  
CC encodes an MN protein (also referred to as MN/CA IX isoenzyme). The MN  
CC protein is a tumour associated carbonic anhydrase isoenzyme. The method  
CC is used for detecting a wide variety of preneoplastic/neoplastic diseases  
CC in a vertebrate, preferably a human. The disease detected is mammary,  
CC bladder, renal, urinary tract, ovarian, uterine, cervical, endometrial,  
CC vaginal, vulval, prostate, liver, lung, skin, thyroid, pancreatic,  
CC testicular, brain, head and neck, mesodermal, gallbladder, rectal,  
CC duodenal, jejunal, ileal, gastric, pancreatic duct, liver duct, gastric  
CC mucosa, gallbladder epithelium, small intestinal mucosa, colorectal  
CC mucosa, pancreatic duct epithelium or liver duct epithelium  
CC preneoplastic/neoplastic disease. AAA16540 to AAA16617 and AAY53228 to  
CC AAY53245 represent sequences used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 11 BP; 5 A; 2 C; 4 G; 0 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 8 CCTGCTGTGT 17  
|||||  
Db 10 CCTTCTGTGT 1  
  
RESULT 316  
AAA52527/c  
ID AAA52527 standard; DNA; 11 BP.  
XX  
AC AAA52527;  
XX  
DT 25-SEP-2000 (first entry)  
XX

DE Human MN gene intron 10 splice acceptor sequence.

XX MN protein; tumour associated cell adhesion molecule; oncoprotein;

KW proteoglycan domain; PG domain; carbonic anhydrase; CA domain;

KW abnormal expression; neoplastic disease; cancer; gene therapy; ds.

XX Homo sapiens.

OS

XX WO200024913-A2.

PN

XX 04-MAY-2000.

PD

XX 22-OCT-1999; 99WO-US024879.

PF

XX 23-OCT-1998; 98US-00177776.

PR

XX 23-OCT-1998; 98US-00178115.

XX

PA (FARB ) BAYER CORP.

PA (VIRO-) INST VIROLOGY.

XX

PI Zavada J, Pastorekova S, Pastorek J;

XX

DR WPI; 2000-350752/30.

XX

PT A molecule which specifically binds to a site on MN protein (oncoprotein)

PT and prevents adhesion of vertebrate cells to the protein, useful for

PT treating preneoplastic or neoplastic diseases such as cancer.

XX

PS Disclosure; Page 26; 154pp; English.

XX

CC The invention relates to the inhibition of cell adhesion mediated by the

CC MN oncoprotein (also known as the MN/CA IX isoenzyme or the MN/G250

CC protein). The MN protein is a tumour-associated adhesion molecule which

CC comprises a proteoglycan-like (PG) domain (AAB03017) which contains the

CC protein's binding site, and a carbonic anhydrase (CA) domain (AAB03018).

CC Abnormal expression of the MN protein is associated with tumorigenicity.

CC The invention encompasses molecules (e.g., proteins and peptides) which

CC which specifically bind to a site on the MN protein, thereby preventing

CC adhesion of vertebrate cells to the protein in a cell adhesion assay. It

CC also encompasses MN proteins or MN protein fragments which can be added

CC to the extracellular environment to prevent the adhesion of vertebrate

CC cells to each other. The invention also relates to the identification of

CC the binding site of the MN protein and to a method of identifying a site

CC on an MN protein to which cells adhere, comprising testing a series of

CC overlapping peptides from the protein in a cell adhesion assay. The

CC invention encompasses a vector comprising an expression control sequence

CC operatively linked to a nucleic acid encoding the variable domains of a

CC MN-specific antibody, where the domains are separated by a flexible

CC linker peptide (AAB03035) and the vector inhibits the growth of a

CC vertebrate preneoplastic or neoplastic cell that abnormally expresses MN

CC protein. The invention also encompasses a vector comprising a nucleic

CC acid encoding a cytotoxic protein or peptide operatively linked to the MN

CC gene promoter, which inhibits the growth of a vertebrate preneoplastic or

CC neoplastic cell. Also claimed is a repressor complex that binds to the MN

CC gene promoter (AAA52473). MN proteins and peptides, MN-binding proteins

CC and peptides, and expression vectors encoding such proteins and peptides

CC are useful for treating patients with preneoplastic or neoplastic disease

CC (e.g., cancers) associated with or characterised by abnormal MN

CC expression. The present sequence represents a fragment of the human MN

CC gene (AAA52462) specified in the invention

XX

SQ Sequence 11 BP; 5 A; 2 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 1.8e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGT 17

Db ||| |||||

10 CCTTCTGTGT 1

RESULT 317

AAF75228

ID AAF75228 standard; DNA; 11 BP.

XX

AC AAF75228;

XX

DT 09-MAY-2001 (first entry)

XX

DE Human RXR binding element, SEQ ID NO: 28.

XX

KW Human; peroxisome proliferator-activator receptor delta; PPARDelta; RXR;

KW cytosolic; neurotropic; neuroprotective; anti-HIV; cardiant;

KW cerebroprotective; vasotropic; antitumor; immunosuppressive;

KW nephrotropic; antibacterial; antiviral; antifungal; protozoacide;

KW non-steroidal anti-inflammatory disease; NSAID; infection;

KW Alzheimer's disease; AIDS; muscle wasting disease; autoimmune disease;

KW binding element; ds.

XX

OS Homo sapiens.

XX

PN WO200112858-A1.

XX

PD 22-FEB-2001.

XX

PF 16-AUG-2000; 2000WO-US022411.

XX

PR 16-AUG-1999; 99US-0148701P.

PR 15-AUG-2000; 2000US-00638623.

XX

PA (UYJO ) UNIV JOHNS HOPKINS.

XX

PI He T, Kinzler KW, Vogelstein B;

XX

DR WPI; 2001-211236/21.

XX

PT Novel subgenomic polynucleotide having peroxisome proliferator-activator

PT receptor proliferator (PPAR-Delta) and RXR binding elements used to

PT identify downregulators of PPAR-delta transcriptional activity.

XX

PS Claim 1; Fig 3A; 70pp; English.

XX

CC The present sequence is provided in a specification relating to an

CC isolated subgenomic polynucleotide comprising a peroxisome proliferator-

CC activator receptor (PPAR)delta binding element and an RXR binding

CC element. The polynucleotide is useful for identifying potential

CC therapeutic agents for cancer treatment and for ameliorating negative

CC side effects of non-steroidal anti-inflammatory diseases (NSAIDs). Test

CC compounds which increase transcription of PPARDelta protein, PPARDelta

CC protein binding to a PPARDelta binding element, or expression of a

CC reporter gene which is under the control of a PPARDelta binding element,

CC are identified. These are candidates for use in encouraging cell

CC proliferation or preventing cell apoptosis in a disease state such as

CC Alzheimer's disease, AIDS, muscular dystrophy, amyotrophic lateral

CC sclerosis, or other muscle wasting diseases, autoimmune diseases, heart

CC attack, stroke, ischaemic heart disease, kidney failure, septic shock, or

CC a disease in which the cell is infected with a pathogen, such as a virus,

CC bacterium, fungus, mycoplasma, or protozoan, to promote healing of the

CC stomach or intestines, or to ameliorate negative side effects of NSAIDs,

CC such as gastric and intestinal ulceration

XX

SQ Sequence 11 BP; 2 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 1.8e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 20 CCTGTTAAAT 29

Db ||||| |||

1 CCTGGTCAAT 10

RESULT 318

ABQ86838/c

ID ABQ86838 standard; cDNA; 11 BP.

```
XX AC ABQ86838;
XX DT 10-SEP-2002 (first entry)
XX DE Human skin stress/ageing related EST SEQ ID NO 593.
XX KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX PN WO200253773-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015178.
XX PR 03-JAN-2001; 2001DE-01000121.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX DR WPI; 2002-528865/56.
XX PT Identifying genes involved in skin stress and aging, useful e.g. in
XX PT screening for cosmetic or therapeutic agents, based on differential gene
XX PT expression.
XX PS Claim 8; Page 61; 325pp; German.
XX CC The invention relates to identifying (M1) genes in vitro that, in humans
XX CC or animals, are important for skin ageing and/or skin stress by serial
XX CC analysis of gene expression between mixtures of transcribed and
XX CC optionally translated, genetically encoded factors (A) obtained from
XX CC young and aged skin, to identify that genes that show strong differential
XX CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
XX CC useful for: identifying markers of skin ageing and/or stress; determining
XX CC skin ageing and/or stress; and identifying or determining the effects of
XX CC pharmaceutical or cosmetic agents for control of skin ageing. The present
XX CC sequence is one of a group of human skin ageing/stress related expressed
XX CC sequence tags (ABQ86246-ABQ87680) of the invention
XX SQ Sequence 11 BP; 2 A; 2 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATCCACCTGC 12
Db ||||| |||||
10 ATCCAACTGC 1

RESULT 319
ABQ86763/c
ID ABQ86763 standard; cDNA; 11 BP.
XX AC ABQ86763;
XX DT 10-SEP-2002 (first entry)
XX DE Human skin stress/ageing related EST SEQ ID NO 518.
XX KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX PN WO200253773-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015178.
```

```
XX PR 03-JAN-2001; 2001DE-01000121.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX DR WPI; 2002-528865/56.
XX PT Identifying genes involved in skin stress and aging, useful e.g. in
XX PT screening for cosmetic or therapeutic agents, based on differential gene
XX PT expression.
XX PS Claim 8; Page 58; 325pp; German.
XX CC The invention relates to identifying (M1) genes in vitro that, in humans
XX CC or animals, are important for skin ageing and/or skin stress by serial
XX CC analysis of gene expression between mixtures of transcribed and
XX CC optionally translated, genetically encoded factors (A) obtained from
XX CC young and aged skin, to identify that genes that show strong differential
XX CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
XX CC useful for: identifying markers of skin ageing and/or stress; determining
XX CC skin ageing and/or stress; and identifying or determining the effects of
XX CC pharmaceutical or cosmetic agents for control of skin ageing. The present
XX CC sequence is one of a group of human skin ageing/stress related expressed
XX CC sequence tags (ABQ86246-ABQ87680) of the invention
XX SQ Sequence 11 BP; 5 A; 2 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGT 17
Db ||||| |||||
11 CCTCCTGTGT 2

RESULT 320
ABQ86990
ID ABQ86990 standard; cDNA; 11 BP.
XX AC ABQ86990;
XX DT 10-SEP-2002 (first entry)
XX DE Human skin stress/ageing related EST SEQ ID NO 745.
XX KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX PN WO200253773-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015178.
XX PR 03-JAN-2001; 2001DE-01000121.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX DR WPI; 2002-528865/56.
XX PT Identifying genes involved in skin stress and aging, useful e.g. in
XX PT screening for cosmetic or therapeutic agents, based on differential gene
XX PT expression.
XX PS Claim 8; Page 68; 325pp; German.
XX CC The invention relates to identifying (M1) genes in vitro that, in humans
```

CC or animals, are important for skin ageing and/or skin stress by serial  
CC analysis of gene expression between mixtures of transcribed and  
CC optionally translated, genetically encoded factors (A) obtained from  
CC young and aged skin, to identify that genes that show strong differential  
CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is  
CC useful for: identifying markers of skin ageing and/or stress; determining  
CC skin ageing and/or stress; and identifying or determining the effects of  
CC pharmaceutical or cosmetic agents for control of skin ageing. The present  
CC sequence is one of a group of human skin ageing/stress related expressed  
CC sequence tags (ABQ86246-ABQ87680) of the invention  
XX  
SQ Sequence 11 BP; 1 A; 6 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATCCACCTGC 12  
Db 1 ATCGCCTGC 10

RESULT 321  
ABQ87167/C  
ID ABQ87167 standard; cDNA; 11 BP.

AC ABQ87167;  
DT 10-SEP-2002 (first entry)  
XX Human skin stress/ageing related EST SEQ ID NO 922.  
DE Human; skin ageing; skin stress; EST; expressed sequence tag; ss.  
XX Homo sapiens.  
OS WO200253773-A2.  
PN 11-JUL-2002.  
XX 20-DEC-2001; 2001WO-EP015178.  
XX 03-JAN-2001; 2001DE-01000121.  
XX (HENK ) HENKEL KGAA.  
PI Petersohn D, Conradt M, Hofmann K;  
XX WPI; 2002-528865/56.  
DR Identifying genes involved in skin stress and aging, useful e.g. in  
PT screening for cosmetic or therapeutic agents, based on differential gene  
PT expression.  
XX Claim 8; Page 75; 325pp; German.

XX The invention relates to identifying (M1) genes in vitro that, in humans  
CC or animals, are important for skin ageing and/or skin stress by serial  
CC analysis of gene expression between mixtures of transcribed and  
CC optionally translated, genetically encoded factors (A) obtained from  
CC young and aged skin, to identify that genes that show strong differential  
CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is  
CC useful for: identifying markers of skin ageing and/or stress; determining  
CC skin ageing and/or stress; and identifying or determining the effects of  
CC pharmaceutical or cosmetic agents for control of skin ageing. The present  
CC sequence is one of a group of human skin ageing/stress related expressed  
CC sequence tags (ABQ86246-ABQ87680) of the invention  
XX  
SQ Sequence 11 BP; 3 A; 6 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 GTGACCTGGT 25  
Db 10 GTGGCCTGGT 1

RESULT 322  
ABQ87430  
ID ABQ87430 standard; cDNA; 11 BP.  
XX AC ABQ87430;  
XX 10-SEP-2002 (first entry)  
DT Human skin stress/ageing related EST SEQ ID NO 1185.  
DE Human; skin ageing; skin stress; EST; expressed sequence tag; ss.  
XX Homo sapiens.  
OS WO200253773-A2.  
PN 11-JUL-2002.  
XX 20-DEC-2001; 2001WO-EP015178.  
XX 03-JAN-2001; 2001DE-01000121.  
XX (HENK ) HENKEL KGAA.  
PI Petersohn D, Conradt M, Hofmann K;  
XX WPI; 2002-528865/56.  
DR Identifying genes involved in skin stress and aging, useful e.g. in  
PT screening for cosmetic or therapeutic agents, based on differential gene  
PT expression.  
XX Claim 8; Page 86; 325pp; German.

XX The invention relates to identifying (M1) genes in vitro that, in humans  
CC or animals, are important for skin ageing and/or skin stress by serial  
CC analysis of gene expression between mixtures of transcribed and  
CC optionally translated, genetically encoded factors (A) obtained from  
CC young and aged skin, to identify that genes that show strong differential  
CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is  
CC useful for: identifying markers of skin ageing and/or stress; determining  
CC skin ageing and/or stress; and identifying or determining the effects of  
CC pharmaceutical or cosmetic agents for control of skin ageing. The present  
CC sequence is one of a group of human skin ageing/stress related expressed  
CC sequence tags (ABQ86246-ABQ87680) of the invention  
XX  
SQ Sequence 11 BP; 1 A; 4 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCCACCTGCT 13  
Db 2 TCCAGCTGCT 11

RESULT 323  
ABQ86674  
ID ABQ86674 standard; cDNA; 11 BP.  
XX AC ABQ86674;  
XX 10-SEP-2002 (first entry)

DT Human skin stress/ageing related EST SEQ ID NO 429.  
DE  
XX



KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253773-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015178.  
XX  
PR 03-JAN-2001; 2001DE-01000121.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX WPI; 2002-528865/56.  
DR  
XX Identifying genes involved in skin stress and aging, useful e.g. in  
PT screening for cosmetic or therapeutic agents, based on differential gene  
PT expression.  
XX  
PS Claim 8; Page 54; 325pp; German.  
XX  
CC The invention relates to identifying (M1) genes in vitro that, in humans  
CC or animals, are important for skin ageing and/or skin stress by serial  
CC analysis of gene expression between mixtures of transcribed and  
CC optionally translated, genetically encoded factors (A) obtained from  
CC young and aged skin, to identify that genes that show strong differential  
CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is  
CC useful for: identifying markers of skin ageing and/or stress; determining  
CC skin ageing and/or stress; and identifying or determining the effects of  
CC pharmaceutical or cosmetic agents for control of skin ageing. The present  
CC sequence is one of a group of human skin ageing/stress related expressed  
CC sequence tags (ABQ86246-ABQ87680) of the invention  
XX  
SQ Sequence 11 BP; 2 A; 7 C; 1 G; 1 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 ATCCACCTGC 12  
Db 1 ATCCACCCGC 10  
  
RESULT 324  
ABV63315  
ID ABV63315 standard; cDNA; 11 BP.  
XX  
AC ABV63315;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 1101.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX

PI Petersohn D, Conradt M, Hofmann K;  
XX WPI; 2002-590638/63.  
DR  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 55; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 1 A; 6 C; 2 G; 2 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 ATCCACCTGC 12  
Db 1 ATCCGCCTGC 10  
  
RESULT 325  
ABV66003/C  
ID ABV66003 standard; cDNA; 11 BP.  
XX  
AC ABV66003;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 3789.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 130; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)



CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 3 A; 6 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 GTGACCTGGT 25  
Db 10 GTGGCCTGGT 1  
||| |||||

RESULT 326  
ABV68983  
ID ABV68983 standard; cDNA; 11 BP.  
XX  
AC ABV68983;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 6769.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 213; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 1 A; 3 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 TGTGTGACCT 22  
Db 1 TCTGTGACCT 10  
||| |||||

RESULT 327  
ABV67130/c  
ID ABV67130 standard; cDNA; 11 BP.  
XX  
AC ABV67130;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 4916.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 160; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 3 A; 0 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCCACCTGCT 13  
Db 11 TCCACCTCCT 2  
||| ||||| ||

RESULT 328  
ABV67225  
ID ABV67225 standard; cDNA; 11 BP.  
XX  
AC ABV67225;

XX 21-OCT-2002 (first entry)  
XX Human skin EST 5011.  
DE  
DE Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200253774-A2.  
PN  
XX 11-JUL-2002.  
PD  
XX 20-DEC-2001; 2001WO-EP015179.  
PF  
XX 03-JAN-2001; 2001DE-01000127.  
PR  
XX (HENK ) HENKEL KGAA.  
PA  
XX Petersohn D, Conradt M, Hofmann K;  
PI  
XX WPI; 2002-590638/63.  
DR  
XX In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 163; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 3 A; 6 C; 1 G; 1 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 ATCCACCTGC 12  
| | | | | | | |  
Db 1 ACCCACCTGC 10  
  
RESULT 329  
ABV67773/c  
ID ABV67773 standard; cDNA; 11 BP.  
XX  
AC ABV67773;  
XX  
DT 21-OCT-2002 (first entry)  
DE Human skin EST 5559.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX

PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX (HENK ) HENKEL KGAA.  
PA  
XX Petersohn D, Conradt M, Hofmann K;  
PI  
XX WPI; 2002-590638/63.  
DR  
XX In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 178; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 3 A; 0 C; 5 G; 3 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 ATCCACCTGC 12  
| | | | | | | |  
Db 11 ATCCACCTTC 2  
  
RESULT 330  
ABV62764/c  
ID ABV62764 standard; cDNA; 11 BP.  
XX  
AC ABV62764;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 550.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX (HENK ) HENKEL KGAA.  
PA  
XX Petersohn D, Conradt M, Hofmann K;  
PI  
XX WPI; 2002-590638/63.  
DR  
XX In vitro identification of skin-expressed genes, useful for determining  
PT

PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 40; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 4 A; 0 C; 6 G; 1 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 4 TCCACCTGCT 13  
Db 11 TCCACCTCCT 2  
  
RESULT 331  
ABV62815/c  
ID ABV62815 standard; cDNA; 11 BP.  
XX  
AC ABV62815;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 601.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 601.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 42; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;

CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 5 A; 2 C; 4 G; 0 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 8 CCTGCTGTGT 17  
Db 11 CCTCCTGTGT 2  
  
RESULT 332  
ABV69214  
ID ABV69214 standard; cDNA; 11 BP.  
XX  
AC ABV69214;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 7000.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 220; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 1 A; 2 C; 5 G; 3 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 10 TGCTGTGTGA 19  
||||| |||||

Db 2 TGCTGCGTGA 11

RESULT 333

ABV70185/c

ID ABV70185 standard; cDNA; 11 BP.

XX AC ABV70185;

XX 21-OCT-2002 (first entry)

XX Human skin EST 7971.

DE

XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

OS Homo sapiens.

XX WO200253774-A2.

PN 11-JUL-2002.

PD 20-DEC-2001; 2001WO-EP015179.

XX 03-JAN-2001; 2001DE-01000127.

PR (HENK ) HENKEL KGAA.

PA Petersohn D, Conradt M, Hofmann K;

XX WPI; 2002-590638/63.

DR In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

XX Claim 24; Page 254; 1345pp; German.

PS The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention

XX Sequence 11 BP; 4 A; 0 C; 6 G; 1 T; 0 U; 0 Other;

SQ Query Match 29.0%; Score 8.4; DB 1; Length 11; Best Local Similarity 90.0%; Pred. No. 1.8e+02; Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCCACCTGCT 13

Db 11 TCCACCTCCT 2

RESULT 334

ABV70837/c

ID ABV70837 standard; cDNA; 11 BP.

XX AC ABV70837;

XX 21-OCT-2002 (first entry)

DT Human skin EST 8623.

XX

KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

XX Homo sapiens.

OS WO200253774-A2.

PN 11-JUL-2002.

PD 20-DEC-2001; 2001WO-EP015179.

XX 03-JAN-2001; 2001DE-01000127.

PR (HENK ) HENKEL KGAA.

PA Petersohn D, Conradt M, Hofmann K;

XX WPI; 2002-590638/63.

DR In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

XX Claim 24; Page 276; 1345pp; German.

PS The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention

XX Sequence 11 BP; 6 A; 3 C; 2 G; 0 T; 0 U; 0 Other;

SQ Query Match 29.0%; Score 8.4; DB 1; Length 11; Best Local Similarity 90.0%; Pred. No. 1.8e+02; Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGT 17

Db 10 CTTGCTGTGT 1

RESULT 335

ABV65404

ID ABV65404 standard; cDNA; 11 BP.

XX AC ABV65404;

XX 21-OCT-2002 (first entry)

DT Human skin EST 3190.

XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

OS Homo sapiens.

XX WO200253774-A2.

PN 11-JUL-2002.

PD 20-DEC-2001; 2001WO-EP015179.

XX 03-JAN-2001; 2001DE-01000127.



XX (HENK ) HENKEL KGAA.  
PA  
XX Petersohn D, Conradt M, Hofmann K;  
PI  
XX WPI; 2002-590638/63.  
DR  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 113; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 1 A; 4 C; 2 G; 4 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 TCCACCTGCT 13  
Db 2 TCCAGCTGCT 11  
  
RESULT 336  
ABV66252/c  
ID ABV66252 standard; cDNA; 11 BP.  
XX  
AC ABV66252;  
XX  
DT 21-OCT-2002 (first entry)  
DE Human skin EST 4038.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX (HENK ) HENKEL KGAA.  
PI Petersohn D, Conradt M, Hofmann K;  
XX WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 137; 1345pp; German.  
XX

CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 7 ACCTGCTGTG 16  
Db 10 ACCTGCTGGG 1  
  
RESULT 337  
ABV67008  
ID ABV67008 standard; cDNA; 11 BP.  
XX  
AC ABV67008;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 4794.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX (HENK ) HENKEL KGAA.  
PI Petersohn D, Conradt M, Hofmann K;  
XX WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 157; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX



SQ Sequence 11 BP; 2 A; 7 C; 1 G; 1 T; 0 U; 0 Other;  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 ATCCACCTGC 12  
| | | | | | | |  
Db 1 ATCCACCCGC 10  
| | | | | | | |  
RESULT 338  
ABV69518/c  
ID ABV69518 standard; cDNA; 11 BP.  
XX  
AC ABV69518;  
XX  
DT 21-OCT-2002 (first entry)  
XX Human skin EST 7304.  
DE  
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
AC ABV69518;  
XX  
DT 21-OCT-2002 (first entry)  
XX Human skin EST 7304.  
DE  
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX (HENK ) HENKEL KGAA.  
PA  
XX Petersohn D, Conradt M, Hofmann K;  
PI  
XX WPI; 2002-590638/63.  
DR  
XX In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX (HENK ) HENKEL KGAA.  
PA  
XX Petersohn D, Conradt M, Hofmann K;  
PI  
XX WPI; 2002-590638/63.  
DR  
XX In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PF Disclosure; Page 229; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 1 A; 1 C; 5 G; 4 T; 0 U; 0 Other;  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 ATCCACCTGC 12  
| | | | | | | |  
Db 10 AACACCTGC 1  
| | | | | | | |  
RESULT 339  
ABV70736

ID ABV70736 standard; cDNA; 11 BP.  
XX  
AC ABV70736;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 8522.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX (HENK ) HENKEL KGAA.  
PA  
XX Petersohn D, Conradt M, Hofmann K;  
PI  
XX WPI; 2002-590638/63.  
DR  
XX In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Claim 24; Page 273; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 1 A; 6 C; 2 G; 2 T; 0 U; 0 Other;  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 ATCCACCTGC 12  
| | | | | | | |  
Db 1 ATCCGCCTGC 10  
| | | | | | | |  
RESULT 340  
ABV66438  
ID ABV66438 standard; cDNA; 11 BP.  
XX  
AC ABV66438;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 4224.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.



CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 1 A; 5 C; 2 G; 3 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 TCCACCTGCT 13  
Db 2 TCCACCTGGT 11  
||| |||||  
  
RESULT 343  
ABV70236/C  
ID ABV70236 standard; cDNA; 11 BP.  
XX  
AC ABV70236;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 8022.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Claim 24; Page 255; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 5 A; 2 C; 4 G; 0 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGT 17  
||| |||||  
Db 11 CCTCCTGTGT 2  
  
RESULT 344  
ABV63416/C  
ID ABV63416 standard; cDNA; 11 BP.  
XX  
AC ABV63416;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 1202.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 58; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 6 A; 3 C; 2 G; 0 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 8 CCTGCTGTGT 17  
||| |||||  
Db 10 CTTGCTGTGT 1  
  
RESULT 345  
ABV64243/C  
ID ABV64243 standard; cDNA; 11 BP.  
XX  
AC ABV64243;  
XX  
DT 21-OCT-2002 (first entry)

XX Human skin EST 2029.  
DE  
XX  
KW Human; skin; dermatological; vulnerrary; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 81; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 2 A; 2 C; 4 G; 3 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 ATCCACCTGC 12  
|||  
Db 10 ATCCAACCTGC 1  
  
RESULT 346  
ABV67475/c  
ID ABV67475 standard; cDNA; 11 BP.  
XX  
AC ABV67475;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 5261.  
XX  
KW Human; skin; dermatological; vulnerrary; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX

PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 170; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 2 A; 5 C; 2 G; 2 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 17 TGACCTGGTA 26  
|||  
Db 11 TGACCTGGGA 2  
  
RESULT 347  
ABV71664/c  
ID ABV71664 standard; cDNA; 11 BP.  
XX  
AC ABV71664;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 9450.  
XX  
KW Human; skin; dermatological; vulnerrary; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
PT

XX Claim 24; Page 305; 1345pp; German.

XX The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention

XX Sequence 11 BP; 2 A; 2 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATCCACCTGC 12  
|||||

Db 10 ATCCAACCTGC 1

RESULT 348  
ABV67586

ID ABV67586 standard; cDNA; 11 BP.

XX

AC ABV67586;

XX 21-OCT-2002 (first entry)

XX Human skin EST 5372.

XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

OS Homo sapiens.

XX WO200253774-A2.

XX 11-JUL-2002.

XX 20-DEC-2001; 2001WO-EP015179.

XX 03-JAN-2001; 2001DE-01000127.

XX (HENK ) HENKEL KGAA.

XX Petersohn D, Conradt M, Hofmann K;

XX WPI; 2002-590638/63.

XX In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

XX Disclosure; Page 173; 1345pp; German.

XX The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the

CC skin. The present sequence is that of a human expressed sequence tag (EST) of the invention

XX Sequence 11 BP; 2 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 GTGTGACCTG 23  
|||||

Db 2 GTGAGACCTG 11

RESULT 349  
ABV68554/C

ID ABV68554 standard; cDNA; 11 BP.

XX

AC ABV68554;

XX 21-OCT-2002 (first entry)

XX Human skin EST 6340.

XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

OS Homo sapiens.

XX WO200253774-A2.

XX 11-JUL-2002.

XX 20-DEC-2001; 2001WO-EP015179.

XX 03-JAN-2001; 2001DE-01000127.

XX (HENK ) HENKEL KGAA.

XX Petersohn D, Conradt M, Hofmann K;

XX WPI; 2002-590638/63.

XX In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

XX Disclosure; Page 201; 1345pp; German.

XX The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention

XX Sequence 11 BP; 3 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCCACCTGCT 13  
|||||

Db 11 TCCAGCTGCT 2



RESULT 350  
AAD40434  
ID AAD40434 standard; DNA; 11 BP.  
XX  
AC AAD40434;  
XX  
DT 22-OCT-2002 (first entry)  
XX  
DE Bovine DGAT1 gene fragment #11.  
XX  
KW Bovine; diacylglycerol acyltransferase; genotyping; milk production;  
KW DGAT1; polymorphism; farming industry; transgenic; ds.  
XX  
OS Bos taurus.  
XX  
PN WO200236824-A1.  
XX  
PD 10-MAY-2002.  
XX  
PF 31-OCT-2001; 2001WO-NZ000245.  
XX  
PR 31-OCT-2000; 2000NZ-00507888.  
PR 06-DEC-2000; 2000NZ-00508662.  
XX  
PA (GEOR/) GEORGES M A J.  
PA (COPP/) COPPIETERS W H R.  
PA (GRIS/) GRISART B M J.  
PA (SNEL/) SNELL R G.  
PA (REID/) REID S J.  
PA (FORD/) FORD C A.  
PA (SPEL/) SPELMAN R J.  
XX  
PI Georges MAJ, Coppieters WHR, Grisart BMJ, Snell RG, Reid SJ;  
PI Ford CA, Spelman RJ;  
XX  
DR WPI; 2002-500128/53.  
XX  
PT Determining genetic merit of a bovine with respect to milk composition  
PT and volume for improved milk production, comprises determining the  
PT diacylglycerol acyltransferase gene genotypic state of the bovine.  
XX  
PS Claim 4; Page 8; 128pp; English.  
XX  
CC The invention relates to a method of genotyping bovine for improved milk  
CC production traits which comprises determining the diacylglycerol  
CC acyltransferase (DGAT1) genotypic state of the bovine, wherein the DGAT1  
CC gene and polymorphisms have been found to be associated with such  
CC improved milk production traits. The method is useful for selecting a  
CC bovine having a desired DGAT1 genotypic state. It is also useful for the  
CC identification and selection of a bovine having one of the polymorphisms  
CC in its DGAT1 gene. Milk produced from selected bovine which is useful for  
CC making a dairy product provides a beneficial health effect. An antibody  
CC to the protein having DGAT1 activity is useful for inhibiting the  
CC activity of bovine DGAT1 in a lactating bovine so as to modulate milk  
CC production and/or milk solids content. DGAT1 nucleic acid and its  
CC fragments are useful in the farming industry. They are also useful to  
CC generate transgenic animals which are useful to investigate the molecular  
CC basis of DGAT1 action and to test a substance for the ability to prevent,  
CC slow or enhance DGAT1 activity. The present sequence is bovine DGAT1 gene  
CC fragment. This sequence is used to illustrate the method of the invention  
XX  
SQ Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 14 GTGTGACCTG 23  
| | | | | | | |  
Db 1 GAGTGACCTG 10

RESULT 351  
ABV78654  
ID ABV78654 standard; DNA; 11 BP.  
XX  
AC ABV78654;  
XX  
DT 26-NOV-2002 (first entry)  
XX  
DE RXR binding site from clone X9TOP.  
XX  
KW PPARDelta; peroxisome proliferator-activated receptor delta; nootropic;  
KW neuroprotective; anti-HIV; cardiant; cytostatic; antiinflammatory;  
KW immunosuppressive; cerebroprotective; gene therapy; inflammation; cancer;  
KW Alzheimer's disease; AIDS; muscular dystrophy; autoimmune disease;  
KW heart attack; stroke; fecundity; RXR; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200268386-A2.  
XX  
PD 06-SEP-2002.  
XX  
PF 27-FEB-2002; 2002WO-US003408.  
XX  
PR 27-FEB-2001; 2001US-0271412P.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Park BH, Kinzler KW, Vogelstein B;  
XX  
DR WPI; 2002-691649/74.  
XX  
PT Homozygous PPAR gene-defective cell line, useful for treating  
PT inflammation and cancer and disorders associated with premature cell  
PT death such as Alzheimer's disease, AIDS, muscular dystrophy, autoimmune  
PT diseases and heart attacks.  
XX  
PS Example 2; Fig 6; 33pp; English.  
XX  
CC The invention relates to a novel homoygous peroxisome proliferator-  
CC activated receptor delta (PPARDelta) gene-defective cell line. The  
CC compositions of the invention have nootropic, neuroprotective, anti-HIV,  
CC cardiant, cytostatic, antiinflammatory, immunosuppressive, and  
CC cerebroprotective activity. The cell lines may have a use in gene  
CC therapy. The methods and compositions are useful for treating cell  
CC inflammation and cancer and other disorders with increased cell  
CC proliferation or in which cells are dying prematurely such as Alzheimer's  
CC disease, AIDS, muscular dystrophy, autoimmune diseases, heart attack and  
CC stroke, improving fecundity and/or ameliorating toxic effects of non-  
CC steroidal antiinflammatory drugs. The sequence represents a PCR product  
CC of an oligonucleotide template that bound a fusion protein containing the  
CC DNA binding domain of RXR  
XX  
SQ Sequence 11 BP; 2 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 20 CCTGGTAAAT 29  
| | | | | | | |  
Db 1 CCTGGTCAAT 10

RESULT 352  
ADG13667/c  
ID ADG13667 standard; RNA; 11 BP.  
XX  
AC ADG13667;  
XX  
DT 26-FEB-2004 (first entry)  
XX  
DE Human EGFR Amberzyme target sequence #15.

XX Human; ss; EGFR; epidermal growth factor receptor; HER1; HER2; HER3;  
KW HER4; hammerhead ribozyme; inozyme; zinzyme; DNazyme; amberzyme; cancer;  
KW brain tumour; cytostatic; short interfering RNA; siRNA; RNA interference;  
KW prostate cancer; colorectal cancer; brain cancer; oesophageal cancer;  
KW stomach cancer; bladder cancer; pancreatic cancer; cervical cancer;  
KW head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma;  
KW multidrug resistant cancer.  
XX  
OS Homo sapiens.  
XX  
PN US2003186909-A1.  
XX  
PD 02-OCT-2003.  
XX  
PF 21-OCT-2002; 2002US-00277494.  
XX  
PR 27-JAN-1997; 97US-0036749P.  
PR 04-DEC-1997; 97US-00985162.  
PR 22-SEP-1999; 99US-00401063.  
PR 03-MAY-2001; 2001US-00848754.  
PR 25-JUL-2001; 2001US-00916466.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Mcswiggen J;  
XX  
DR WPI; 2004-032029/03.  
XX  
PT New double stranded short interfering ribonucleic acid molecule for  
PT inhibiting expression of epidermal growth factor receptor gene.  
XX  
PS Claim 7; SEQ ID NO 94; 113pp; English.  
XX  
CC The invention relates to a double stranded short interfering RNA (siRNA)  
CC molecule that inhibits expression of epidermal growth factor receptor  
CC (EGFR) gene (e.g. HER1-4) by RNA interference is new. Also included is an  
CC expression vector comprising a nucleic acid sequence encoding siRNA  
CC molecule(s) in a manner that allows expression of the nucleic acid  
CC molecule. The siRNA molecules comprise hammerhead ribozymes, inozymes,  
CC amberzymes zinzymes and DNazymes. The invention is used for inhibiting  
CC expression of EGFR. It can be used for treatment of cancer, prostate  
CC cancer, colorectal cancer, brain cancer, oesophageal cancer, stomach  
CC cancer, bladder cancer, pancreatic cancer, cervical cancer, head and neck  
CC cancer, ovarian cancer, melanoma, lymphoma, glioma, multidrug resistant  
CC cancer or a brain tumour. The invention has enhanced shelf-life, half-  
CC life in vitro , stability, and ease of introduction of oligonucleotide to  
CC target site. The present sequence is an EGFR/HER1-4 target sequence for  
CC an siRNA of the invention.  
XX  
SQ Sequence 11 BP; 3 A; 1 C; 5 G; 0 T; 2 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCCACCT 10  
Db |||||  
10 CCATCCACTT 1

RESULT 353  
ADK41836/c  
ID ADK41836 standard; DNA; 11 BP.  
XX  
AC ADK41836;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Human MN gene intron-exon boundary sequence SeqID65.  
XX  
KW carbonic anhydrase IX; CA IX; precancerous cell; MN; cancerous cell;  
KW human; vertebrate; cytostatic; vaccine; gene therapy;

KW renal cell carcinoma; breast cancer; colorectal cancer; splice acceptor;  
KW ds.  
XX  
OS Homo sapiens.  
XX  
PN WO2004005348-A1.  
XX  
PD 15-JAN-2004.  
XX  
PF 22-FEB-2003; 2003WO-US005137.  
XX  
PR 23-MAY-2002; 2002US-0383068P.  
PR 05-DEC-2002; 2002US-0431499P.  
XX  
PA (FARB ) BAYER CORP.  
PA (VIRO-) INST VIROLOGY.  
XX  
PI Zavada J, Pastorekova S, Pastorek J, Zavadova Z;  
XX WPI; 2004-083500/08.  
DR  
XX  
PT New soluble form of the carbonic anhydrase IX (CA IX) protein for  
PT screening, diagnosing or prognosing diseases associated with abnormal  
PT expression of CA IX protein, e.g. renal cell carcinoma, breast cancer or  
PT colorectal cancer.  
XX  
PS Disclosure; SEQ ID NO 65; 159pp; English.  
XX  
CC This invention relates to a novel soluble form of the carbonic anhydrase  
CC IX (CA IX) (or MN) protein or CA IX polypeptide which is released from  
CC precancerous and/or cancerous cells of a vertebrate into a body fluid.  
CC The invention may be useful for the development of compounds with a  
CC cytostatic activity or a vaccine whilst the disclosed sequences may be  
CC used for gene therapy. The protein and method are useful for screening,  
CC diagnosing or prognosing diseases associated with abnormal expression of  
CC carbonic anhydrase IX protein, such as precancerous and cancerous  
CC diseases like renal cell carcinoma, breast cancer or colorectal cancer.  
CC The monoclonal antibody may also be used for treating or preventing  
CC precancerous and cancerous diseases. The present sequence is that of a  
CC splice acceptor site from a human MN gene intron-exon boundary which is  
CC related to the invention.  
XX  
SQ Sequence 11 BP; 5 A; 2 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGT 17  
Db |||||  
10 CCTTCTGTGT 1

RESULT 354  
ADQ35801/c  
ID ADQ35801 standard; DNA; 11 BP.  
XX  
AC ADQ35801;  
XX  
DT 23-SEP-2004 (first entry)  
XX  
DE Human hair-bearing skin-associated DNA fragment SEQ ID NO 618.  
XX  
KW hair-bearing skin; human; serial analysis of gene expression; SAGE;  
KW homeostasis; cosmetic; pharmaceutical; biochip; ds.  
XX  
OS Homo sapiens.  
XX  
PN DE10260931-A1.  
XX  
PD 08-JUL-2004.  
XX  
PF 20-DEC-2002; 2002DE-01060931.

XX 20-DEC-2002; 2002DE-01060931.  
PR (HENK ) HENKEL KGAA.  
XX  
PA  
XX  
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;  
PI Conradt M, Hofmann K;  
XX  
DR WPI; 2004-518857/50.  
XX  
XX In vitro identification of genes important for hair-bearing skin, useful  
PT for assessing homeostasis and in screening for pharmaceutical or cosmetic  
PT agents, based on differential expression analysis.  
XX  
PS Claim 5; SEQ ID NO 618; 250pp; German.  
XX  
CC This invention describes a novel in vitro method for identifying genes  
CC that are significant for hair-bearing skin in humans. The method  
CC comprises recovering, from hair-bearing skin, a first mixture of  
CC genetically expressed (transcribed and optionally translated) factors  
CC (i.e. proteins, mRNA or their fragments), recovering a second, similar  
CC mixture from skin on which hair does not grow and subjecting both  
CC mixtures to serial analysis of gene expression (SAGE) to identify those  
CC genes for which expression is markedly different between the two types of  
CC skin. The invention also describes in vitro methods for determining  
CC homeostasis of human hair-bearing skin and for determining activity of  
CC cosmetic and pharmaceutical agents for use against disorders or  
CC disturbances of the homeostasis of human hair-bearing skin. A biochip and  
CC a test kit comprising a solid support (flexible or rigid) with  
CC immobilised probes are also described for determining homeostasis. The  
CC hair-bearing skin is from the scalp and the other skin is from the face.  
CC The method allows identification of as many as possible of the genes  
CC important for hair-bearing skin, and therefore, of a very wide range of  
CC potential therapeutic and cosmetic agents. ADQ35184-ADQ36518 represent  
CC human DNA Tag fragments used to identify genes associated with hair-  
CC bearing skin.  
XX  
SQ Sequence 11 BP; 4 A; 2 C; 4 G; 1 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 TCCACCTGCT 13  
DB 11 TCCACCTGGT 2  
  
RESULT 355  
ADQ35910  
ID ADQ35910 standard; DNA; 11 BP.  
XX  
AC ADQ35910;  
XX  
DT 23-SEP-2004 (first entry)  
XX  
DE Human hair-bearing skin-associated DNA fragment SEQ ID NO 727.  
XX  
KW hair-bearing skin; human; serial analysis of gene expression; SAGE;  
KW homeostasis; cosmetic; pharmaceutical; biochip; ds.  
XX  
OS Homo sapiens.  
XX  
PN DE10260931-A1.  
XX  
PD 08-JUL-2004.  
XX  
XX 20-DEC-2002; 2002DE-01060931.  
XX  
PR 20-DEC-2002; 2002DE-01060931.  
XX  
PA (HENK ) HENKEL KGAA.

PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;  
PI Conradt M, Hofmann K;  
XX  
DR WPI; 2004-518857/50.  
XX  
PT In vitro identification of genes important for hair-bearing skin, useful  
PT for assessing homeostasis and in screening for pharmaceutical or cosmetic  
PT agents, based on differential expression analysis.  
XX  
PS Claim 5; SEQ ID NO 727; 250pp; German.  
XX  
CC This invention describes a novel in vitro method for identifying genes  
CC that are significant for hair-bearing skin in humans. The method  
CC comprises recovering, from hair-bearing skin, a first mixture of  
CC genetically expressed (transcribed and optionally translated) factors  
CC (i.e. proteins, mRNA or their fragments), recovering a second, similar  
CC mixture from skin on which hair does not grow and subjecting both  
CC mixtures to serial analysis of gene expression (SAGE) to identify those  
CC genes for which expression is markedly different between the two types of  
CC skin. The invention also describes in vitro methods for determining  
CC homeostasis of human hair-bearing skin and for determining activity of  
CC cosmetic and pharmaceutical agents for use against disorders or  
CC disturbances of the homeostasis of human hair-bearing skin. A biochip and  
CC a test kit comprising a solid support (flexible or rigid) with  
CC immobilised probes are also described for determining homeostasis. The  
CC hair-bearing skin is from the scalp and the other skin is from the face.  
CC The method allows identification of as many as possible of the genes  
CC important for hair-bearing skin, and therefore, of a very wide range of  
CC potential therapeutic and cosmetic agents. ADQ35184-ADQ36518 represent  
CC human DNA Tag fragments used to identify genes associated with hair-  
CC bearing skin.  
XX  
SQ Sequence 11 BP; 3 A; 6 C; 1 G; 1 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 ATCCACCTGC 12  
DB 1 ACCCACCTGC 10  
  
RESULT 356  
ADQ35843/C  
ID ADQ35843 standard; DNA; 11 BP.  
XX  
AC ADQ35843;  
XX  
DT 23-SEP-2004 (first entry)  
XX  
DE Human hair-bearing skin-associated DNA fragment SEQ ID NO 660.  
XX  
KW hair-bearing skin; human; serial analysis of gene expression; SAGE;  
KW homeostasis; cosmetic; pharmaceutical; biochip; ds.  
XX  
OS Homo sapiens.  
XX  
PN DE10260931-A1.  
XX  
PD 08-JUL-2004.  
XX  
PF 20-DEC-2002; 2002DE-01060931.  
XX  
PR 20-DEC-2002; 2002DE-01060931.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;  
PI Conradt M, Hofmann K;  
XX  
DR WPI; 2004-518857/50.  
XX

PT In vitro identification of genes important for hair-bearing skin, useful  
PT for assessing homeostasis and in screening for pharmaceutical or cosmetic  
PT agents, based on differential expression analysis.  
XX  
PS  
XX Claim 5; SEQ ID NO 660; 250pp; German.  
XX  
CC This invention describes a novel in vitro method for identifying genes  
CC that are significant for hair-bearing skin in humans. The method  
CC comprises recovering, from hair-bearing skin, a first mixture of  
CC genetically expressed (transcribed and optionally translated) factors  
CC (i.e. proteins, mRNA or their fragments), recovering a second, similar  
CC mixture from skin on which hair does not grow and subjecting both  
CC mixtures to serial analysis of gene expression (SAGE) to identify those  
CC genes for which expression is markedly different between the two types of  
CC skin. The invention also describes in vitro methods for determining  
CC homeostasis of human hair-bearing skin and for determining activity of  
CC cosmetic and pharmaceutical agents for use against disorders or  
CC disturbances of the homeostasis of human hair-bearing skin. A biochip and  
CC a test kit comprising a solid support (flexible or rigid) with  
CC immobilised probes are also described for determining homeostasis. The  
CC hair-bearing skin is from the scalp and the other skin is from the face.  
CC The method allows identification of as many as possible of the genes  
CC important for hair-bearing skin, and therefore, of a very wide range of  
CC potential therapeutic and cosmetic agents. ADQ35184-ADQ36518 represent  
CC human DNA Tag fragments used to identify genes associated with hair-  
CC bearing skin.  
XX  
SQ Sequence 11 BP; 3 A; 0 C; 5 G; 3 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 ATCCACCTGC 12  
Db 11 ATCCACCTTC 2  
  
RESULT 357  
ADQ33204  
ID ADQ33204 standard; DNA; 11 BP.  
XX  
AC ADQ33204;  
XX  
DT 23-SEP-2004 (first entry)  
XX  
DE Human facial skin-associated DNA fragment SEQ ID NO 1294.  
XX  
KW facial skin; human; serial analysis of gene expression; SAGE;  
KW homeostasis; biochip; cosmetic; pharmaceutical; ds.  
XX  
OS Homo sapiens.  
XX  
PN DE10260928-A1.  
XX  
PD 08-JUL-2004.  
XX  
PF 20-DEC-2002; 2002DE-01060928.  
XX  
PR 20-DEC-2002; 2002DE-01060928.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;  
PI Conradt M, Hofmann K;  
XX  
DR WPI; 2004-518855/50.  
XX  
PT In vitro identification of genes important for facial skin, useful for  
PT assessing homeostasis and in screening for pharmaceutical or cosmetic  
PT agents, based on differential expression analysis.  
XX  
PS Claim 5; SEQ ID NO 1294; 577pp; German.

XX  
CC This invention describes a novel in vitro method for identifying genes  
CC that are significant for facial skin in humans. The method comprises  
CC recovering, from facial skin, a first mixture of genetically expressed  
CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or  
CC their fragments), recovering a second, similar mixture from some other  
CC human tissue, preferably skin from a protected area, especially from the  
CC breast and subjecting the mixtures to serial analysis of gene expression  
CC (SAGE) to identify those genes for which expression is markedly different  
CC between facial skin and the other tissue. The invention also describes an  
CC in vitro method for determining homeostasis of human facial skin; a test  
CC kit which comprises a solid support (flexible or rigid) on which are  
CC immobilised probes that bind specifically to the factors of interest and  
CC a biochip for determining homeostasis of human facial skin. The products  
CC of the invention are also used in a method which determines activity of  
CC cosmetic and pharmaceutical agents for use against disorders or  
CC disturbances of the homeostasis of human skin and a screening method for  
CC identifying cosmetic and pharmaceutical agents. The method allows  
CC identification of as many as possible of the genes important for facial  
CC skin and thus of a very wide range of potential therapeutic and cosmetic  
CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to  
CC identify the facial skin-associated genes described in the invention.  
XX  
SQ Sequence 11 BP; 2 A; 7 C; 1 G; 1 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 ATCCACCTGC 12  
Db 1 ATCCACCCGC 10  
  
RESULT 358  
ADQ33521/c  
ID ADQ33521 standard; DNA; 11 BP.  
XX  
AC ADQ33521;  
XX  
DT 23-SEP-2004 (first entry)  
XX  
DE Human facial skin-associated DNA fragment SEQ ID NO 1611.  
XX  
KW facial skin; human; serial analysis of gene expression; SAGE;  
KW homeostasis; biochip; cosmetic; pharmaceutical; ds.  
XX  
OS Homo sapiens.  
XX  
PN DE10260928-A1.  
XX  
PD 08-JUL-2004.  
XX  
PF 20-DEC-2002; 2002DE-01060928.  
XX  
PR 20-DEC-2002; 2002DE-01060928.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;  
PI Conradt M, Hofmann K;  
XX  
DR WPI; 2004-518855/50.  
XX  
PT In vitro identification of genes important for facial skin, useful for  
PT assessing homeostasis and in screening for pharmaceutical or cosmetic  
PT agents, based on differential expression analysis.  
XX  
PS Claim 5; SEQ ID NO 1611; 577pp; German.  
XX  
CC This invention describes a novel in vitro method for identifying genes  
CC that are significant for facial skin in humans. The method comprises  
CC recovering, from facial skin, a first mixture of genetically expressed



CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or  
CC their fragments), recovering a second, similar mixture from some other  
CC human tissue, preferably skin from a protected area, especially from the  
CC breast and subjecting the mixtures to serial analysis of gene expression  
CC (SAGE) to identify those genes for which expression is markedly different  
CC between facial skin and the other tissue. The invention also describes an  
CC in vitro method for determining homeostasis of human facial skin; a test  
CC kit which comprises a solid support (flexible or rigid) on which are  
CC immobilised probes that bind specifically to the factors of interest and  
CC a biochip for determining homeostasis of human facial skin. The products  
CC of the invention are also used in a method which determines activity of  
CC cosmetic and pharmaceutical agents for use against disorders or  
CC disturbances of the homeostasis of human skin and a screening method for  
CC identifying cosmetic and pharmaceutical agents. The method allows  
CC identification of as many as possible of the genes important for facial  
CC skin and thus of a very wide range of potential therapeutic and cosmetic  
CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to  
CC identify the facial skin-associated genes described in the invention.

XX  
SQ Sequence 11 BP; 5 A; 3 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTG 18  
Db 10 CTGCTTTGTG 1

RESULT 359  
ADQ33660/C  
ID ADQ33660 standard; DNA; 11 BP.  
XX  
AC ADQ33660;  
XX  
DT 23-SEP-2004 (first entry)  
XX  
DE Human facial skin-associated DNA fragment SEQ ID NO 1750.  
KW facial skin; human; serial analysis of gene expression; SAGE;  
KW homeostasis; biochip; cosmetic; pharmaceutical; ds.  
XX  
OS Homo sapiens.  
XX  
PN DE10260928-A1.  
XX  
PD 08-JUL-2004.  
XX  
PF 20-DEC-2002; 2002DE-01060928.  
XX  
PR 20-DEC-2002; 2002DE-01060928.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;  
PI Conradt M, Hofmann K;  
XX  
DR WPI; 2004-518855/50.  
XX  
PT In vitro identification of genes important for facial skin, useful for  
PT assessing homeostasis and in screening for pharmaceutical or cosmetic  
PT agents, based on differential expression analysis.  
XX  
PS Claim 5; SEQ ID NO 1750; 577pp; German.  
XX  
CC This invention describes a novel in vitro method for identifying genes  
CC that are significant for facial skin in humans. The method comprises  
CC recovering, from facial skin, a first mixture of genetically expressed  
CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or  
CC their fragments), recovering a second, similar mixture from some other  
CC human tissue, preferably skin from a protected area, especially from the  
CC breast and subjecting the mixtures to serial analysis of gene expression

CC (SAGE) to identify those genes for which expression is markedly different  
CC between facial skin and the other tissue. The invention also describes an  
CC in vitro method for determining homeostasis of human facial skin; a test  
CC kit which comprises a solid support (flexible or rigid) on which are  
CC immobilised probes that bind specifically to the factors of interest and  
CC a biochip for determining homeostasis of human facial skin. The products  
CC of the invention are also used in a method which determines activity of  
CC cosmetic and pharmaceutical agents for use against disorders or  
CC disturbances of the homeostasis of human skin and a screening method for  
CC identifying cosmetic and pharmaceutical agents. The method allows  
CC identification of as many as possible of the genes important for facial  
CC skin and thus of a very wide range of potential therapeutic and cosmetic  
CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to  
CC identify the facial skin-associated genes described in the invention.

XX  
SQ Sequence 11 BP; 4 A; 0 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCCACCTGCT 13  
Db 11 TCCACCTTCT 2

RESULT 360  
ADQ33652  
ID ADQ33652 standard; DNA; 11 BP.  
XX  
AC ADQ33652;  
XX  
DT 23-SEP-2004 (first entry)  
XX  
DE Human facial skin-associated DNA fragment SEQ ID NO 1742.  
KW facial skin; human; serial analysis of gene expression; SAGE;  
KW homeostasis; biochip; cosmetic; pharmaceutical; ds.  
XX  
OS Homo sapiens.  
XX  
PN DE10260928-A1.  
XX  
PD 08-JUL-2004.  
XX  
PF 20-DEC-2002; 2002DE-01060928.  
XX  
PR 20-DEC-2002; 2002DE-01060928.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;  
PI Conradt M, Hofmann K;  
XX  
DR WPI; 2004-518855/50.  
XX  
PT In vitro identification of genes important for facial skin, useful for  
PT assessing homeostasis and in screening for pharmaceutical or cosmetic  
PT agents, based on differential expression analysis.  
XX  
PS Claim 5; SEQ ID NO 1742; 577pp; German.  
XX  
CC This invention describes a novel in vitro method for identifying genes  
CC that are significant for facial skin in humans. The method comprises  
CC recovering, from facial skin, a first mixture of genetically expressed  
CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or  
CC their fragments), recovering a second, similar mixture from some other  
CC human tissue, preferably skin from a protected area, especially from the  
CC breast and subjecting the mixtures to serial analysis of gene expression  
CC (SAGE) to identify those genes for which expression is markedly different  
CC between facial skin and the other tissue. The invention also describes an  
CC in vitro method for determining homeostasis of human facial skin; a test  
CC kit which comprises a solid support (flexible or rigid) on which are



CC immobilised probes that bind specifically to the factors of interest and  
CC a biochip for determining homeostasis of human facial skin. The products  
CC of the invention are also used in a method which determines activity of  
CC cosmetic and pharmaceutical agents for use against disorders or  
CC disturbances of the homeostasis of human skin and a screening method for  
CC identifying cosmetic and pharmaceutical agents. The method allows  
CC identification of as many as possible of the genes important for facial  
CC skin and thus of a very wide range of potential therapeutic and cosmetic  
CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to  
CC identify the facial skin-associated genes described in the invention.  
XX  
SQ Sequence 11 BP; 1 A; 3 C; 2 G; 5 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 6 CACCTGCTGT 15  
Db 2 CACTTGCTGT 11  
  
RESULT 361  
ADQ34937/c  
ID ADQ34937 standard; DNA; 11 BP.  
XX  
AC ADQ34937;  
XX  
DT 23-SEP-2004 (first entry)  
XX  
DE Human facial skin-associated DNA fragment SEQ ID NO 3027.  
XX  
KW facial skin; human; serial analysis of gene expression; SAGE;  
KW homeostasis; biochip; cosmetic; pharmaceutical; ds.  
XX  
OS Homo sapiens.  
XX  
PN DE10260928-A1.  
XX  
PD 08-JUL-2004.  
XX  
PF 20-DEC-2002; 2002DE-01060928.  
XX  
PR 20-DEC-2002; 2002DE-01060928.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;  
PI Conradt M, Hofmann K;  
XX  
DR WPI; 2004-518855/50.  
XX  
PT In vitro identification of genes important for facial skin, useful for  
PT assessing homeostasis and in screening for pharmaceutical or cosmetic  
PT agents, based on differential expression analysis.  
XX  
PS Claim 4; SEQ ID NO 3027; 577pp; German.  
XX  
CC This invention describes a novel in vitro method for identifying genes  
CC that are significant for facial skin in humans. The method comprises  
CC recovering, from facial skin, a first mixture of genetically expressed  
CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or  
CC their fragments), recovering a second, similar mixture from some other  
CC human tissue, preferably skin from a protected area, especially from the  
CC breast and subjecting the mixtures to serial analysis of gene expression  
CC (SAGE) to identify those genes for which expression is markedly different  
CC between facial skin and the other tissue. The invention also describes an  
CC in vitro method for determining homeostasis of human facial skin; a test  
CC kit which comprises a solid support (flexible or rigid) on which are  
CC immobilised probes that bind specifically to the factors of interest and  
CC a biochip for determining homeostasis of human facial skin. The products  
CC of the invention are also used in a method which determines activity of  
CC cosmetic and pharmaceutical agents for use against disorders or

CC disturbances of the homeostasis of human skin and a screening method for  
CC identifying cosmetic and pharmaceutical agents. The method allows  
CC identification of as many as possible of the genes important for facial  
CC skin and thus of a very wide range of potential therapeutic and cosmetic  
CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to  
CC identify the facial skin-associated genes described in the invention.  
XX  
SQ Sequence 11 BP; 3 A; 2 C; 5 G; 1 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 TCCACCTGCT 13  
Db 11 TCCAGCTGCT 2  
  
RESULT 362  
ADQ32556/c  
ID ADQ32556 standard; DNA; 11 BP.  
XX  
AC ADQ32556;  
XX  
DT 23-SEP-2004 (first entry)  
XX  
DE Human facial skin-associated DNA fragment SEQ ID NO 646.  
XX  
KW facial skin; human; serial analysis of gene expression; SAGE;  
KW homeostasis; biochip; cosmetic; pharmaceutical; ds.  
XX  
OS Homo sapiens.  
XX  
PN DE10260928-A1.  
XX  
PD 08-JUL-2004.  
XX  
PF 20-DEC-2002; 2002DE-01060928.  
XX  
PR 20-DEC-2002; 2002DE-01060928.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;  
PI Conradt M, Hofmann K;  
XX  
DR WPI; 2004-518855/50.  
XX  
PT In vitro identification of genes important for facial skin, useful for  
PT assessing homeostasis and in screening for pharmaceutical or cosmetic  
PT agents, based on differential expression analysis.  
XX  
PS Claim 6; SEQ ID NO 646; 577pp; German.  
XX  
CC This invention describes a novel in vitro method for identifying genes  
CC that are significant for facial skin in humans. The method comprises  
CC recovering, from facial skin, a first mixture of genetically expressed  
CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or  
CC their fragments), recovering a second, similar mixture from some other  
CC human tissue, preferably skin from a protected area, especially from the  
CC breast and subjecting the mixtures to serial analysis of gene expression  
CC (SAGE) to identify those genes for which expression is markedly different  
CC between facial skin and the other tissue. The invention also describes an  
CC in vitro method for determining homeostasis of human facial skin; a test  
CC kit which comprises a solid support (flexible or rigid) on which are  
CC immobilised probes that bind specifically to the factors of interest and  
CC a biochip for determining homeostasis of human facial skin. The products  
CC of the invention are also used in a method which determines activity of  
CC cosmetic and pharmaceutical agents for use against disorders or  
CC disturbances of the homeostasis of human skin and a screening method for  
CC identifying cosmetic and pharmaceutical agents. The method allows  
CC identification of as many as possible of the genes important for facial  
CC skin and thus of a very wide range of potential therapeutic and cosmetic

CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to  
CC identify the facial skin-associated genes described in the invention.  
XX  
SQ Sequence 11 BP; 5 A; 2 C; 4 G; 0 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 8 CCTGCTGTGT 17  
Db 11 CCTCCTGTGT 2  
  
RESULT 363  
ADQ33878  
ID ADQ33878 standard; DNA; 11 BP.  
XX  
AC ADQ33878;  
XX  
DT 23-SEP-2004 (first entry)  
DE Human facial skin-associated DNA fragment SEQ ID NO 1968.  
XX  
KW facial skin; human; serial analysis of gene expression; SAGE;  
KW homeostasis; biochip; cosmetic; pharmaceutical; ds.  
XX  
OS Homo sapiens.  
XX  
PN DE10260928-A1.  
XX  
PD 08-JUL-2004.  
XX  
PF 20-DEC-2002; 2002DE-01060928.  
XX  
PR 20-DEC-2002; 2002DE-01060928.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;  
PI Conradt M, Hofmann K;  
XX  
DR WPI; 2004-518855/50.  
XX  
PT In vitro identification of genes important for facial skin, useful for  
PT assessing homeostasis and in screening for pharmaceutical or cosmetic  
PT agents, based on differential expression analysis.  
XX  
PS Claim 5; SEQ ID NO 1968; 577pp; German.  
XX  
CC This invention describes a novel in vitro method for identifying genes  
CC that are significant for facial skin in humans. The method comprises  
CC recovering, from facial skin, a first mixture of genetically expressed  
CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or  
CC their fragments), recovering a second, similar mixture from some other  
CC human tissue, preferably skin from a protected area, especially from the  
CC breast and subjecting the mixtures to serial analysis of gene expression  
CC (SAGE) to identify those genes for which expression is markedly different  
CC between facial skin and the other tissue. The invention also describes an  
CC in vitro method for determining homeostasis of human facial skin; a test  
CC kit which comprises a solid support (flexible or rigid) on which are  
CC immobilised probes that bind specifically to the factors of interest and  
CC a biochip for determining homeostasis of human facial skin. The products  
CC of the invention are also used in a method which determines activity of  
CC cosmetic and pharmaceutical agents for use against disorders or  
CC disturbances of the homeostasis of human skin and a screening method for  
CC identifying cosmetic and pharmaceutical agents. The method allows  
CC identification of as many as possible of the genes important for facial  
CC skin and thus of a very wide range of potential therapeutic and cosmetic  
CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to  
CC identify the facial skin-associated genes described in the invention.  
XX  
SQ Sequence 11 BP; 1 A; 5 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 TCCACCTGCT 13  
Db 2 TCCACCTGGT 11  
  
RESULT 364  
ADQ32289  
ID ADQ32289 standard; DNA; 11 BP.  
XX  
AC ADQ32289;  
XX  
DT 23-SEP-2004 (first entry)  
XX  
DE Human facial skin-associated DNA fragment SEQ ID NO 379.  
XX  
KW facial skin; human; serial analysis of gene expression; SAGE;  
KW homeostasis; biochip; cosmetic; pharmaceutical; ds.  
XX  
OS Homo sapiens.  
XX  
PN DE10260928-A1.  
XX  
PD 08-JUL-2004.  
XX  
PF 20-DEC-2002; 2002DE-01060928.  
XX  
PR 20-DEC-2002; 2002DE-01060928.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;  
PI Conradt M, Hofmann K;  
XX  
DR WPI; 2004-518855/50.  
XX  
PT In vitro identification of genes important for facial skin, useful for  
PT assessing homeostasis and in screening for pharmaceutical or cosmetic  
PT agents, based on differential expression analysis.  
XX  
PS Claim 8; SEQ ID NO 379; 577pp; German.  
XX  
CC This invention describes a novel in vitro method for identifying genes  
CC that are significant for facial skin in humans. The method comprises  
CC recovering, from facial skin, a first mixture of genetically expressed  
CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or  
CC their fragments), recovering a second, similar mixture from some other  
CC human tissue, preferably skin from a protected area, especially from the  
CC breast and subjecting the mixtures to serial analysis of gene expression  
CC (SAGE) to identify those genes for which expression is markedly different  
CC between facial skin and the other tissue. The invention also describes an  
CC in vitro method for determining homeostasis of human facial skin; a test  
CC kit which comprises a solid support (flexible or rigid) on which are  
CC immobilised probes that bind specifically to the factors of interest and  
CC a biochip for determining homeostasis of human facial skin. The products  
CC of the invention are also used in a method which determines activity of  
CC cosmetic and pharmaceutical agents for use against disorders or  
CC disturbances of the homeostasis of human skin and a screening method for  
CC identifying cosmetic and pharmaceutical agents. The method allows  
CC identification of as many as possible of the genes important for facial  
CC skin and thus of a very wide range of potential therapeutic and cosmetic  
CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to  
CC identify the facial skin-associated genes described in the invention.  
XX  
SQ Sequence 11 BP; 2 A; 2 C; 5 G; 2 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 GTGTGACCTG 23  
Db 2 GTGAGACCTG 11

RESULT 365  
ADQ32669  
ID ADQ32669 standard; DNA; 11 BP.  
XX AC ADQ32669;  
XX DT 23-SEP-2004 (first entry)  
XX DE Human facial skin-associated DNA fragment SEQ ID NO 759.  
XX KW facial skin; human; serial analysis of gene expression; SAGE;  
XX KW homeostasis; biochip; cosmetic; pharmaceutical; ds.  
XX OS Homo sapiens.  
XX PN DE10260928-A1.  
XX PD 08-JUL-2004.  
XX PF 20-DEC-2002; 2002DE-01060928.  
XX PD 08-JUL-2004.  
XX PF 20-DEC-2002; 2002DE-01060928.  
XX PR 20-DEC-2002; 2002DE-01060928.  
XX PA (HENK ) HENKEL KGAA.  
XX PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;  
PI Conradt M, Hofmann K;  
XX WPI; 2004-518855/50.  
XX In vitro identification of genes important for facial skin, useful for  
PT assessing homeostasis and in screening for pharmaceutical or cosmetic  
PT agents, based on differential expression analysis.  
XX Claim 5; SEQ ID NO 759; 577pp; German.  
XX This invention describes a novel in vitro method for identifying genes  
CC that are significant for facial skin in humans. The method comprises  
CC recovering, from facial skin, a first mixture of genetically expressed  
CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or  
CC their fragments), recovering a second, similar mixture from some other  
CC human tissue, preferably skin from a protected area, especially from the  
CC breast and subjecting the mixtures to serial analysis of gene expression  
CC (SAGE) to identify those genes for which expression is markedly different  
CC between facial skin and the other tissue. The invention also describes an  
CC in vitro method for determining homeostasis of human facial skin; a test  
CC kit which comprises a solid support (flexible or rigid) on which are  
CC immobilised probes that bind specifically to the factors of interest and  
CC a biochip for determining homeostasis of human facial skin. The products  
CC of the invention are also used in a method which determines activity of  
CC cosmetic and pharmaceutical agents for use against disorders or  
CC disturbances of the homeostasis of human skin and a screening method for  
CC identifying cosmetic and pharmaceutical agents. The method allows  
CC identification of as many as possible of the genes important for facial  
CC skin and thus of a very wide range of potential therapeutic and cosmetic  
CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to  
CC identify the facial skin-associated genes described in the invention.  
XX Sequence 11 BP; 2 A; 4 C; 1 G; 4 T; 0 U; 0 Other;  
SQ Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATCCACCTG 11  
Db 1 CATCCATCTG 10

RESULT 366  
ADQ34474/c  
ID ADQ34474 standard; DNA; 11 BP.  
XX AC ADQ34474;  
XX DT 23-SEP-2004 (first entry)  
XX DE Human facial skin-associated DNA fragment SEQ ID NO 2564.  
XX KW facial skin; human; serial analysis of gene expression; SAGE;  
XX KW homeostasis; biochip; cosmetic; pharmaceutical; ds.  
XX OS Homo sapiens.  
XX PN DE10260928-A1.  
XX PD 08-JUL-2004.  
XX PF 20-DEC-2002; 2002DE-01060928.  
XX PR 20-DEC-2002; 2002DE-01060928.  
XX PA (HENK ) HENKEL KGAA.  
XX PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;  
PI Conradt M, Hofmann K;  
XX WPI; 2004-518855/50.  
XX In vitro identification of genes important for facial skin, useful for  
PT assessing homeostasis and in screening for pharmaceutical or cosmetic  
PT agents, based on differential expression analysis.  
XX Claim 4; SEQ ID NO 2564; 577pp; German.  
XX This invention describes a novel in vitro method for identifying genes  
CC that are significant for facial skin in humans. The method comprises  
CC recovering, from facial skin, a first mixture of genetically expressed  
CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or  
CC their fragments), recovering a second, similar mixture from some other  
CC human tissue, preferably skin from a protected area, especially from the  
CC breast and subjecting the mixtures to serial analysis of gene expression  
CC (SAGE) to identify those genes for which expression is markedly different  
CC between facial skin and the other tissue. The invention also describes an  
CC in vitro method for determining homeostasis of human facial skin; a test  
CC kit which comprises a solid support (flexible or rigid) on which are  
CC immobilised probes that bind specifically to the factors of interest and  
CC a biochip for determining homeostasis of human facial skin. The products  
CC of the invention are also used in a method which determines activity of  
CC cosmetic and pharmaceutical agents for use against disorders or  
CC disturbances of the homeostasis of human skin and a screening method for  
CC identifying cosmetic and pharmaceutical agents. The method allows  
CC identification of as many as possible of the genes important for facial  
CC skin and thus of a very wide range of potential therapeutic and cosmetic  
CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to  
CC identify the facial skin-associated genes described in the invention.  
XX Sequence 11 BP; 3 A; 0 C; 7 G; 1 T; 0 U; 0 Other;  
SQ Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCCACCTGCT 13  
Db 11 TCCACCTCCT 2

RESULT 367  
AAQ52115/c

ID AAQ52115 standard; RNA; 12 BP.  
XX  
AC AAQ52115;  
XX  
DT 25-MAR-2003 (revised)  
DT 26-MAY-1994 (first entry)  
XX  
DE Breast cancer specific mRNA ribozyme cleavable nucleotide (2833).  
DE  
XX  
KW Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;  
KW resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;  
KW actinomycin D; vinblastine; small intestine; kidney; adrenal gland;  
KW adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;  
KW human; chronic myelogenous leukemia; CML; follicular lymphoma;  
KW B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;  
KW neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;  
KW hairpin; hepatitis delta virus; group I intron; RNaseP; leukaemia; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO9323057-A1.  
PN  
XX  
PD 25-NOV-1993.  
XX  
XX 13-MAY-1993; 93WO-US004573.  
PF  
XX 14-MAY-1992; 92US-00882822.  
PR 14-MAY-1992; 92US-00882885.  
PR 26-AUG-1992; 92US-00936110.  
PR 26-AUG-1992; 92US-00936421.  
PR 26-AUG-1992; 92US-00936422.  
PR 26-AUG-1992; 92US-00936531.  
PR 26-AUG-1992; 92US-00936532.  
PR 07-DEC-1992; 92US-00987131.  
PR 19-JAN-1993; 93US-00006122.  
PR 19-JAN-1993; 93US-00008910.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Thompson JD, Draper KG;  
XX  
DR WPI; 1993-386203/48.  
XX  
PT New enzymatic RNA molecules (ribozymes) - which cleave mRNA associated  
PT with tumours or mRNA expressed from gene encoding multiple drug  
PT resistance.  
XX  
PS Claim 3; Fig 8; 69pp; English.  
XX  
CC The sequences given in AAQ51825-2266 represent areas of mRNAs which are  
CC associated with development or maintenance of chronic myelogenous  
CC leukemia (CML), promyelocytic leukemia, Burkitt's lymphoma, or acute  
CC lymphocytic leukemia, follicular lymphoma, B-cell acute lymphocytic  
CC leukemia, breast cancer, colon carcinoma, neuroblastoma and lung cancer.  
CC The full length mRNAs containing these target sequences, encode aberrant  
CC cellular proteins which are able to control cellular proliferation and  
CC are directly linked to a leukemic phenotype. These target sequences are  
CC identified by the ribozyme of the invention. The ribozymes is formed in a  
CC hammerhead motif, but may also be formed in the motif of a hairpin,  
CC hepatitis delta virus, group I intron or RNaseP-like RNA. These ribozymes  
CC may be used to inhibit the development or expression of a transformed  
CC phenotype in man and other animals by modulating expression of the  
CC corresponding gene. Cleavage of target mRNAs expressed in pre-neoplastic  
CC and transformed cells elicits inhibition of the transformed state.  
CC Multiple drug resistance (mdr-1) mRNA specific ribozymes remove the  
CC mechanism of drug resistance used by transformed cells and thus enhances  
CC drug therapies for tumours. The ribozymes may also be used to study  
CC genetic drift and mutations within cells. (Updated on 25-MAR-2003 to  
CC correct PN field.)  
XX  
SQ Sequence 12 BP; 3 A; 1 C; 6 G; 0 T; 2 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;

Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CCATCCACCT 10  
Db 10 CCATCCACTT 1  
RESULT 368  
AAV32307/c  
ID AAV32307 standard; DNA; 12 BP.  
XX  
AC AAV32307;  
XX 18-AUG-1998 (first entry)  
DT  
XX Random primed reverse transcription PCR primer 139.  
DE  
XX RT-PCR; primer; amplification; reverse transcription; RNA fingerprinting;  
KW differential gene expression; ss.  
XX Synthetic.  
OS  
XX WO9813521-A1.  
PN  
XX 02-APR-1998.  
PD  
XX 26-SEP-1997; 97WO-EP005290.  
PF  
XX 27-SEP-1996; 96GB-00020216.  
PR  
XX (SANR-) FOND CENT SAN RAFFAELE DEL MONTE TABOR.  
PA  
XX Consalez G, Fesce R;  
PI  
XX WPI; 1998-230725/20.  
DR  
XX Differential screening of gene expression by reverse transcription  
PT polymerase chain reaction - uses random priming with primers selected for  
PT high efficiency and selectivity by computer screening of database(s).  
XX  
PS Claim 9; Page 24; 37pp; English.  
XX  
CC The invention provides a method for the differential screening of gene  
CC expression by random primed reverse transcription PCR (RT-PCR). The  
CC primer sequences are generated by stimulating PCR reactions on non-  
CC redundant mammalian nucleotide sequence databank entries containing at  
CC least 1,000 bp of coding region. The primers selected, such as the  
CC present one, had to meet various criteria such as having an efficiency  
CC index between 2-10, having a selectivity index higher than 1, being 12 bp  
CC long i.e. 8 C or G and 4 T or A, and each primer differed from the others  
CC in at least 5 of the 8 bases at the 3'-end. The invention claims the  
CC selected primers make it possible to use internally primed, PCR-based RNA  
CC fingerprinting for simple, exhaustive and systematic analysis of  
CC differential gene expression as an advantageous alternative to  
CC differential display. The method can also be useful for isolating new  
CC coding sequences and to compare known and new genes  
XX  
SQ Sequence 12 BP; 1 A; 0 C; 7 G; 3 T; 0 U; 1 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CCATCCACCT 10  
Db 10 CCACCCACCT 1  
RESULT 369  
AAV32258/c  
ID AAV32258 standard; DNA; 12 BP.  
XX



AC AAV32258;  
XX  
DT 18-AUG-1998 (first entry)  
XX  
DE Random primed reverse transcription PCR primer 164.  
XX  
KW RT-PCR; primer; amplification; reverse transcription; RNA fingerprinting;  
KW differential gene expression; ss.  
XX  
OS Synthetic.  
XX  
PN WO9813521-A1.  
XX  
PD 02-APR-1998.  
XX  
PF 26-SEP-1997; 97WO-EP005290.  
XX  
PR 27-SEP-1996; 96GB-00020216.  
XX  
PS Claim 9; Page 24; 37pp; English.  
XX  
CC The invention provides a method for the differential screening of gene  
CC expression by random primed reverse transcription PCR (RT-PCR). The  
CC primer sequences are generated by stimulating PCR reactions on non-  
CC redundant mammalian nucleotide sequence databank entries containing at  
CC least 1,000 bp of coding region. The primers selected, such as the  
CC present one, had to meet various criteria such as having an efficiency  
CC index between 2-10, having a selectivity index higher than 1, being 12 bp  
CC long i.e. 8 C or G and 4 T or A, and each primer differed from the others  
CC in at least 5 of the 8 bases at the 3'-end. The invention claims the  
CC selected primers make it possible to use internally primed, PCR-based RNA  
CC fingerprinting for simple, exhaustive and systematic analysis of  
CC differential gene expression as an advantageous alternative to  
CC differential display. The method can also be useful for isolating new  
CC coding sequences and to compare known and new genes  
XX  
SQ Sequence 12 BP; 3 A; 3 C; 4 G; 1 T; 0 U; 1 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 75.0%; Pred. No. 2e+02;  
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 12 CTGTGTGACCTG 23  
Db :|||||  
12 STCCGTGACCTG 1  
  
RESULT 370  
AAV32253/c  
ID AAV32253 standard; DNA; 12 BP.  
XX  
AC AAV32253;  
XX  
DT 18-AUG-1998 (first entry)  
XX  
DE Random primed reverse transcription PCR primer 192.  
XX  
KW RT-PCR; primer; amplification; reverse transcription; RNA fingerprinting;  
KW differential gene expression; ss.  
XX  
OS Synthetic.  
XX  
PN WO9813521-A1.

XX 02-APR-1998.  
PD  
XX  
PF 26-SEP-1997; 97WO-EP005290.  
XX  
PR 27-SEP-1996; 96GB-00020216.  
XX  
PA (SANR-) FOND CENT SAN RAFFAELE DEL MONTE TABOR.  
XX  
PI Consalez G, Fesce R;  
XX  
XX WPI; 1998-230725/20.  
DR  
XX  
PT Differential screening of gene expression by reverse transcription  
PT polymerase chain reaction - uses random priming with primers selected for  
PT high efficiency and selectivity by computer screening of database(s).  
XX  
PS Claim 9; Page 24; 37pp; English.  
XX  
CC The invention provides a method for the differential screening of gene  
CC expression by random primed reverse transcription PCR (RT-PCR). The  
CC primer sequences are generated by stimulating PCR reactions on non-  
CC redundant mammalian nucleotide sequence databank entries containing at  
CC least 1,000 bp of coding region. The primers selected, such as the  
CC present one, had to meet various criteria such as having an efficiency  
CC index between 2-10, having a selectivity index higher than 1, being 12 bp  
CC long i.e. 8 C or G and 4 T or A, and each primer differed from the others  
CC in at least 5 of the 8 bases at the 3'-end. The invention claims the  
CC selected primers make it possible to use internally primed, PCR-based RNA  
CC fingerprinting for simple, exhaustive and systematic analysis of  
CC differential gene expression as an advantageous alternative to  
CC differential display. The method can also be useful for isolating new  
CC coding sequences and to compare known and new genes  
XX  
SQ Sequence 12 BP; 3 A; 2 C; 5 G; 1 T; 0 U; 1 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 75.0%; Pred. No. 2e+02;  
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2 CATCCACCTGCT 13  
Db :|||||  
12 SATCCTCCGGCT 1  
  
RESULT 371  
AAZ41830/c  
ID AAZ41830 standard; DNA; 12 BP.  
XX  
AC AAZ41830;  
XX  
DT 20-MAR-2003 (revised)  
DT 21-JAN-2000 (first entry)  
XX  
DE Organic material detecting primer 191.  
XX  
KW Amplification; polymerase chain reaction; PCR; microorganism; compost;  
KW detection; pollutant; soil; food; agricultural chemical; polymer;  
KW organochlorine; primer; ss.  
XX  
OS Synthetic.  
XX  
PN DE19914461-A1.  
XX  
PD 21-OCT-1999.  
XX  
PF 30-MAR-1999; 99DE-01014461.  
XX  
PR 31-MAR-1998; 98JP-00087651.  
PR 16-MAR-1999; 99JP-00069694.  
XX  
XX  
PA (SAOL ) SANYO ELECTRIC CO LTD.  
PA (NORQ ) SOC TECHNO-INNOVATION AGRIC FORESTY & FI.



XX Inoue T;  
PI WPI; 1999-592157/51.  
XX Novel polymerase chain reaction method, for differentiating between  
PT microorganisms and for detecting contaminants.  
PT Example 1; Page 22; 78pp; German.  
PS  
XX This invention describes a novel method for the amplification of DNA  
CC comprising (i) preparing many primers (P) with different probabilities of  
CC amplification and (ii) simultaneous polymerase chain reaction (PCR) of  
CC many different DNA using these primers. The method is used (i) to  
CC differentiate between different microorganisms in a mixed population and  
CC (ii) to determine presence/absence of an impurity (pollutant), or its  
CC concentration, in e.g. soil, foods, compost etc., typically metals,  
CC agricultural chemicals, polymers, organochlorine compounds etc. A  
CC particular use is monitoring composting of organic material.  
CC Amplification with many primers produces a lot of information, so  
CC reliability of the test is improved, and many samples may be tested  
CC quickly. AAZ41640-241855 represent the primers described in the method of  
CC the invention. (Updated on 20-MAR-2003 to correct PR field.)  
XX  
SQ Sequence 12 BP; 2 A; 2 C; 6 G; 2 T; 0 U; 0 Other;  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 5 CCACCTGCTG 14  
DB 11 CCACCTCCTG 2  
RESULT 372  
AAZ41780  
ID AAZ41780 standard; DNA; 12 BP.  
XX  
AC AAZ41780;  
XX  
DT 20-MAR-2003 (revised)  
DT 21-JAN-2000 (first entry)  
XX  
DE Organic material detecting primer 141.  
XX  
KW Amplification; polymerase chain reaction; PCR; microorganism; compost;  
KW detection; pollutant; soil; food; agricultural chemical; polymer;  
KW organochlorine; primer; ss.  
XX  
OS Synthetic.  
XX  
PN DE19914461-A1.  
XX  
PD 21-OCT-1999.  
XX  
PF 30-MAR-1999; 99DE-01014461.  
XX  
PR 31-MAR-1998; 98JP-00087651.  
PR 16-MAR-1999; 99JP-00069694.  
XX  
XX (SAOL ) SANYO ELECTRIC CO LTD.  
PA (NORQ ) SOC TECHNO-INNOVATION AGRIC FORESTY & FI.  
XX  
PI Inoue T;  
XX  
DR WPI; 1999-592157/51.  
XX  
PT Novel polymerase chain reaction method, for differentiating between  
PT microorganisms and for detecting contaminants.  
XX  
PS Example 1; Page 20; 78pp; German.  
XX

CC This invention describes a novel method for the amplification of DNA  
CC comprising (i) preparing many primers (P) with different probabilities of  
CC amplification and (ii) simultaneous polymerase chain reaction (PCR) of  
CC many different DNA using these primers. The method is used (i) to  
CC differentiate between different microorganisms in a mixed population and  
CC (ii) to determine presence/absence of an impurity (pollutant), or its  
CC concentration, in e.g. soil, foods, compost etc., typically metals,  
CC agricultural chemicals, polymers, organochlorine compounds etc. A  
CC particular use is monitoring composting of organic material.  
CC Amplification with many primers produces a lot of information, so  
CC reliability of the test is improved, and many samples may be tested  
CC quickly. AAZ41640-241855 represent the primers described in the method of  
CC the invention. (Updated on 20-MAR-2003 to correct PR field.)  
XX  
SQ Sequence 12 BP; 0 A; 4 C; 3 G; 5 T; 0 U; 0 Other;  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 6 CACCTGCTGT 15  
DB 1 CTCCTGCTGT 10  
RESULT 373  
AAZ41564  
ID AAZ41564 standard; DNA; 12 BP.  
XX  
AC AAZ41564;  
XX  
DT 19-JAN-2000 (first entry)  
XX  
DE Microbe detection in organic waste arbitrarily primed PCR primer #141.  
XX  
KW Microbe; detection; organic waste; arbitrarily primer PCR;  
KW random amplified polymorphic DNA; amplification; PCR primer; ss.  
XX  
OS Synthetic.  
XX  
PN JP11276176-A.  
XX  
PD 12-OCT-1999.  
XX  
PF 31-MAR-1998; 98JP-00087652.  
XX  
PR 31-MAR-1998; 98JP-00087652.  
XX  
PA (SAOL ) SANYO ELECTRIC CO LTD.  
PA (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.  
XX  
DR WPI; 1999-626940/54.  
XX  
PT Amplification of a DNA fragment - in order to establish the state of  
PT existence of a microbe.  
XX  
PS Example; Page 9; 40pp; Japanese.  
XX  
CC A method has been developed for the amplification of a DNA fragment in  
CC which amplification is carried out on the DNA fragments of a number of  
CC different DNAs. The method comprises a PCR reaction repeatedly carrying  
CC out a heat-denaturing step, a primer annealing step and a polymerase  
CC extending step, to amplify the DNA fragments of a plural of different  
CC DNAs. The method can detect the existence of a microbe in organic waste.  
CC AAZ41424 to AAZ41639 represent PCR primers used in random amplified  
CC polymorphic DNA arbitrarily primed PCR, for the detection of microbes in  
CC organic waste  
XX  
SQ Sequence 12 BP; 0 A; 4 C; 3 G; 5 T; 0 U; 0 Other;  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CACCTGCTGT 15  
Db 1 CTCCTGCTGT 10

RESULT 374  
AAZ41614/c  
ID AAZ41614 standard; DNA; 12 BP.  
XX  
AC AAZ41614;  
XX  
DT 19-JAN-2000 (first entry)  
XX  
DE Microbe detection in organic waste arbitrarily primed PCR primer #191.  
XX  
KW Microbe; detection; organic waste; arbitrarily primer PCR;  
KW random amplified polymorphic DNA; amplification; PCR primer; ss.  
XX  
OS Synthetic.  
XX  
PN JP11276176-A.  
XX  
PD 12-OCT-1999.  
XX  
PF 31-MAR-1998; 98JP-00087652.  
XX  
PR 31-MAR-1998; 98JP-00087652.  
XX  
PA (SAOL ) SANYO ELECTRIC CO LTD.  
PA (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.  
XX  
DR WPI; 1999-626940/54.  
XX  
PT Amplification of a DNA fragment - in order to establish the state of  
PT existence of a microbe.  
XX  
PS Example; Page 10; 40pp; Japanese.  
XX  
CC A method has been developed for the amplification of a DNA fragment in  
CC which amplification is carried out on the DNA fragments of a number of  
CC different DNAs. The method comprises a PCR reaction repeatedly carrying  
CC out a heat-denaturing step, a primer annealing step and a polymerase  
CC extending step, to amplify the DNA fragments of a plural of different  
CC DNAs. The method can detect the existence of a microbe in organic waste.  
CC AAZ41424 to AAZ41639 represent PCR primers used in random amplified  
CC polymorphic DNA arbitrarily primed PCR, for the detection of microbes in  
CC organic waste  
XX  
SQ Sequence 12 BP; 2 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTG 14  
Db 11 CCACCTCCTG 2

RESULT 375  
AAF74730/c  
ID AAF74730 standard; DNA; 12 BP.  
XX  
AC AAF74730;  
XX  
DT 17-MAY-2001 (first entry)  
XX  
DE Human smoothelin variant intron-exon splice recognition sequence #26.  
XX  
KW Human; smoothelin; smoothelin B gene; smooth muscle cell promoter;  
KW vascular contractile smooth muscle cell; gene therapy; PCR primer;  
KW visceral contractile smooth muscle cell; cardiovascular; ss.

XX  
OS Homo sapiens.  
XX  
PN EP1083231-A1.  
XX  
PD 14-MAR-2001.  
XX  
PF 09-SEP-1999; 99EP-00202943.  
XX  
PR 09-SEP-1999; 99EP-00202943.  
XX  
PA (INTR-) INTROGENE BV.  
XX  
DR WPI; 2001-236858/25.  
XX  
PT Nucleic acids encoding smooth muscle cell specific promoters, useful e.g.  
PT for treating cardiovascular diseases or in targeting transgene expression  
PT to smooth muscle cells expressing endogenous smoothelin proteins.  
XX  
PS Example 3; Page 16; 51pp; English.  
XX  
CC The present invention describes a nucleic acid delivery vehicle (I)  
CC comprising a nucleic acid capable of expressing specifically in a  
CC contractile smooth muscle cell, preferably a vascular contractile smooth  
CC muscle cell and/or a visceral contractile smooth muscle cell. Also  
CC described are smooth muscle cell specific promoters which can be  
CC incorporated into a nucleic acid delivery vehicle, where the nucleic acid  
CC delivery vehicle preferably comprises a virus-like particle such as an  
CC adenovirus particle, an adeno-associated virus particle or a retrovirus  
CC particle. (I) has cardiovascular activity and can be used in gene  
CC therapy. The nucleic acid delivery vehicle is useful for the preparation  
CC of a pharmaceutical for the treatment of a cardiovascular disease. The  
CC promoter of the smoothelin gene (a smooth muscle cell specific promoter)  
CC is useful for providing a particular nucleic acid with the capacity to  
CC express proteins specifically in contractile smooth muscle cells. The  
CC promoter may also be used in targeting transgene expression to smooth  
CC muscle cells that express endogenous smoothelin protein, in  
CC distinguishing subsets of smooth muscle cells, and in expressing foreign  
CC genetic material specifically in contractile smooth muscle cells.  
CC AAF74719 to AAF74756 represent human smoothelin variant intron-exon  
CC splice recognition sites, which are used in an example from the present  
CC invention  
XX  
SQ Sequence 12 BP; 3 A; 2 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATCCACCTGC 12  
Db 12 ATCCAGCTGC 3

RESULT 376  
AAS01805/c  
ID AAS01805 standard; DNA; 12 BP.  
XX  
AC AAS01805;  
XX  
DT 12-SEP-2001 (first entry)  
XX  
DE Human smoothelin gene intron-exon splice recognition sequence #12.  
XX  
KW Human; smoothelin; promoter; nucleic acid delivery vehicle; restenosis;  
KW contractile smooth muscle cell; pharmaceutical; cardiovascular disease;  
KW hypertension; atherosclerosis; transgene expression; oligo linker; ds;  
KW percutaneous transluminal coronary angioplasty.  
XX  
OS Homo sapiens.  
XX  
PN WO200118048-A2.  
XX

```
PD 15-MAR-2001.
XX
PF 08-SEP-2000; 2000WO-NL000638.
XX
PR 09-SEP-1999; 99EP-00202943.
XX 09-SEP-1999; 99US-0153284P.
XX (INTR-) INTROGENE BV.
XX
PI Van Eijs GJJM, Hateboer G, Havenga MJE;
XX WPI; 2001-244559/25.
DR
XX New nucleic acids encoding smooth muscle cell specific promoters, useful
PT for treating a cardiovascular disease or in targeting transgene
PT expression to smooth muscle cells expressing endogenous smoothelin
PT protein.
XX
PS Example 3; Page 45; 60pp; English.
XX
CC The sequence represents an intron-exon splice recognition sequence of the
CC human smoothelin gene. The smoothelin gene promoter, or its functional
CC part, derivative and/or analogue, can be used as part of a nucleic acid
CC delivery vehicle, comprising a nucleic acid capable of expressing
CC specifically in a contractile smooth muscle cell. The nucleic acid
CC delivery vehicle is useful for the preparation of a pharmaceutical for
CC the treatment of cardiovascular diseases, such as hypertension,
CC atherosclerosis and restenosis after percutaneous transluminal coronary
CC angioplasty. The promoter of a smoothelin gene is useful for providing a
CC particular nucleic acid with the capacity to express foreign genetic
CC material specifically in a contractile smooth muscle cell. The promoter
CC may also be used in targeting transgene expression to smooth muscle cells
CC that express endogenous smoothelin protein, in distinguishing subsets of
CC smooth muscle cells, and in expressing foreign genetic material
CC specifically in contractile smooth muscle cells
XX
SQ Sequence 12 BP; 3 A; 2 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATCCACCTGC 12
Db 12 ATCCAGCTGC 3

RESULT 377
AAC97965/c
ID AAC97965 standard; DNA; 12 BP.
XX
AC AAC97965;
XX
DT 28-FEB-2001 (first entry)
XX
DE Primer used to illustrate DNA amplification method SEQ ID 191.
XX
KW Primer; amplification; selective; ss.
XX
OS Synthetic.
XX
PN JP2000270867-A.
XX
PD 03-OCT-2000.
XX
PF 19-MAR-1999; 99JP-00076844.
XX
PR 19-MAR-1999; 99JP-00076844.
XX
PA (SAOL ) SANYO ELECTRIC CO LTD.
XX (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
XX WPI; 2001-011047/02.
DR

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATCCACCTGC 12
Db 12 ATCCAGCTGC 3

RESULT 377
AAC97965/c
ID AAC97965 standard; DNA; 12 BP.
XX
AC AAC97965;
XX
DT 28-FEB-2001 (first entry)
XX
DE Primer used to illustrate DNA amplification method SEQ ID 191.
XX
KW Primer; amplification; selective; ss.
XX
OS Synthetic.
XX
PN JP2000270867-A.
XX
PD 03-OCT-2000.
XX
PF 19-MAR-1999; 99JP-00076844.
XX
PR 19-MAR-1999; 99JP-00076844.
XX
PA (SAOL ) SANYO ELECTRIC CO LTD.
XX (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
XX WPI; 2001-011047/02.
DR

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTG 14
Db 11 CCACCTCCTG 2

RESULT 378
AAC97915
ID AAC97915 standard; DNA; 12 BP.
XX
AC AAC97915;
XX
DT 28-FEB-2001 (first entry)
XX
DE Primer used to illustrate DNA amplification method SEQ ID 141.
XX
KW Primer; amplification; selective; ss.
XX
OS Synthetic.
XX
PN JP2000270867-A.
XX
PD 03-OCT-2000.
XX
PF 19-MAR-1999; 99JP-00076844.
XX
PR 19-MAR-1999; 99JP-00076844.
XX
PA (SAOL ) SANYO ELECTRIC CO LTD.
XX (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
XX
DR WPI; 2001-011047/02.
XX
PT Amplification of a DNA fragment and its apparatus.
XX
PS Example 1; Page 10; 32pp; Japanese.
XX
CC This invention relates to a method for amplifying a DNA fragment. The
CC method comprises successive repetitions of heat-denaturing, annealing of
CC a primer and an extending step using a DNA polymerase. The method makes
CC use of a cDNA pool in which the primer is one primer or a pair of primer
CC sets and has an amplification probability which allows it to amplify a
CC DNA fragment from a limited number of the cDNAs among the DNA pool (where
CC the limited number is in the range of 1 to 25). Also included in the
CC invention are apparatus used for carrying out the method, a primer and a
CC DNA polymerase and a kit used for amplifying a DNA fragment. The method
CC can be used to amplify a limited number of cDNAs from a pool in which a
CC wide variety of cDNAs are present. Oligonucleotides AAC97775 - AAC97990
CC represent primers used in an example illustrating the method of the
CC invention
XX
SQ Sequence 12 BP; 2 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTG 14
Db 11 CCACCTCCTG 2

RESULT 378
AAC97915
ID AAC97915 standard; DNA; 12 BP.
XX
AC AAC97915;
XX
DT 28-FEB-2001 (first entry)
XX
DE Primer used to illustrate DNA amplification method SEQ ID 141.
XX
KW Primer; amplification; selective; ss.
XX
OS Synthetic.
XX
PN JP2000270867-A.
XX
PD 03-OCT-2000.
XX
PF 19-MAR-1999; 99JP-00076844.
XX
PR 19-MAR-1999; 99JP-00076844.
XX
PA (SAOL ) SANYO ELECTRIC CO LTD.
XX (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
XX
DR WPI; 2001-011047/02.
XX
PT Amplification of a DNA fragment and its apparatus.
XX
PS Example 1; Page 10; 32pp; Japanese.
XX
CC This invention relates to a method for amplifying a DNA fragment. The
CC method comprises successive repetitions of heat-denaturing, annealing of
CC a primer and an extending step using a DNA polymerase. The method makes
CC use of a cDNA pool in which the primer is one primer or a pair of primer
CC sets and has an amplification probability which allows it to amplify a
CC DNA fragment from a limited number of the cDNAs among the DNA pool (where
CC the limited number is in the range of 1 to 25). Also included in the
CC invention are apparatus used for carrying out the method, a primer and a
CC DNA polymerase and a kit used for amplifying a DNA fragment. The method
CC can be used to amplify a limited number of cDNAs from a pool in which a
CC wide variety of cDNAs are present. Oligonucleotides AAC97775 - AAC97990
CC represent primers used in an example illustrating the method of the
CC invention
```

```
CC invention
XX
SQ Sequence 12 BP; 0 A; 4 C; 3 G; 5 T; 0 U; 0 Other;

Query Match          29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CACCTGCTGT 15
Db 1 CTCCTGCTGT 10

RESULT 379
ABI29917
ID ABI29917 standard; DNA; 12 BP.
XX
AC ABI29917;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 329890 for detecting SNP TSC0035228.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
DR WPI; 2001-657177/75.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 329890; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 1 A; 0 C; 5 G; 6 T; 0 U; 0 Other;

This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligomers are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 1 A; 0 C; 5 G; 6 T; 0 U; 0 Other;

Query Match          29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 TGCTGTGTGA 19
Db 3 TGTGTGTGA 12

RESULT 381
ABI59162/c
ID ABI59162 standard; DNA; 12 BP.
XX
AC ABI59162;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 359135 for detecting SNP TSC0051475.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
```

```
RESULT 380
ABH85587/c
ID ABH85587 standard; DNA; 12 BP.
XX
AC ABH85587;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 285580 for detecting SNP TSC0012360.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 285580; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 0 Other;

Query Match          29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 TGCTGTGTGA 19
Db 10 TGTGTGTGA 1

RESULT 381
ABI59162/c
ID ABI59162 standard; DNA; 12 BP.
XX
AC ABI59162;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 359135 for detecting SNP TSC0051475.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
```



XX Homo sapiens.  
OS  
XX  
XX WO200177384-A2.  
PN  
XX  
XX 18-OCT-2001.  
PD  
XX  
XX 06-APR-2001; 2001WO-IB0000713.  
PF  
XX  
XX 07-APR-2000; 2000DE-01019173.  
PR  
XX  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
PI  
XX  
XX WPI; 2001-657177/75.  
DR  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
PT  
XX  
XX Claim 1; SEQ ID NO 359135; 29pp + Sequence Listing; German.  
PS  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 1 A; 0 C; 8 G; 3 T; 0 U; 0 Other;  
XX  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 CCATCCACCT 10  
DB 10 CCACCCACCT 1  
RESULT 382  
ABH74750/C  
ID ABH74750 standard; DNA; 12 BP.  
XX  
XX ABH74750;  
AC  
XX 22-FEB-2002 (first entry)  
DT  
XX Oligonucleotide primer SEQ ID NO 274735 for detecting SNP TSC0003662.  
DE  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200177384-A2.  
PN  
XX  
XX 18-OCT-2001.  
PD  
XX  
XX 06-APR-2001; 2001WO-IB0000713.  
PF  
XX  
XX 07-APR-2000; 2000DE-01019173.  
PR  
XX  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX  
XX

PI Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
DR  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
PT  
XX  
XX Claim 1; SEQ ID NO 274735; 29pp + Sequence Listing; German.  
PS  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 0 C; 7 G; 2 T; 0 U; 0 Other;  
XX  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 CCATCCACCT 10  
DB 11 CCACCCACCT 2  
RESULT 383  
ABH75922  
ID ABH75922 standard; DNA; 12 BP.  
XX  
XX ABH75922;  
AC  
XX 22-FEB-2002 (first entry)  
DT  
XX Oligonucleotide primer SEQ ID NO 275915 for detecting SNP TSC0004038.  
DE  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200177384-A2.  
PN  
XX  
XX 18-OCT-2001.  
PD  
XX  
XX 06-APR-2001; 2001WO-IB0000713.  
PF  
XX  
XX 07-APR-2000; 2000DE-01019173.  
PR  
XX  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
PI  
XX  
XX WPI; 2001-657177/75.  
DR  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
PT  
XX  
XX Claim 1; SEQ ID NO 275915; 29pp + Sequence Listing; German.  
PS  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The



CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCCACCT 10  
Db 1 CCATCCAACT 10  
|||||

RESULT 384  
ABI26643  
ID ABI26643 standard; DNA; 12 BP.  
XX  
AC ABI26643;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 326616 for detecting SNP TSC0033176.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 326616; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 1 A; 6 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCCACCT 10  
Db 1 CCATCCAACT 10  
|||||

RESULT 386  
ABI59024  
ID ABI59024 standard; DNA; 12 BP.  
XX  
AC ABI59024;

Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCCACCTGCT 13  
Db 2 TCCACCTCCT 11  
|||||

RESULT 385  
ABI53560  
ID ABI53560 standard; DNA; 12 BP.  
XX  
AC ABI53560;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 353533 for detecting SNP TSC0048564.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 353533; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 5 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCCACCT 10  
Db 1 CTATCCACCT 10  
|||||

RESULT 386  
ABI59024  
ID ABI59024 standard; DNA; 12 BP.  
XX  
AC ABI59024;

XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 358997 for detecting SNP TSC0010504.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
OS Homo sapiens.  
XX WO200177384-A2.  
XX PN 18-OCT-2001.  
PD XX 06-APR-2001; 2001WO-IB000713.  
XX PF 07-APR-2000; 2000DE-01019173.  
XX PR (EPIG-) EPIGENOMICS AG.  
XX PA Olek A, Piepenbrock C, Berlin K;  
PI WPI; 2001-657177/75.  
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 358997; 29pp + Sequence Listing; German.  
XX SQ This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 12 BP; 1 A; 8 C; 0 G; 3 T; 0 U; 0 Other;  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 CCATCCACCT 10  
Db 3 CCATCCCCCT 12  
RESULT 387  
AB160693/c  
ID AB160693 standard; DNA; 12 BP.  
XX AC AB160693;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 360666 for detecting SNP TSC0052209.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is

XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 358997 for detecting SNP TSC0010504.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
OS Homo sapiens.  
XX WO200177384-A2.  
XX PN 18-OCT-2001.  
PD XX 06-APR-2001; 2001WO-IB000713.  
XX PF 07-APR-2000; 2000DE-01019173.  
XX PR (EPIG-) EPIGENOMICS AG.  
XX PA Olek A, Piepenbrock C, Berlin K;  
PI WPI; 2001-657177/75.  
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 358997; 29pp + Sequence Listing; German.  
XX SQ This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 12 BP; 1 A; 8 C; 0 G; 3 T; 0 U; 0 Other;  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 CCATCCACCT 10  
Db 3 CCATCCCCCT 12  
RESULT 387  
AB160693/c  
ID AB160693 standard; DNA; 12 BP.  
XX AC AB160693;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 360666 for detecting SNP TSC0052209.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is

PD 18-OCT-2001.  
XX 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 360666; 29pp + Sequence Listing; German.  
XX SQ This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 12 BP; 2 A; 0 C; 8 G; 2 T; 0 U; 0 Other;  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 CCATCCACCT 10  
Db 11 CCACCCACCT 2  
RESULT 388  
AB118617  
ID AB118617 standard; DNA; 12 BP.  
XX AC AB118617;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 318590 for detecting SNP TSC0028751.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 318590; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 CCATCCACCT 10  
Db 2 CCTTCCACCT 11  
||| |||||  
RESULT 389  
ABH71661  
ID ABH71661 standard; DNA; 12 BP.  
XX  
AC ABH71661;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 271638 for detecting SNP TSC0002575.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 271638; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 7 C; 0 G; 2 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 CCATCCACCT 10  
Db 3 CCTTCCACCT 12  
||| |||||  
RESULT 390  
ABH77312  
ID ABH77312 standard; DNA; 12 BP.  
XX  
AC ABH77312;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 277305 for detecting SNP TSC0004433.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 277305; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 TCCACCTGCT 13  
||||| ||

Db 1 TCCACCTCCT 10

RESULT 391

ABI18206

ID ABI18206 standard; DNA; 12 BP.

XX

AC ABI18206;

XX

DT 22-FEB-2002 (first entry)

XX

DE Oligonucleotide primer SEQ ID NO 318179 for detecting SNP TSC0028503.

XX

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX

OS Homo sapiens.

XX

PN WO200177384-A2.

XX

PD 18-OCT-2001.

XX

PF 06-APR-2001; 2001WO-IB000713.

XX

PR 07-APR-2000; 2000DE-01019173.

XX

PA (EPIG-) EPIGENOMICS AG.

XX

PI Olek A, Piepenbrock C, Berlin K;

XX

WPI; 2001-657177/75.

XX

DR Set of oligonucleotides, useful for diagnosis and cell typing, is

XX

PT designed to detect single-nucleotide polymorphisms and cytosine

PT methylation status.

XX

PS Claim 1; SEQ ID NO 318179; 29pp + Sequence Listing; German.

XX

CC This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence

CC data for this patent did not form part of the printed specification, but

CC was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences

XX

Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

XX

Query Match 29.0%; Score 8.4; DB 1; Length 12;

Best Local Similarity 90.0%; Pred. No. 2e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATCCACCTGC 12

DB 3 ATCCACCTAC 12

RESULT 392

ABI43158

ID ABI43158 standard; DNA; 12 BP.

XX

AC ABI43158;

XX

DT 22-FEB-2002 (first entry)

XX

DE Oligonucleotide primer SEQ ID NO 343131 for detecting SNP TSC0042904.

XX

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX

PN WO200177384-A2.

XX

PD 18-OCT-2001.

XX

PF 06-APR-2001; 2001WO-IB000713.

XX

PR 07-APR-2000; 2000DE-01019173.

XX

PA (EPIG-) EPIGENOMICS AG.

XX

PI Olek A, Piepenbrock C, Berlin K;

XX

WPI; 2001-657177/75.

XX

PT Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single-nucleotide polymorphisms and cytosine

PT methylation status.

XX

PS Claim 1; SEQ ID NO 343131; 29pp + Sequence Listing; German.

XX

CC This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence

CC data for this patent did not form part of the printed specification, but

CC was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences

XX

Sequence 12 BP; 2 A; 6 C; 1 G; 3 T; 0 U; 0 Other;

XX

Query Match 29.0%; Score 8.4; DB 1; Length 12;

Best Local Similarity 90.0%; Pred. No. 2e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCCACCT 10

DB 3 CCGTCCACCT 12

RESULT 393

ABI69159/c

ID ABI69159 standard; DNA; 12 BP.

XX

AC ABI69159;

XX

DT 22-FEB-2002 (first entry)

XX

DE Oligonucleotide primer SEQ ID NO 369132 for detecting SNP TSC0057463.

XX

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX

PN WO200177384-A2.

XX

PD 18-OCT-2001.

XX

PF 06-APR-2001; 2001WO-IB000713.

XX

PR 07-APR-2000; 2000DE-01019173.



XX (EPIG-) EPIGENOMICS AG.  
PA Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
PT Claim 1; SEQ ID NO 369132; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 2 A; 0 C; 6 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 3 ATCCACCTGC 12  
DB 11 ATCCACCTAC 2  
XX  
RESULT 394  
ABH81976/C  
ID ABH81976 standard; DNA; 12 BP.  
XX  
AC ABH81976;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 281969 for detecting SNP TSC0010212.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 281969 for detecting SNP TSC0010212.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB0000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 281969; 29pp + Sequence Listing; German.  
XX

CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 1 A; 0 C; 9 G; 2 T; 0 U; 0 Other;  
XX  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 1 CCATCCACCT 10  
DB 11 CCACCCACCT 2  
XX  
RESULT 395  
ABI69157/C  
ID ABI69157 standard; DNA; 12 BP.  
XX  
AC ABI69157;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 369130 for detecting SNP TSC0057462.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB0000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 369130; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX

SQ Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATCCACCTGC 12  
|||||||  
Db 10 ATCCACCTAC 1

RESULT 396  
ABI80903/c  
ID ABI80903 standard; DNA; 12 BP.  
XX  
AC ABI80903;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 380876 for detecting SNP TSC0064024.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 380876 for detecting SNP TSC0064024.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 380876; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCCACCT 10  
|||||||  
Db 10 CCATCCATCT 1

RESULT 397  
ABH97813/c

ID ABH97813 standard; DNA; 12 BP.  
XX  
AC ABH97813;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 297806 for detecting SNP TSC0017781.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 297806; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 4 A; 0 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCCACCTGCT 13  
|||||||  
Db 12 TCCACCTCCT 3

RESULT 398  
ABH93473/c  
ID ABH93473 standard; DNA; 12 BP.  
XX  
AC ABH93473;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 293466 for detecting SNP TSC0015629.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.

XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB0000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX DR WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 293466; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 12 BP; 3 A; 1 C; 4 G; 4 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 19 ACCTGGTAAA 28  
Db 12 ACCTCGTAAA 3  
  
RESULT 399  
ABI43157  
ID ABI43157 standard; DNA; 12 BP.  
XX AC ABI43157;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 343130 for detecting SNP TSC0042904.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB0000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX

DR WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 343130; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 12 BP; 2 A; 6 C; 1 G; 3 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 CCATCCACCT 10  
Db 3 CCATCCGCCT 12  
  
RESULT 400  
ABI72787  
ID ABI72787 standard; DNA; 12 BP.  
XX AC ABI72787;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 372760 for detecting SNP TSC0059601.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB0000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX DR WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 372760; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published pct sequences

```

Query Match      29.0%;   Score 8.4;   DB 1;   Length 12;
Best Local Similarity 90.0%;   Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

|    |   |            |    |
|----|---|------------|----|
| Qy | 4 | TCCACCTGCT | 13 |
|    |   |            |    |
| Db | 2 | TCCACCTCCT | 11 |

RESULT 401  
ABI05466  
ID ABI05466 standard; DNA; 12 BP.

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 305439 for detecting SNP TSC0021446.

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

**Homo sapiens.**

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

PA (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

WPI: 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 305439; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF0010-ABF99989, ABH0010-ABH99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at <ftp.wipo.int/pub/published/pct/sequences>

```

Query Match      29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

|    |   |            |    |
|----|---|------------|----|
| Qy | 1 | CCATCCACCT | 10 |
|    |   |            |    |
| Db | 2 | CCGTCCACCT | 11 |

RESULT 402  
 AB113967  
 ID AB113967 standard; DNA; 12 BP.

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 313940 for detecting SNP TSC0026041.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW  
peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW  
central nervous system; gastrointestinal; respiratory; immune; metabolic;  
KW

**Homo sapiens.**

WO200177384-A2.

18-OCT-2001.

PF 06-APR-2001: 2001WO-IB0000713.

PR 07-APR-2000; 2000DE-01019173.

PA (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

DR WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

PS Claim 1; SEQ ID NO 313940; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at [ftp.wipo.int/pub/published](http://wipo.int/pub/published) pct sequences

```

Query Match          29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

|    |   |            |    |
|----|---|------------|----|
| Qy | 1 | CCATCCACCT | 10 |
|    |   |            |    |
| Dy | 1 | CCACCCACCT | 10 |

RESULT 403  
ABI16340/c  
ID ABI16340 standard; DNA; 12 BP.

DT 22-FEB-2002 (first entry)





XX PS Claim 1; SEQ ID NO 337514; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX XX  
SQ Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 10 TGCTGTGTGA 19  
Db 2 TGATGTGTGA 11  
  
RESULT 406  
ABH77664/c  
ID ABH77664 standard; DNA; 12 BP.  
XX AC ABH77664;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 277657 for detecting SNP TSC0004662.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX DR WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 277657; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX XX  
SQ Sequence 12 BP; 3 A; 2 C; 4 G; 3 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 18 GACCTGGTAA 27  
Db 11 GACCTCGTAA 2  
  
RESULT 407  
ABH86388  
ID ABH86388 standard; DNA; 12 BP.  
XX AC ABH86388;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 286381 for detecting SNP TSC0012703.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX DR WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 286381; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX XX  
SQ Sequence 12 BP; 3 A; 7 C; 0 G; 2 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 CCATCCACCT 10  
Db 2 CCCTCCACCT 11

RESULT 408  
ABH74692/c  
ID ABH74692 standard; DNA; 12 BP.  
XX AC ABH74692;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 274677 for detecting SNP TSC0003635.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 274677; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 0 Other;  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 3 ATCCACCTGC 12  
Db 12 ATCCACCTAC 3  
RESULT 409  
ABI02272  
ID ABI02272 standard; DNA; 12 BP.  
XX AC ABI02272;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 302245 for detecting SNP TSC0019886.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 302245; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 12 BP; 3 A; 7 C; 0 G; 2 T; 0 U; 0 Other;  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 CCATCCACCT 10  
Db 2 CCACCCACCT 11  
RESULT 410  
ABI77388  
ID ABI77388 standard; DNA; 12 BP.  
XX AC ABI77388;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 377361 for detecting SNP TSC0062291.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;  
XX DR WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 377361; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 12 BP; 2 A; 0 C; 5 G; 5 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 10 TGCTGTGTGA 19  
Db 1 TGTGTGTGA 10  
  
RESULT 411  
ABH97611/c  
ID ABH97611 standard; DNA; 12 BP.  
XX AC ABH97611;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 297604 for detecting SNP TSC0017656.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX DR WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 297604; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 CCATCCACCT 10  
Db 12 CCATCTACCT 3  
  
RESULT 412  
ABH84024  
ID ABH84024 standard; DNA; 12 BP.  
XX AC ABH84024;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 284017 for detecting SNP TSC0011628.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX DR WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 284017; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;



```

Query Match      29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 ATCCACCTGC 12
      |||||
Db      1 ATCCACCTAC 10

RESULT 413
ABH85692/c
ID  ABH85692 standard; DNA; 12 BP.
XX
AC  ABH85692;
XX
DT  22-FEB-2002 (first entry)
XX
DE  Oligonucleotide primer SEQ ID NO 285685 for detecting SNP TSC0012400.
XX
KW  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW  peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW  central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS  Homo sapiens.
XX
PN  WO200177384-A2.
XX
PD  18-OCT-2001.
XX
PF  06-APR-2001; 2001WO-IB000713.
XX
PR  07-APR-2000; 2000DE-01019173.
XX
PA  (EPIG-) EPIGENOMICS AG.
XX
PI  Olek A, Piepenbrock C, Berlin K;
XX  WPI; 2001-657177/75.
XX
PT  Set of oligonucleotides, useful for diagnosis and cell typing, is
PT  designed to detect single-nucleotide polymorphisms and cytosine
PT  methylation status.
XX
PS  Claim 1; SEQ ID NO 285685; 29pp + Sequence Listing; German.
XX
CC  This invention describes novel oligonucleotide primers or peptide nucleic
CC  acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC  and cytosine methylation status in chemically pretreated genomic DNA. The
CC  oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC  range of diseases including immune system, gastrointestinal, respiratory,
CC  central nervous system, cardiovascular and metabolic disorders. The
CC  oligomers are also used for detecting cell type differentiation. ABC00010
CC  -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC  represent the oligomers described in the invention. NOTE: The sequence
CC  data for this patent did not form part of the printed specification, but
CC  was obtained in electronic format from WIPO at
CC  ftp.wipo.int/pub/published_pct_sequences
XX
SQ  Sequence 12 BP; 2 A; 1 C; 6 G; 3 T; 0 U; 0 Other;

Query Match      29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 ATCCACCTGC 12
      |||||
Db      10 ATCCACCCGC 1

RESULT 414
ABI53806/c
ID  ABI53806 standard; DNA; 12 BP.
XX
```

```

AC  ABI53806;
XX
DT  22-FEB-2002 (first entry)
XX
DE  Oligonucleotide primer SEQ ID NO 353779 for detecting SNP TSC0048711.
XX
KW  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW  peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW  central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS  Homo sapiens.
XX
PN  WO200177384-A2.
XX
PD  18-OCT-2001.
XX
PF  06-APR-2001; 2001WO-IB000713.
XX
PR  07-APR-2000; 2000DE-01019173.
XX
PA  (EPIG-) EPIGENOMICS AG.
XX
PI  Olek A, Piepenbrock C, Berlin K;
XX  WPI; 2001-657177/75.
XX
PT  Set of oligonucleotides, useful for diagnosis and cell typing, is
PT  designed to detect single-nucleotide polymorphisms and cytosine
PT  methylation status.
XX
PS  Claim 1; SEQ ID NO 353779; 29pp + Sequence Listing; German.
XX
CC  This invention describes novel oligonucleotide primers or peptide nucleic
CC  acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC  and cytosine methylation status in chemically pretreated genomic DNA. The
CC  oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC  range of diseases including immune system, gastrointestinal, respiratory,
CC  central nervous system, cardiovascular and metabolic disorders. The
CC  oligomers are also used for detecting cell type differentiation. ABC00010
CC  -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC  represent the oligomers described in the invention. NOTE: The sequence
CC  data for this patent did not form part of the printed specification, but
CC  was obtained in electronic format from WIPO at
CC  ftp.wipo.int/pub/published_pct_sequences
XX
SQ  Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

Query Match      29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCATCCACCT 10
      |||||
Db      11 CCATCCATCT 2

RESULT 415
ABI19386
ID  ABI19386 standard; DNA; 12 BP.
XX
AC  ABI19386;
XX
DT  22-FEB-2002 (first entry)
XX
DE  Oligonucleotide primer SEQ ID NO 319359 for detecting SNP TSC0029177.
XX
KW  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW  peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW  central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS  Homo sapiens.
XX
PN  WO200177384-A2.
```



```
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match      29.0%; Score 8.4; DB 1; Length 12;
  Best Local Similarity 90.0%; Pred. No. 2e+02;
  Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATCCACCTGC 12
   |||||
Db 2 ATCCACCTAC 11

RESULT 418
ABH84793
ID ABH84793 standard; DNA; 12 BP.
XX
AC ABH84793;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 284786 for detecting SNP TSC0011996.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 284786; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 1 A; 8 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match      29.0%; Score 8.4; DB 1; Length 12;
  Best Local Similarity 90.0%; Pred. No. 2e+02;
  Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCCACCT 10
```

```
Db 3 CCCTCCACCT 12
   |||||
RESULT 419
ABI73341/c
ID ABI73341 standard; DNA; 12 BP.
XX
AC ABI73341;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 373314 for detecting SNP TSC0059971.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 373314; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 0 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match      29.0%; Score 8.4; DB 1; Length 12;
  Best Local Similarity 90.0%; Pred. No. 2e+02;
  Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCCACCTGCT 13
   |||||
Db 10 TCCACCTTCT 1

RESULT 420
ABI59818/c
ID ABI59818 standard; DNA; 12 BP.
XX
AC ABI59818;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 359791 for detecting SNP TSC0008946.
```

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIC-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
DR  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 359791; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 2 A; 0 C; 7 G; 3 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 CCATCCACCT 10  
Db 10 CCAACCCACCT 1  
  
RESULT 421  
ABK72569  
ID ABK72569 standard; DNA; 12 BP.  
XX  
AC ABK72569;  
XX  
DT 13-AUG-2002 (first entry)  
XX  
DE Human OPAl gene, exon/intron junction #36.  
XX  
KW Human; ophthalmological; OPAl; autosomal dominant optic atrophy; ADOA;  
KW gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200227022-A2.  
XX  
PD 04-APR-2002.  
XX  
PF 26-SEP-2001; 2001WO-GB004284.  
XX  
PR 26-SEP-2000; 2000GB-00023555.  
XX

XX (UNLO ) UNIV COLLEGE LONDON.  
PA (UYEY-) UNIV EYE HOSPITAL.  
XX  
PI Bhattacharya S, Wissinger B, Alexander C, Votruba M;  
XX WPI; 2002-416484/44.  
DR  
XX Novel human normal or mutant OPAl (the predominant locus for autosomal  
PT dominant optic atrophy (ADOA)) polypeptides and the OPAl gene, useful in  
PT the diagnosis and treatment of autosomal dominant optic atrophy ADOA.  
XX  
PS Disclosure; Fig 12; 75pp; English.  
XX  
CC The invention relates to an isolated human normal or mutant OPAl (the  
CC predominant locus for autosomal dominant optic atrophy (ADOA))  
CC polypeptide (I), characterised by a molecular weight of about 112 kDa,  
CC and substantially free of other human proteins. Also described is the DNA  
CC (II) encoding (I). (I) and (II) are useful as a medicament, for the  
CC treatment of a medical condition resulting from a defect in the OPAl  
CC gene, which results in autosomal dominant optic atrophy. The nucleic acid  
CC and antibodies to (I) are useful in a variety of hybridisation and  
CC immunological assays to screen for, and to detect the presence of, either  
CC a normal or a defective OPAl gene or gene product. ABK72533-ABK72593  
CC represent the human OPAl gene and intron/exon splice junctions  
XX  
SQ Sequence 12 BP; 4 A; 2 C; 4 G; 2 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 18 GACCTGGTAA 27  
Db 1 GACCGGGTAA 10  
  
RESULT 422  
ABK72535  
ID ABK72535 standard; DNA; 12 BP.  
XX  
AC ABK72535;  
XX  
DT 13-AUG-2002 (first entry)  
XX  
DE Human OPAl gene, exon/intron junction #2.  
XX  
KW Human; ophthalmological; OPAl; autosomal dominant optic atrophy; ADOA;  
KW gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200227022-A2.  
XX  
PD 04-APR-2002.  
XX  
PF 26-SEP-2001; 2001WO-GB004284.  
XX  
PR 26-SEP-2000; 2000GB-00023555.  
XX  
PA (UNLO ) UNIV COLLEGE LONDON.  
PA (UYEY-) UNIV EYE HOSPITAL.  
XX  
PI Bhattacharya S, Wissinger B, Alexander C, Votruba M;  
XX WPI; 2002-416484/44.  
DR  
XX Novel human normal or mutant OPAl (the predominant locus for autosomal  
PT dominant optic atrophy (ADOA)) polypeptides and the OPAl gene, useful in  
PT the diagnosis and treatment of autosomal dominant optic atrophy ADOA.  
XX  
PS Disclosure; Fig 12; 75pp; English.  
XX



CC The invention relates to an isolated human normal or mutant OPA1 (the  
CC predominant locus for autosomal dominant optic atrophy (ADOA))  
CC polypeptide (I), characterised by a molecular weight of about 112 kDa,  
CC and substantially free of other human proteins. Also described is the DNA  
CC (II) encoding (I). (I) and (II) are useful as a medicament, for the  
CC treatment of a medical condition resulting from a defect in the OPA1  
CC gene, which results in autosomal dominant optic atrophy. The nucleic acid  
CC and antibodies to (I) are useful in a variety of hybridisation and  
CC immunological assays to screen for, and to detect the presence of, either  
CC a normal or a defective OPA1 gene or gene product. ABK72533-ABK72593  
CC represent the human OPA1 gene and intron/exon splice junctions  
XX  
SQ Sequence 12 BP; 2 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 GACCTGGTAA 27  
| | | | | | | |  
Db 1 GGCCTGGTAA 10

RESULT 423  
AAL42695/c  
ID AAL42695 standard; DNA; 12 BP.

XX AAL42695;

DT 08-AUG-2002 (first entry)

DE Rice seed bZIP transcription factor-related nucleotide 13.

KW Rice seed b-zipper 1; RISBZ1; ds; rice; b-ZIP transcription factor;  
KW novel plant; transgenic plant; seed production; higher nutrition;  
KW denser protein storage.

OS Unidentified.

PN WO200231154-A1.

PD 18-APR-2002.

PF 11-OCT-2001; 2001WO-JP008936.

PR 11-OCT-2000; 2000JP-00311295.

PA (NORQ ) NAT INST AGROBIOLOGICAL SCI.

PA (BIOO-) BIO-ORIENTED TECHNOLOGY RES ADVANCEMENT.

PI Takaiwa F, Onodera Y;

XX WPI; 2002-372276/40.

PT Rice seed-originated bZIP type transcription factors regulating  
PT expression of rice storage protein with binding activity to GCN4 motif,  
PT useful in constructing new breeds of plants to produce seeds with higher  
PT nutrition.

PS Example 11; Fig 13; 124pp; Japanese.

XX The invention comprises the amino acid and coding sequences of rice seed  
CC b-ZIP type transcriptions factors (RISBZ1, RISBZ4 and RISBZ5). The DNA and  
CC protein sequences of the rice seed b-ZIP transcription factors are useful  
CC in constructing new breeds of plants (e.g. rice) - to produce seeds with  
CC higher nutrition and denser protein storage. The present DNA sequence is  
CC included in the specification

SQ Sequence 12 BP; 4 A; 5 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 TGTGACCTGG 24  
| | | | | | | |  
Db 12 TGTGACGTGG 3

RESULT 424  
AAL42645/c  
ID AAL42645 standard; DNA; 12 BP.

XX AAL42645;

DT 08-AUG-2002 (first entry)

DE Rice seed bZIP transcription factor PCR primer 1.

XX Rice seed b-zipper 1; RISBZ1; ss; rice; b-ZIP transcription factor;

KW novel plant; transgenic plant; seed production; higher nutrition;

OS Oryza sativa.

PN WO200231154-A1.

PD 18-APR-2002.

PF 11-OCT-2001; 2001WO-JP008936.

PR 11-OCT-2000; 2000JP-00311295.

PA (NORQ ) NAT INST AGROBIOLOGICAL SCI.

PA (BIOO-) BIO-ORIENTED TECHNOLOGY RES ADVANCEMENT.

PI Takaiwa F, Onodera Y;

XX WPI; 2002-372276/40.

PT Rice seed-originated bZIP type transcription factors regulating  
PT expression of rice storage protein with binding activity to GCN4 motif,  
PT useful in constructing new breeds of plants to produce seeds with higher  
PT nutrition.

PS Disclosure; Page 21; 124pp; Japanese.

XX The invention comprises the amino acid and coding sequences of rice seed  
CC b-ZIP type transcriptions factors (RISBZ1, RISBZ4 and RISBZ5). The DNA and  
CC protein sequences of the rice seed b-ZIP transcription factors are useful  
CC in constructing new breeds of plants (e.g. rice) - to produce seeds with  
CC higher nutrition and denser protein storage. DNA sequences AAL42638 -  
CC AAL42682 represent rice seed bZIP transcription factor PCR primers

SQ Sequence 12 BP; 4 A; 5 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 TGTGACCTGG 24  
| | | | | | | |  
Db 12 TGTGACGTGG 3

RESULT 425

ID ABK29928 standard; DNA; 12 BP.

XX ABK29928;

DT 23-APR-2002 (first entry)

DE Beta-lactamase promoter wild type sequence for the start site.

XX Cyclin D1 promoter; CD40L promoter; hepatitis B virus promoter;

|                                                            |                                                                           |
|------------------------------------------------------------|---------------------------------------------------------------------------|
| KW                                                         | HBV promoter; vancomycin-resistant enterococci promoter; VRE promoter;    |
| KW                                                         | vanH promoter; androgen receptor promoter; AR promoter;                   |
| KW                                                         | human epidermal growth factor receptor 2 promoter; her2 promoter;         |
| KW                                                         | beta lactamase promoter; Bla promoter; transgene; cancer; breast cancer;  |
| KW                                                         | colon cancer; immunological disorder; prostate cancer; cytostatic;        |
| KW                                                         | autoimmune disease; HBV pre-S promoter; HBV-X promoter;                   |
| KW                                                         | Enterococcus infection; immunosuppressive; antibacterial; antiviral;      |
| KW                                                         | gene expression modulator; multiple sclerosis; MS;                        |
| KW                                                         | chronic hepatic insufficiency; cirrhosis; hepatocellular carcinoma;       |
| KW                                                         | systematic lupus erythematosus; SLE; graft-vs-host disease; GVHD;         |
| KW                                                         | familial adenomatous polyposis; rheumatoid arthritis; PCR; primer;        |
| KW                                                         | transgenic; ss.                                                           |
| XX                                                         |                                                                           |
| OS                                                         | Escherichia coli.                                                         |
| XX                                                         |                                                                           |
| PN                                                         | WO200194600-A2.                                                           |
| XX                                                         |                                                                           |
| PD                                                         | 13-DEC-2001.                                                              |
| XX                                                         |                                                                           |
| PF                                                         | 06-JUN-2001; 2001WO-US018343.                                             |
| XX                                                         |                                                                           |
| PR                                                         | 06-JUN-2000; 2000US-0209549P.                                             |
| XX                                                         |                                                                           |
| PA                                                         | (GENE-) GENELABS TECHNOLOGIES INC.                                        |
| XX                                                         |                                                                           |
| PI                                                         | Kim JP, Starr DB, Tam AW, Laurance ME, Michelotti EF;                     |
| PI                                                         | Velligan MD, Latour DR, Thomas RL, Kongpachith A, Sheppard LT;            |
| PI                                                         | Lim MY, Bruice TW;                                                        |
| XX                                                         |                                                                           |
| DR                                                         | WPI; 2002-130595/17.                                                      |
| XX                                                         |                                                                           |
| PT                                                         | New nucleic acid regulatory sequences, which are able to regulate         |
| PT                                                         | expression of a gene operably linked to a promoter, useful for regulating |
| PT                                                         | the expression of transgenes and for treating e.g., cancer and            |
| PT                                                         | immunological diseases.                                                   |
| XX                                                         |                                                                           |
| PS                                                         | Claim 17; Page 60; 95pp; English.                                         |
| XX                                                         |                                                                           |
| CC                                                         | The invention describes an isolated nucleic acid regulatory sequence for  |
| CC                                                         | a cyclin D1 promoter, a CD40L promoter, vancomycin-resistant enterococci  |
| CC                                                         | (VRE) promoter, an HBV promoter, androgen receptor (AR) promoter, Human   |
| CC                                                         | epidermal growth factor receptor 2 (HER2) promoter, or a beta lactamase   |
| CC                                                         | (Bla) promoter. Transcription regulatory sequences may be used to         |
| CC                                                         | regulate expression of the endogenous, autologous or heterologous genes   |
| CC                                                         | operably linked to the promoter, and may be incorporated into             |
| CC                                                         | heterologous nucleic acid constructs for use in regulated expression of   |
| CC                                                         | transgenes. Regulated expression of cyclin D1 can be used in cancer       |
| CC                                                         | therapies, such as breast, colon or pancreatic cancers and familial       |
| CC                                                         | adenomatous polyposis. Regulation of the activity of CD40L gene promoter  |
| CC                                                         | may be used in the treatment of immunological disorders, such as          |
| CC                                                         | autoimmune diseases e.g. multiple sclerosis (MS), systematic lupus        |
| CC                                                         | erythematosus (SLE), graft-vs-host disease (GVHD) and rheumatoid          |
| CC                                                         | arthritis. Regulated expression of genes under the control of the HBV     |
| CC                                                         | (hepatitis B)-specific core, pre-S and X promoters can be used in the     |
| CC                                                         | therapy of HBV disease, chronic hepatic insufficiency, cirrhosis,         |
| CC                                                         | hepatocellular carcinoma, and in the regulated expression of liver cell-  |
| CC                                                         | specific genes. Regulated expression of the vanH gene promoter can be     |
| CC                                                         | used in treatment of Enterococcus infection, while regulated expression   |
| CC                                                         | of the androgen receptor gene can be used in the treatment of prostate    |
| CC                                                         | cancer. This sequence represents a primer used in the invention to        |
| CC                                                         | determine the functions of regions within the selected promoters,         |
| CC                                                         | described in the method of the invention                                  |
| XX                                                         |                                                                           |
| SQ                                                         | Sequence 12 BP; 5 A; 3 C; 1 G; 3 T; 0 U; 0 Other;                         |
| Query Match 29.0%; Score 8.4; DB 1; Length 12;             |                                                                           |
| Best Local Similarity 90.0%; Pred. No. 2e+02;              |                                                                           |
| Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0; |                                                                           |
| Qy                                                         | 20 CCTGGTAAAT 29                                                          |
|                                                            |                                                                           |
| Db                                                         | 3 CCTGATAAAT 12                                                           |

|                                                                              |
|------------------------------------------------------------------------------|
| RESULT 426                                                                   |
| ABK30092                                                                     |
| ID ABK30092 standard; DNA; 12 BP.                                            |
| XX                                                                           |
| AC ABK30092;                                                                 |
| XX                                                                           |
| DT 23-APR-2002 (first entry)                                                 |
| XX                                                                           |
| DE Beta-lactamase promoter, wild type -5 to +7 region.                       |
| XX                                                                           |
| KW Cyclin D1 promoter; CD40L promoter; hepatitis B virus promoter;           |
| KW HBV promoter; vancomycin-resistant enterococci promoter; VRE promoter;    |
| KW vanH promoter; androgen receptor promoter; AR promoter;                   |
| KW human epidermal growth factor receptor 2 promoter; her2 promoter;         |
| KW beta lactamase promoter; Bla promoter; transgene; cancer; breast cancer;  |
| KW colon cancer; immunological disorder; prostate cancer; cytostatic;        |
| KW autoimmune disease; HBV pre-S promoter; HBV-X promoter;                   |
| KW Enterococcus infection; immunosuppressive; antibacterial; antiviral;      |
| KW gene expression modulator; multiple sclerosis; MS;                        |
| KW chronic hepatic insufficiency; cirrhosis; hepatocellular carcinoma;       |
| KW systematic lupus erythematosus; SLE; graft-vs-host disease; GVHD;         |
| KW familial adenomatous polyposis; rheumatoid arthritis; PCR; primer;        |
| KW mutant; transgenic; ds.                                                   |
| XX                                                                           |
| OS Escherichia coli.                                                         |
| XX                                                                           |
| PN WO200194600-A2.                                                           |
| XX                                                                           |
| PD 13-DEC-2001.                                                              |
| XX                                                                           |
| PF 06-JUN-2001; 2001WO-US018343.                                             |
| XX                                                                           |
| PR 06-JUN-2000; 2000US-0209549P.                                             |
| XX                                                                           |
| PA (GENE-) GENELABS TECHNOLOGIES INC.                                        |
| XX                                                                           |
| PI Kim JP, Starr DB, Tam AW, Laurance ME, Michelotti EF;                     |
| PI Velligan MD, Latour DR, Thomas RL, Kongpachith A, Sheppard LT;            |
| PI Lim MY, Bruice TW;                                                        |
| XX                                                                           |
| DR WPI; 2002-130595/17.                                                      |
| XX                                                                           |
| PT New nucleic acid regulatory sequences, which are able to regulate         |
| PT expression of a gene operably linked to a promoter, useful for regulating |
| PT the expression of transgenes and for treating e.g., cancer and            |
| PT immunological diseases.                                                   |
| XX                                                                           |
| PS Example 7; Page 57; 95pp; English.                                        |
| XX                                                                           |
| CC The invention describes an isolated nucleic acid regulatory sequence for  |
| a cyclin D1 promoter, a CD40L promoter, vancomycin-resistant enterococci     |
| (VRE) promoter, an HBV promoter, androgen receptor (AR) promoter, Human      |
| epidermal growth factor receptor 2 (HER2) promoter, or a beta lactamase      |
| (Bla) promoter. Transcription regulatory sequences may be used to            |
| regulate expression of the endogenous, autologous or heterologous genes      |
| operably linked to the promoter, and may be incorporated into                |
| heterologous nucleic acid constructs for use in regulated expression of      |
| transgenes. Regulated expression of cyclin D1 can be used in cancer          |
| therapies, such as breast, colon or pancreatic cancers and familial          |
| adenomatous polyposis. Regulation of the activity of CD40L gene promoter     |
| may be used in the treatment of immunological disorders, such as             |
| autoimmune diseases e.g. multiple sclerosis (MS), systematic lupus           |
| erythematosus (SLE), graft-vs-host disease (GVHD) and rheumatoid             |
| arthritis. Regulated expression of genes under the control of the HBV        |
| (hepatitis B)-specific core, pre-S and X promoters can be used in the        |
| therapy of HBV disease, chronic hepatic insufficiency, cirrhosis,            |
| hepatocellular carcinoma, and in the regulated expression of liver cell-     |
| specific genes. Regulated expression of the vanH gene promoter can be        |
| used in treatment of Enterococcus infection, while regulated expression      |
| of the androgen receptor gene can be used in the treatment of prostate       |
| cancer. This sequence represents a primer used in the invention to           |
| determine the functions of regions within the selected promoters,            |
| described in the method of the invention                                     |
| XX                                                                           |

CC expression, described in the method of the invention  
XX  
SQ Sequence 12 BP; 5 A; 3 C; 1 G; 3 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 20 CCTGGTAAAT 29  
Db 3 CCTGATAAAT 12  
  
RESULT 427  
ABA91368  
ID ABA91368 standard; DNA; 12 BP.  
XX  
AC ABA91368;  
XX  
DT 08-APR-2002 (first entry)  
XX  
DE DNA encoding neuroactive peptide NT-13.  
XX  
KW Neuroactive peptide; NT-13; hypoxia; ischaemia; therapy; gene; ss.  
XX  
OS Synthetic.  
XX  
PN WO200198367-A2.  
XX  
PD 27-DEC-2001.  
XX  
PF 22-JUN-2001; 2001WO-US019839.  
XX  
PR 22-JUN-2000; 2000US-0213614P.  
XX  
PA (NYXI-) NYXIS NEURO THERAPIES INC.  
PI Moskal JR, Yamamoto H, Colley PA;  
XX WPI; 2002-098225/13.  
DR P-PSDB; AAM50692.  
XX  
PT Use of peptide or amino acid compositions for the treatment of hypoxia  
PT and ischemia.  
PT  
PS Disclosure; Page 13; 4lpp; English.  
XX  
CC The present sequence is that of DNA capable of encoding NT-13 (see  
CC AAM50692), a neuroactive peptide that binds to the N-methyl-D-aspartate  
CC (NMDA) receptor, and which can be used to treat hypoxia and ischaemia. A  
CC method of treating hypoxia by administering a peptide or amino acid  
CC composition comprising a neuroactive peptide such as NT-13, a DNA  
CC molecule encoding a neuroactive peptide such as NT-13, and a method of  
CC treating the effects of hypoxia in the central nervous system by  
CC administering a neuroactive peptide, especially NT-13, are claimed. NT-13  
CC was shown to be a partial agonist in a pharmacological NMDA-specific  
CC function assay, a partial agonist in voltage-clamp experiments in an  
CC oocyte expression system, and a partial agonist in a behavioural NMDA-  
CC specific function assay  
XX  
SQ Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 TCCACCTGCT 13  
Db 3 TCCACCTACT 12  
  
RESULT 428  
ADE85925

ID ADE85925 standard; RNA; 12 BP.  
XX  
AC ADE85925;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Immunostimulatory G,U-containing RNA oligomer from HIV-1.  
XX  
KW Toll-like receptor; immunostimulant; antimicrobial; antiallergic;  
KW cytostatic; vaccine; HIV-1; ss.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO2003086280-A2.  
XX  
PD 23-OCT-2003.  
XX  
PF 04-APR-2003; 2003WO-US010406.  
XX  
PR 04-APR-2002; 2002US-0370515P.  
PR 29-OCT-2002; 2002US-0421966P.  
XX  
PA (COLE-) COLEY PHARM GMBH.  
XX  
PI Lipford G, Bauer S;  
XX  
DR WPI; 2003-845251/78.  
XX  
PT New immunostimulatory composition, useful in inducing an immune response  
PT against microbial or cancer antigen or allergen.  
XX  
PS Example 11; SEQ ID NO 2; 220pp; English.  
XX  
CC The present sequence is that of a G,U-containing RNA oligomer  
CC corresponding to nucleotides 112-123 of HIV-1 strain BH10. This is an  
CC example of immunostimulatory RNA oligomers of the invention that comprise  
CC at least one guanine and at least one uracil. The RNA oligomers are  
CC preferably G,U-rich RNA, do not require a CpG dinucleotide, and are at  
CC least 50% self-complementary. They are thought to signal through an MyD88  
CC -dependent pathway, probably through Toll-like receptor (TLR) 7 or TLR8,  
CC and are believed to be ligands of TLR7 or TLR8. Claimed immunostimulatory  
CC compositions comprise a G,U-containing RNA oligomer and optionally an  
CC antigen, especially an allergen, cancer antigen or microbial antigen.  
CC Methods are provided for activating an immune cell, inducing an immune  
CC response, stimulating TLR8 or TLR7 signalling, and supplementing a TLR8-  
CC or TLR7-mediated immune response. The methods and compositions are useful  
CC for activating immune cells in vivo, in vitro and ex vivo, treating  
CC infection, treating cancer, identifying a target receptor, and screening  
CC for additional immunostimulatory compounds. In an example from the  
CC invention, administration of the present RNA oligomer to human peripheral  
CC blood mononuclear cells at micromolar concentrations in the presence of  
CC DOTAP induced 50-100 ng/ml of tumour necrosis factor and 50-200 ng/ml of  
CC interleukin-12 p40.  
XX  
SQ Sequence 12 BP; 0 A; 1 C; 5 G; 0 T; 6 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 50.0%; Pred. No. 2e+02;  
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
  
QY 9 CTGCTGTGTG 18  
Db 3 CUGUUGUGUG 12  
  
RESULT 429  
ADF78662/c  
ID ADF78662 standard; DNA; 12 BP.  
XX  
AC ADF78662;  
XX  
DT 26-FEB-2004 (first entry)  
XX

|                                                            |                                                                           |                                                            |                                                                           |
|------------------------------------------------------------|---------------------------------------------------------------------------|------------------------------------------------------------|---------------------------------------------------------------------------|
| DE                                                         | Chromosomal abnormality detection-related PCR primer 243.                 | DE                                                         | Chromosomal abnormality detection-related PCR primer 67.                  |
| XX                                                         |                                                                           | XX                                                         |                                                                           |
| KW                                                         | chromosomal abnormality; maternal locus; genetic disorder; foetus;        | KW                                                         | chromosomal abnormality; maternal locus; genetic disorder; foetus;        |
| KW                                                         | mutation; translocation; transversion; monosomy; trisomy 21;              | KW                                                         | mutation; translocation; transversion; monosomy; trisomy 21;              |
| KW                                                         | chromosome 21; Down's Syndrome; aneuploidies; chromosome deletion;        | KW                                                         | chromosome 21; Down's Syndrome; aneuploidies; chromosome deletion;        |
| KW                                                         | chromosome addition; chromosome amplification; chromosome translocation;  | KW                                                         | chromosome addition; chromosome amplification; chromosome translocation;  |
| KW                                                         | chromosome rearrangement; single nucleotide polymorphism detection;       | KW                                                         | chromosome rearrangement; single nucleotide polymorphism detection;       |
| KW                                                         | SNP detection; pregnant female; PCR; primer; ss.                          | KW                                                         | SNP detection; pregnant female; PCR; primer; ss.                          |
| XX                                                         |                                                                           | XX                                                         |                                                                           |
| OS                                                         | Homo sapiens.                                                             | OS                                                         | Homo sapiens.                                                             |
| XX                                                         |                                                                           | XX                                                         |                                                                           |
| PN                                                         | WO2003074723-A2.                                                          | PN                                                         | WO2003074723-A2.                                                          |
| XX                                                         |                                                                           | XX                                                         |                                                                           |
| PD                                                         | 12-SEP-2003.                                                              | PD                                                         | 12-SEP-2003.                                                              |
| XX                                                         |                                                                           | XX                                                         |                                                                           |
| PF                                                         | 28-FEB-2003; 2003WO-US006198.                                             | PF                                                         | 28-FEB-2003; 2003WO-US006198.                                             |
| XX                                                         |                                                                           | XX                                                         |                                                                           |
| PR                                                         | 01-MAR-2002; 2002US-0360232P.                                             | PR                                                         | 01-MAR-2002; 2002US-0360232P.                                             |
| PR                                                         | 11-MAR-2002; 2002US-00093618.                                             | PR                                                         | 11-MAR-2002; 2002US-00093618.                                             |
| PR                                                         | 08-MAY-2002; 2002US-0378354P.                                             | PR                                                         | 08-MAY-2002; 2002US-0378354P.                                             |
| XX                                                         |                                                                           | XX                                                         |                                                                           |
| PA                                                         | (DHAL/) DHALLAN R.                                                        | PA                                                         | (DHAL/) DHALLAN R.                                                        |
| XX                                                         |                                                                           | XX                                                         |                                                                           |
| PI                                                         | Dhallan R;                                                                | PI                                                         | Dhallan R;                                                                |
| XX                                                         |                                                                           | XX                                                         |                                                                           |
| DR                                                         | WPI; 2003-845073/78.                                                      | DR                                                         | WPI; 2003-845073/78.                                                      |
| XX                                                         |                                                                           | XX                                                         |                                                                           |
| PT                                                         | Detection of chromosomal abnormalities e.g. Down's Syndrome, non-         | PT                                                         | Detection of chromosomal abnormalities e.g. Down's Syndrome, non-         |
| PT                                                         | invasively in a fetus, comprises forming a ratio of amounts of alleles at | PT                                                         | invasively in a fetus, comprises forming a ratio of amounts of alleles at |
| PT                                                         | a locus of interest and a different heterozygous locus.                   | PT                                                         | a locus of interest and a different heterozygous locus.                   |
| XX                                                         |                                                                           | XX                                                         |                                                                           |
| PS                                                         | Example 11; Page 238; 164pp; English.                                     | PS                                                         | Example 11; Page 214; 164pp; English.                                     |
| XX                                                         |                                                                           | XX                                                         |                                                                           |
| CC                                                         | This invention relates to a novel method of detecting chromosomal         | CC                                                         | This invention relates to a novel method of detecting chromosomal         |
| CC                                                         | abnormalities by determining the sequence of alleles of a locus of        | CC                                                         | abnormalities by determining the sequence of alleles of a locus of        |
| CC                                                         | interest from template DNA, determining which alleles are present and     | CC                                                         | interest from template DNA, determining which alleles are present and     |
| CC                                                         | comparing to amounts of alleles at a different, selected heterozygous     | CC                                                         | comparing to amounts of alleles at a different, selected heterozygous     |
| CC                                                         | locus (for example on another chromosome or a maternal locus); relative   | CC                                                         | locus (for example on another chromosome or a maternal locus); relative   |
| CC                                                         | amounts are expressed as a ratio indicating presence or absence of the    | CC                                                         | amounts are expressed as a ratio indicating presence or absence of the    |
| CC                                                         | abnormality. The method is useful for the detection of genetic disorders, | CC                                                         | abnormality. The method is useful for the detection of genetic disorders, |
| CC                                                         | especially in a foetus, including chromosomal abnormalities and           | CC                                                         | especially in a foetus, including chromosomal abnormalities and           |
| CC                                                         | mutations, for example translocations, transversions, monosomies,         | CC                                                         | mutations, for example translocations, transversions, monosomies,         |
| CC                                                         | trisomies (for example trisomy 21 in which an additional copy of          | CC                                                         | trisomies (for example trisomy 21 in which an additional copy of          |
| CC                                                         | chromosome 21 results in Down's Syndrome) and other aneuploidies,         | CC                                                         | chromosome 21 results in Down's Syndrome) and other aneuploidies,         |
| CC                                                         | deletions, additions, amplifications, translocations and rearrangements.  | CC                                                         | deletions, additions, amplifications, translocations and rearrangements.  |
| CC                                                         | It can be used to detect any alterations in a gene sequence, especially   | CC                                                         | It can be used to detect any alterations in a gene sequence, especially   |
| CC                                                         | single nucleotide polymorphisms (SNPs), and may be used to detect         | CC                                                         | single nucleotide polymorphisms (SNPs), and may be used to detect         |
| CC                                                         | numerous abnormalities simultaneously, for example if several SNPs are    | CC                                                         | numerous abnormalities simultaneously, for example if several SNPs are    |
| CC                                                         | associated with a particular disease. The method provides a rapid, non-   | CC                                                         | associated with a particular disease. The method provides a rapid, non-   |
| CC                                                         | invasive method for determining the sequence of DNA from a foetus using a | CC                                                         | invasive method for determining the sequence of DNA from a foetus using a |
| CC                                                         | sample from a pregnant female, for example to detect genetic disorders as | CC                                                         | sample from a pregnant female, for example to detect genetic disorders as |
| CC                                                         | above or to determine if a foetus is a carrier of a disease or            | CC                                                         | above or to determine if a foetus is a carrier of a disease or            |
| CC                                                         | predisposed to a disease.                                                 | CC                                                         | predisposed to a disease.                                                 |
| XX                                                         |                                                                           | XX                                                         |                                                                           |
| SQ                                                         | Sequence 12 BP; 5 A; 5 C; 1 G; 1 T; 0 U; 0 Other;                         | SQ                                                         | Sequence 12 BP; 4 A; 3 C; 4 G; 1 T; 0 U; 0 Other;                         |
| Query Match 29.0%; Score 8.4; DB 1; Length 12;             |                                                                           | Query Match 29.0%; Score 8.4; DB 1; Length 12;             |                                                                           |
| Best Local Similarity 90.0%; Pred. No. 2e+02;              |                                                                           | Best Local Similarity 90.0%; Pred. No. 2e+02;              |                                                                           |
| Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0; |                                                                           | Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0; |                                                                           |
| QY 10 TGCTGTGTGA 19                                        |                                                                           | QY 7 ACCTGCTGTG 16                                         |                                                                           |
| Db                                                         |                                                                           | Db                                                         |                                                                           |
| 12 TTCTGTGTGA 3                                            |                                                                           | 10 ACCCGCTGTG 1                                            |                                                                           |
| RESULT 430                                                 |                                                                           | RESULT 431                                                 |                                                                           |
| ADF78486/c                                                 |                                                                           | ABZ72938                                                   |                                                                           |
| ID ADF78486 standard; DNA; 12 BP.                          |                                                                           | ID ABZ72938 standard; RNA; 12 BP.                          |                                                                           |
| XX                                                         |                                                                           | XX                                                         |                                                                           |
| AC ADF78486;                                               |                                                                           | AC ABZ72938;                                               |                                                                           |
| XX                                                         |                                                                           | XX                                                         |                                                                           |
| DT 26-FEB-2004 (first entry)                               |                                                                           | DT 09-APR-2003 (first entry)                               |                                                                           |
| XX                                                         |                                                                           | XX                                                         |                                                                           |



DE Rod opsin hammerhead ribozyme oligonucleotide.  
XX  
KW Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;  
KW ophthalmological; Gene therapy; eye; retinal dysfunction; AAV;  
KW diabetic retinopathy; macular degeneration; autosomal dominant retinitis;  
KW blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
PN WO200288320-A2.  
XX  
PD 07-NOV-2002.  
XX  
PF 01-MAY-2002; 2002WO-US013679.  
XX  
PR 01-MAY-2001; 2001US-00847601.  
XX  
PA (UYFL ) UNIV FLORIDA.  
XX  
PI Lewin AS, Shaw LC, Grant MB;  
XX  
DR WPI; 2003-111880/10.  
XX  
PT A recombinant adeno-associated virus-vectored ribozyme composition,  
PT useful for treating a disease or dysfunction of the mammalian eye e.g.  
PT retinal disease, e.g. diabetic retinopathy or age-related macular  
PT degeneration.  
XX  
PS Example 5; Page 73; 115pp; English.  
XX  
CC The present invention describes a recombinant adeno-associated virus  
CC (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a  
CC first ribozyme that specifically cleaves an mRNA encoding a protein,  
CC polypeptide, or peptide selected from the group of rod opsin, iNOS,  
CC RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin  
CC alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a  
CC vector comprising a polynucleotide encoding the ribozyme, where the  
CC polynucleotide operably positioned downstream of at least a first  
CC promoter that directs expression of the polynucleotide in a selected  
CC mammalian cell transformed with the vector; (c) a viral particle  
CC comprising the ribozyme or the polynucleotide; (d) an AAV vector  
CC comprising the ribozyme or the polynucleotide; or (e) a host cell  
CC comprising the ribozyme or the polynucleotide. Also described is a method  
CC for decreasing the amount of mRNA encoding a selected polypeptide in a  
CC retinal cell of a mammalian eye, comprising providing to the eye the  
CC composition described above, and for a time effective to specifically  
CC cleave the mRNA in the cell. (I) has ophthalmological activity, and can  
CC be used in gene therapy. (I) can be used for treating a disease or  
CC dysfunction of the mammalian eye, such as a retinal disease or retinal  
CC degeneration. (I) is also useful for manufacturing a medicament for  
CC treating the diseases mentioned above, including autosomal dominant  
CC retinitis or a blood-retinal barrier dysfunction. (I) can also be useful  
CC for treating, decreasing the severity, or ameliorating the symptoms of a  
CC pathological condition, e.g. atrophic or pigmented lesions of the eye,  
CC blindness, a reduction in central or peripheral vision, or a reduction in  
CC total vision. ABZ72763 to ABZ72953 represent sequences used in the  
CC exemplification of the present invention  
XX  
SQ Sequence 12 BP; 2 A; 6 C; 2 G; 0 T; 2 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 70.0%; Pred. No. 2e+02;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 TCACCTGCT 13  
:|||||  
Db 1 UCCACCAGCU 10  
  
RESULT 432  
ADM56049

ID ADM56049 standard; DNA; 12 BP.  
XX  
AC ADM56049;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Antibacterial peptide related PCR primer.  
XX  
KW antibacterial peptide; bactericidal; antibacterial;  
KW solid-phase chemical process; gene engineering expression;  
KW Gram-negative bacterium; Gram-positive bacterium; fungal infection;  
KW infection; PCR; primer; ss.  
XX  
OS Synthetic.  
XX  
PN CN1398897-A.  
XX  
PD 26-FEB-2003.  
XX  
PF 02-SEP-2002; 2002CN-00136766.  
XX  
PR 02-SEP-2002; 2002CN-00136766.  
XX  
PA (SHAN-) SHANGHAI GAOKE UNION BIOTECHNOLOGY DEV C.  
XX  
PI Huang Q;  
XX  
DR WPI; 2003-457919/44.  
XX  
PT Serial synthetic antibacterial peptide.  
XX  
PS Example 2; Page 10; 4lpp; Chinese.  
XX  
CC The present invention describes a group of synthetic antibacterial  
CC peptides with bactericidal activity stronger than that of a natural  
CC antibacterial peptide. The synthetic antibacterial peptide is prepared by  
CC the solid-phase chemical process or gene engineering expression. The  
CC synthetic antibacterial peptide may be used in preparing medicine for  
CC treating diseases caused by Gram-negative bacterium, Gram-positive  
CC bacterium and fungus infection. The present sequence represents a PCR  
CC primer used in an example from the present invention.  
XX  
SQ Sequence 12 BP; 2 A; 5 C; 3 G; 2 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 CCACCTGCTG 14  
|||  
Db 1 CCGCCTGCTG 10  
  
RESULT 433  
ADM56293/c  
ID ADM56293 standard; DNA; 12 BP.  
XX  
AC ADM56293;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Mouse SLC26A6 anion transporter protein gene splice site #12.  
XX  
KW SLC26A6; SLC26A1; SLC26A2; anion transporter protein; cancer;  
KW splice site; ds; mouse; murine.  
XX  
OS Mus musculus.  
XX  
PN WO2003072759-A2.  
XX  
PD 04-SEP-2003.  
XX  
PF 28-FEB-2003; 2003WO-US0006469.

XX  
PR 28-FEB-2002; 2002US-0360275P.  
XX  
PA (UYVA-) UNIV VANDERBILT.  
PA (UYCA-) UNIV CASE WESTERN RESERVE.  
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
XX  
PI Mount DB, Romero MF;  
XX  
XX WPI; 2003-712726/67.  
DR  
XX  
PT New SLC26A6, SLC26A1 or SLC26A2 polypeptide, useful for preparing a  
composition for treating e.g., cancer.  
XX  
PS Example 2; SEQ ID NO 25; 204pp; English.  
XX  
CC The invention comprises the amino acid and coding sequences of SLC26A6,  
CC SLC26A1 and SLC26A2 anion transporter proteins. The DNA and protein  
CC sequences of the invention are useful for treating cancer. The present  
CC DNA sequence represents a splice site from the gene encoding the mouse  
CC SLC26A6 anion transporter protein.  
XX  
SQ Sequence 12 BP; 3 A; 2 C; 6 G; 1 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 CCACCTGCTG 14  
Db ||||| ||  
10 CCACCTGTTG 1  
  
RESULT 434  
AEB80299  
ID AEB80299 standard; DNA; 12 BP.  
XX  
AC AEB80299;  
XX  
DT 06-OCT-2005 (first entry)  
XX  
DE Organic waste treatment bacteria 16S rDNA PCR primer, SEQ ID 45.  
XX  
KW waste-disposal; degradation; PCR; primer; ss.  
XX  
OS Synthetic.  
XX  
PN JP2003274939-A.  
XX  
PD 30-SEP-2003.  
XX  
PF 22-MAR-2002; 2002JP-00081782.  
XX  
PR 22-MAR-2002; 2002JP-00081782.  
XX  
PA (SAOL ) SANYO ELECTRIC CO LTD.  
PA (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.  
XX  
DR WPI; 2003-857702/80.  
XX  
PT Novel bacteria FERM P-18700, FERM P-18771 and FERM P-18772, useful for  
PT carrying out organic waste processing.  
XX  
PS Example; SEQ ID NO 45; 43pp; Japanese.  
XX  
CC The invention relates to a novel bacteria used in the treatment of  
CC organic waste. The bacteria includes FERM P-18770, FERM P-18771, FERM P-  
CC 18772, FERM P-18773, FERM P-18774, FERM P-18775 and FERM P-18776. The  
CC invention further comprises: processing organic waste using one type of  
CC the bacteria; and a method of processing organic waste, involving adding  
CC a salt to a support of bacteria and supplying organic waste to a  
CC treatment tank present in the apparatus. The bacteria is useful for  
CC carrying out organic waste processing. The bacteria enables stable

CC organic waste processing for a long period of time. This oligo sequence  
CC represents a PCR primer used to amplify the 16S rDNA of a novel bacteria  
CC of the invention.  
XX  
SQ Sequence 12 BP; 0 A; 4 C; 3 G; 5 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 6 CACCTGCTGT 15  
Db | ||||| ||  
1 CTCCTGCTGT 10  
  
RESULT 435  
ADM76195/c  
ID ADM76195 standard; DNA; 12 BP.  
XX  
AC ADM76195;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE NEPHA gene transcriptional control region Pax-4 binding site.  
XX  
KW Human; NEPHA; ephrin receptor; brain; chromosome 1; apoptosis;  
KW drug screening; antisense therapy; gene therapy; cancer; tumour;  
KW lung cancer; ovarian cancer; breast cancer; cervical cancer;  
KW prostate cancer; bladder cancer; stomach cancer; colorectal cancer;  
KW cytostatic; transcriptional control region; promoter;  
KW transcription factor binding site; ds.  
XX  
OS Homo sapiens.  
XX  
PN JP2003289876-A.  
XX  
PD 14-OCT-2003.  
XX  
PF 05-APR-2002; 2002JP-00103497.  
XX  
PR 05-APR-2002; 2002JP-00103497.  
XX  
PA (TAKE ) TAKEDA CHEM IND LTD.  
XX  
DR WPI; 2004-038434/04.  
XX  
PT Novel antisense oligonucleotide useful as anticancer agent for preventing  
PT cancer e.g. lung cancer, stomach cancer, breast cancer.  
XX  
PS Example 2; Page 23; 38pp; Japanese.  
XX  
CC The invention relates to antisense oligonucleotides (ADM76030 and  
CC ADM76031) targeted to the human NEPHA gene (ADM76029), which encodes a  
CC novel brain-derived ephrin receptor (ADM76028). The NEPHA protein has  
CC 50.7% homology to the human EphA7 ephrin receptor and its gene is located  
CC on chromosome 1. Ephrin receptors are overexpressed in various cancers  
CC and it has been found that inhibition of NEPHA expression promotes  
CC apoptosis. The invention also relates to the NEPHA transcriptional  
CC control (promoter) region (ADM76037); recombinant vectors and host cells  
CC comprising the NEPHA promoter operably linked to a reporter gene; a  
CC method of screening for compounds which inhibit or activate transcription  
CC of the NEPHA gene; and pharmaceutical compositions comprising an  
CC antisense oligonucleotide or a transcriptional inhibitor or activator.  
CC The antisense oligonucleotides and modulators of NEPHA transcription are  
CC useful for inducing apoptosis for the treatment and/or prevention of  
CC cancers in which NEPHA is overexpressed such as lung cancer, ovarian  
CC cancer, breast cancer, cervical cancer, prostate cancer, bladder cancer,  
CC stomach cancer and colorectal cancer. Sequences ADM76038-ADM76371  
CC represent transcription factor binding sites within the transcriptional  
CC control region of the NEPHA gene.  
XX  
SQ Sequence 12 BP; 2 A; 0 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCCACCT 10  
| | | | | | | |  
Db 11 CCACCCACCT 2

RESULT 436  
ADQ30184/c  
ID ADQ30184 standard; DNA; 12 BP.  
XX  
AC ADQ30184;  
XX  
DT 09-SEP-2004 (first entry)  
XX  
DE Murine VR1 exon 1d transcription factor binding fragment #76.  
DE ds; VR1 receptor; vanilloid receptor type 1; modulator;  
KW pain transmission; primary sensory neuron; transcription factor;  
KW detection; MZF1; NFkappaB; NFAT; GATA1; sensitivity disorder; analgesia;  
KW hypalgesia; hyperalgesia; neuralgia; myalgia; murine.  
XX  
OS Mus sp.  
XX  
PN WO2004053120-A2.  
XX  
PD 24-JUN-2004.  
XX  
PF 01-DEC-2003; 2003WO-EP013522.  
XX  
PR 09-DEC-2002; 2002DE-01057421.  
XX  
PA (CHEF ) GRUENENTHAL GMBH.  
XX  
PI Weihe E, Bieller A, Schaefer MKH;  
XX  
DR WPI; 2004-468868/44.  
XX  
PT New nucleic acid that modulates expression of the vanilloid receptor-1,  
PT useful for control of pain or sensitivity disorders, comprises sequences  
PT from control regions of the receptor gene.  
XX  
PS Disclosure; Page 50; 68pp; German.  
XX

This invention describes a novel nucleic acid containing a specific segment having at least one region that modulates expression of the VR1 (vanilloid receptor type 1) receptor, or a functional derivative, allele or fragment of this region, or a sequence that hybridises to it under standard conditions. The VR1 modulator is derived from one or more of positions 221931-223344 of GenBank AL670399, 31673-36359 of AL663116, or 44731-43231 or 36616-33151 of AF168787 and is involved in transmission of pain, particularly in primary sensory neurons. The invention also describes a vector that contains the VR1 modulator, host cells containing this vector (other than human germ or embryonal stem cells) and a method for modulating expression of the VR1 receptor by introducing the products of the invention into a cell that contains the VR1 gene. The modulator or the vector into a cell that contains a transcription factor from its binding to a regulatory sequence (or a double-stranded oligonucleotide fragment of it), e.g. by Western blotting or enzyme-linked immunosorbant assay, particularly for diagnosis of diseases associated with overexpression or underexpression of the transcription factor. The region that modulates VR1 receptor expression includes a binding site for a transcription factor, e.g. MZF1, NFkappaB, NFAT or GATA1. The nucleic acids of the invention, or vectors containing them, are used for prevention or treatment of pain, also for treating sensitivity disorders, e.g. analgesia, hypalgesia or hyperalgesia, also neuralgia and myalgia, that are associated with activity of the VR1 receptor. This sequence represents a fragment of murine VR1 exon 1d DNA which is capable of binding to a transcription factor.

SQ Sequence 12 BP; 1 A; 2 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATCCACCTGC 12  
| | | | | | | |  
Db 12 AGCCACCTGC 3

RESULT 437  
ADQ30185/c  
ID ADQ30185 standard; DNA; 12 BP.  
XX  
AC ADQ30185;  
XX  
DT 09-SEP-2004 (first entry)  
XX  
DE Murine VR1 exon 1d transcription factor binding fragment #77.  
DE ds; VR1 receptor; vanilloid receptor type 1; modulator;  
KW pain transmission; primary sensory neuron; transcription factor;  
KW detection; MZF1; NFkappaB; NFAT; GATA1; sensitivity disorder; analgesia;  
KW hypalgesia; hyperalgesia; neuralgia; myalgia; murine.  
XX  
OS Mus sp.  
XX  
PN WO2004053120-A2.  
XX  
PD 24-JUN-2004.  
XX  
PF 01-DEC-2003; 2003WO-EP013522.  
XX  
PR 09-DEC-2002; 2002DE-01057421.  
XX  
PA (CHEF ) GRUENENTHAL GMBH.  
XX  
PI Weihe E, Bieller A, Schaefer MKH;  
XX  
DR WPI; 2004-468868/44.  
XX  
PT New nucleic acid that modulates expression of the vanilloid receptor-1,  
PT useful for control of pain or sensitivity disorders, comprises sequences  
PT from control regions of the receptor gene.  
XX  
PS Disclosure; Page 50; 68pp; German.  
XX

This invention describes a novel nucleic acid containing a specific segment having at least one region that modulates expression of the VR1 (vanilloid receptor type 1) receptor, or a functional derivative, allele or fragment of this region, or a sequence that hybridises to it under standard conditions. The VR1 modulator is derived from one or more of positions 221931-223344 of GenBank AL670399, 31673-36359 of AL663116, or 44731-43231 or 36616-33151 of AF168787 and is involved in transmission of pain, particularly in primary sensory neurons. The invention also describes a vector that contains the VR1 modulator, host cells containing this vector (other than human germ or embryonal stem cells) and a method for modulating expression of the VR1 receptor by introducing the products of the invention into a cell that contains the VR1 gene. The modulator or the vector into a cell that contains a transcription factor from its binding to a regulatory sequence (or a double-stranded oligonucleotide fragment of it), e.g. by Western blotting or enzyme-linked immunosorbant assay, particularly for diagnosis of diseases associated with overexpression or underexpression of the transcription factor. The region that modulates VR1 receptor expression includes a binding site for a transcription factor, e.g. MZF1, NFkappaB, NFAT or GATA1. The nucleic acids of the invention, or vectors containing them, are used for prevention or treatment of pain, also for treating sensitivity disorders, e.g. analgesia, hypalgesia or hyperalgesia, also neuralgia and myalgia, that are associated with activity of the VR1 receptor. This sequence represents a fragment of murine VR1 exon 1d DNA which is capable of binding to a transcription factor.

|            |                                                                           |            |                                                                           |
|------------|---------------------------------------------------------------------------|------------|---------------------------------------------------------------------------|
| SQ         | Sequence 12 BP; 1 A; 2 C; 6 G; 3 T; 0 U; 0 Other;                         | XX         | Sequence 12 BP; 4 A; 1 C; 5 G; 2 T; 0 U; 0 Other;                         |
|            | Query Match 29.0%; Score 8.4; DB 1; Length 12;                            |            | Query Match 29.0%; Score 8.4; DB 1; Length 12;                            |
|            | Best Local Similarity 90.0%; Pred. No. 2e+02;                             |            | Best Local Similarity 90.0%; Pred. No. 2e+02;                             |
|            | Matches 9; Conservative 0; Mismatches 0; Gaps 0;                          |            | Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;                |
| QY         | 3 ATCCACCTGC 12                                                           | QY         | 3 ATCCACCTGC 12                                                           |
|            |                                                                           |            |                                                                           |
| Db         | 12 AGCCACCTGC 3                                                           | Db         | 12 ATTCACCTGC 3                                                           |
| RESULT 438 |                                                                           | RESULT 439 |                                                                           |
| ADQ30343/c |                                                                           | ADR32504   |                                                                           |
| ID         | ADQ30343 standard; DNA; 12 BP.                                            | ID         | ADR32504 standard; DNA; 12 BP.                                            |
| XX         |                                                                           | XX         |                                                                           |
| AC         | ADQ30343;                                                                 | AC         | ADR32504;                                                                 |
| XX         |                                                                           | XX         |                                                                           |
| DT         | 09-SEP-2004 (first entry)                                                 | DT         | 04-NOV-2004 (first entry)                                                 |
| XX         |                                                                           | XX         |                                                                           |
| DE         | Human VR1 exon 1d transcription factor binding fragment #62.              | DE         | Human nicking agent target DNA #45.                                       |
| XX         |                                                                           | XX         |                                                                           |
| KW         | ds; VR1 receptor; vanilloid receptor type 1; modulator;                   | KW         | ss; nicking agent; assay panel; diagnosis; expression pattern;            |
| KW         | pain transmission; primary sensory neuron; transcription factor;          | KW         | DNA fingerprinting; nosocomial infection; microbiological assay;          |
| KW         | detection; MZF1; NFkappaB; NFAT; GATA1; sensitivity disorder; analgesia;  | KW         | bacterial contamination; genome mapping; bioremediation.                  |
| KW         | hypalgesia; hyperalgesia; neuralgia; myalgia; human.                      | XX         |                                                                           |
| XX         |                                                                           | OS         | Homo sapiens.                                                             |
| OS         | Homo sapiens.                                                             | XX         |                                                                           |
| XX         |                                                                           | PN         | WO2004053120-A2.                                                          |
| PN         | WO2004053120-A2.                                                          | XX         |                                                                           |
| XX         |                                                                           | PD         | 24-JUN-2004.                                                              |
| PD         |                                                                           | XX         |                                                                           |
| XX         |                                                                           | XX         |                                                                           |
| PF         | 01-DEC-2003; 2003WO-EP013522.                                             | PF         | 29-JAN-2004; 2004WO-US002720.                                             |
| XX         |                                                                           | XX         |                                                                           |
| PR         | 09-DEC-2002; 2002DE-01057421.                                             | PR         | 29-JAN-2003; 2003US-0443811P.                                             |
| XX         |                                                                           | XX         |                                                                           |
| PA         | (CHEF ) GRUENENTHAL GMBH.                                                 | PA         | (KECK-) KECK GRADUATE INST.                                               |
| XX         |                                                                           | XX         |                                                                           |
| PI         | Weihe E, Bieller A, Schaefer MKH;                                         | PI         | Van Ness J, Galas DJ, Van Ness LK;                                        |
| XX         |                                                                           | XX         |                                                                           |
| DR         | WPI; 2004-468868/44.                                                      | DR         | WPI; 2004-581010/56.                                                      |
| XX         |                                                                           | XX         |                                                                           |
| PT         | New nucleic acid that modulates expression of the vanilloid receptor-1,   | PT         | Identifying nucleic acid sample source, useful for identifying bacterial  |
| PT         | useful for control of pain or sensitivity disorders, comprises sequences  | PT         | strains involved in nosocomial infections, comprises treating the nucleic |
| PT         | from control regions of the receptor gene.                                | PT         | acid sample with components comprising a nicking agent under nicking      |
| XX         |                                                                           | PT         | conditions.                                                               |
| PS         | Disclosure; Page 53; 68pp; German.                                        | XX         |                                                                           |
| XX         |                                                                           | PS         | Example 1; Page 72; 238pp; English.                                       |
| CC         | This invention describes a novel nucleic acid containing a specific       | CC         | The invention relates to a method of treating a nucleic acid sample with  |
| CC         | segment having at least one region that modulates expression of the VR1   | CC         | components under nicking conditions, where the components comprise a      |
| CC         | (vanilloid receptor type 1) receptor, or a functional derivative, allele  | CC         | nicking agent, and the conditions cause the nicking agent to nick the     |
| CC         | or fragment of this region, or a sequence that hybridises to it under     | CC         | nucleic acid sample to thus produce a family of initiating                |
| CC         | standard conditions. The VR1 modulator is derived from one or more of     | CC         | oligonucleotide fragments, and subjecting one or more members of the      |
| CC         | positions 221931-223344 of GenBank AL670399, 31673-36359 of AL663116, or  | CC         | family of initiating oligonucleotide fragments to a characterization      |
| CC         | 44731-43231 or 36616-33151 of AF168787 and is involved in transmission of | CC         | process to thus provide results. The method is useful for creating an     |
| CC         | pain, particularly in primary sensory neurons. The invention also         | CC         | assay panel of diagnostic oligonucleotides that can identify any organism |
| CC         | describes a vector that contains the VR1 modulator, host cells containing | CC         | or individual. The method is useful for characterizing other DNA          |
| CC         | this vector (other than human germ or embryonal stem cells) and a method  | CC         | molecules e.g., cDNA, and for characterizing cDNA expression patterns.    |
| CC         | for modulating expression of the VR1 receptor by introducing the          | CC         | The method, kit or composition is useful for identifying the source       |
| CC         | modulator or the vector into a cell that contains the VR1 gene. The       | CC         | organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,  |
| CC         | products of the invention are used for detecting a transcription factor   | CC         | non-human animal or human. The method is particularly useful for rapidly  |
| CC         | from its binding to a regulatory sequence (or a double-stranded           | CC         | fingerprinting DNA to identifying prokaryotic and eukaryotic species,     |
| CC         | oligonucleotide fragment of it), e.g. by Western blotting or enzyme-      | CC         | subspecies, and especially strains or individuals of the subspecies. It   |
| CC         | linked immunosorbant assay, particularly for diagnosis of diseases        | CC         | is especially useful for identifying different bacterial strains involved |
| CC         | associated with overexpression or underexpression of the transcription    | CC         | in e.g., nosocomial infections. Furthermore, the method is useful for     |
| CC         | factor. The region that modulates VR1 receptor expression includes a      | CC         | diagnosing bacterial disease in plants and humans, monitoring for         |
| CC         | binding site for a transcription factor, e.g. MZF1, NFkappaB, NFAT or     | CC         | bacterial content and/or contamination in the environment, monitoring     |
| CC         | GATA1. The nucleic acids of the invention, or vectors containing them,    | CC         | food for bacterial contamination, monitoring manufacturing processes for  |
| CC         | are used for prevention or treatment of pain, also for treating           | CC         | bacterial contamination, monitoring quality assurance/quality control of  |
| CC         | sensitivity disorders, e.g. analgesia, hypalgesia or hyperalgesia, also   | CC         | laboratory tests involving microbiological assays, tracing bacterial      |
| CC         | neuralgia and myalgia, that are associated with activity of the VR1       | CC         | contamination and/or outbreaks of bacterial infections, genome mapping,   |
| CC         | receptor. This sequence represents a fragment of human VR1 exon 1d DNA    | CC         | monitoring bioremediation sites, and for monitoring agricultural sites    |
| CC         | which is capable of binding to a transcription factor.                    |            |                                                                           |



|    |                                                                            |    |                                                                            |
|----|----------------------------------------------------------------------------|----|----------------------------------------------------------------------------|
| CC | for test crops, bacteria and recombinant molecules. This sequence          | CC | cleavage of the products, mixing the products with CleanResin,             |
| CC | corresponds to nucleic acid used in the method of the invention.           | CC | transferring products to SpectroCHIP, and analysing the SpectroCHIP. The   |
| XX |                                                                            | CC | dephosphorylation reaction is with shrimp alkaline phosphatase.            |
| SQ | Sequence 12 BP; 0 A; 3 C; 5 G; 4 T; 0 U; 0 Other;                          | CC | Alternatively, the determination of the sequence of the alleles comprises  |
|    | Query Match 29.0%; Score 8.4; DB 1; Length 12;                             | CC | Amplifying the locus of interest, dephosphorylation of the unused          |
|    | Best Local Similarity 90.0%; Pred. No. 2e+02;                              | CC | reagents, hybridising a primer to the locus of interest, incorporating a   |
|    | Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;                 | CC | nucleotide, mixing the products with CleanResin, transferring products to  |
| QY | 8 CCTGCTGTGT 17                                                            | CC | SpectroCHIP, and analysing the SpectroCHIP. The hybridisation of primer    |
| Db | 3 CCTGCGGTGT 12                                                            | CC | is adjacent to the locus of interest. The determination of the sequence    |
|    |                                                                            | CC | of the alleles may also comprise amplifying the locus of interest,         |
|    |                                                                            | CC | treating the products with exonuclease, single stranded DNA is annealed    |
|    |                                                                            | CC | to an oligonucleotide, incorporating a nucleotide using the annealed       |
|    |                                                                            | CC | template and primer, and detecting the incorporated nucleotide. The        |
|    |                                                                            | CC | method is useful for detecting a chromosomal abnormality in a sample.      |
|    |                                                                            | CC | Specifically, the method is useful for detecting chromosomal               |
|    |                                                                            | CC | abnormalities in a fetus including translocations, transversions,          |
|    |                                                                            | CC | monosomies, trisomies, and other aneuploidies, deletions, additions,       |
|    |                                                                            | CC | amplifications, and arrangements. The method of the invention can also be  |
|    |                                                                            | CC | used for prenatal diagnosis. This sequence represents a PCR primer used    |
|    |                                                                            | CC | to amplify human SNP's from chromosome 21.                                 |
| XX |                                                                            | XX |                                                                            |
| SQ | Sequence 12 BP; 5 A; 5 C; 1 G; 1 T; 0 U; 0 Other;                          | SQ | Sequence 12 BP; 5 A; 5 C; 1 G; 1 T; 0 U; 0 Other;                          |
|    |                                                                            |    | Query Match 29.0%; Score 8.4; DB 1; Length 12;                             |
|    |                                                                            |    | Best Local Similarity 90.0%; Pred. No. 2e+02;                              |
|    |                                                                            |    | Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;                 |
| QY | 10 TGCTGTGTGA 19                                                           | QY | 10 TGCTGTGTGA 19                                                           |
| Db | 12 TTCTGTGTGA 3                                                            | Db | 12 TTCTGTGTGA 3                                                            |
|    |                                                                            |    |                                                                            |
|    |                                                                            |    | RESULT 441                                                                 |
|    |                                                                            |    | ADR98062/c                                                                 |
| ID | ADR98062 standard; DNA; 12 BP.                                             | ID | ADR98062 standard; DNA; 12 BP.                                             |
| XX |                                                                            | XX |                                                                            |
| AC | ADR98062;                                                                  | AC | ADR98062;                                                                  |
| XX |                                                                            | XX |                                                                            |
| DT | 02-DEC-2004 (first entry)                                                  | DT | 02-DEC-2004 (first entry)                                                  |
| XX |                                                                            | XX |                                                                            |
| DE | Human SNP TSC0470003 multiplex PCR primer #2.                              | DE | Human SNP TSC0470003 multiplex PCR primer #2.                              |
| XX |                                                                            | XX |                                                                            |
| KW | ss; chromosomal abnormality; detection; foetus; translocation;             | KW | ss; chromosomal abnormality; detection; foetus; translocation;             |
| KW | transversion; monosomy; trisomy; aneuploidy; deletion; addition;           | KW | transversion; monosomy; trisomy; aneuploidy; deletion; addition;           |
| KW | amplification; prenatal diagnosis; PCR; primer; SNP;                       | KW | amplification; prenatal diagnosis; PCR; primer; SNP;                       |
| KW | single nucleotide polymorphism; human; chromosome 21.                      | KW | single nucleotide polymorphism; human; multiplex; TSC0470003.              |
| XX |                                                                            | XX |                                                                            |
| OS | Homo sapiens.                                                              | OS | Homo sapiens.                                                              |
| XX |                                                                            | XX |                                                                            |
| PN | WO2004079011-A1.                                                           | PN | WO2004079011-A1.                                                           |
| XX |                                                                            | XX |                                                                            |
| PD | 16-SEP-2004.                                                               | PD | 16-SEP-2004.                                                               |
| XX |                                                                            | XX |                                                                            |
| PF | 29-AUG-2003; 2003WO-US027308.                                              | PF | 29-AUG-2003; 2003WO-US027308.                                              |
| XX |                                                                            | XX |                                                                            |
| PR | 28-FEB-2003; 2003WO-US006198.                                              | PR | 28-FEB-2003; 2003WO-US006198.                                              |
| XX |                                                                            | XX |                                                                            |
| PA | (RAVG-) RAVGEN INC.                                                        | PA | (RAVG-) RAVGEN INC.                                                        |
| XX |                                                                            | XX |                                                                            |
| PI | Dhallan R;                                                                 | PI | Dhallan R;                                                                 |
| XX |                                                                            | XX |                                                                            |
| DR | WPI; 2004-677127/66.                                                       | DR | WPI; 2004-677127/66.                                                       |
| XX |                                                                            | XX |                                                                            |
| PT | Detecting a chromosomal abnormality, e.g. translocations, transversions,   | PT | Detecting a chromosomal abnormality, e.g. translocations, transversions,   |
| PT | monosomies, trisomies, aneuploidies, deletions, or arrangements, comprises | PT | monosomies, trisomies, aneuploidies, deletions, or arrangements, comprises |
| PT | determining the sequence of alleles of a locus of interest in the sample   | PT | determining the sequence of alleles of a locus of interest in the sample   |
| PT | from template DNA.                                                         | PT | from template DNA.                                                         |
| XX |                                                                            | XX |                                                                            |
| PS | Example 12; Page 223; 429pp; English.                                      | PS | Example 12; Page 200; 429pp; English.                                      |
| XX |                                                                            | XX |                                                                            |
| CC | This invention describes a novel method for detecting a chromosomal        | CC | Detecting a chromosomal abnormality, e.g. translocations, transversions,   |
| CC | abnormality in a sample which comprises determining the sequence of        | CC | monosomies, trisomies, aneuploidies, deletions, or arrangements, comprises |
| CC | alleles of a locus of interest in a sample from template DNA where         | CC | determining the sequence of alleles of a locus of interest in the sample   |
| CC | determining the sequence of the alleles comprises amplifying the locus of  | CC | from template DNA.                                                         |
| CC | interest, hybridising the amplified loci to GeneCHIP array, washing        |    |                                                                            |
| CC | GeneCHIP array, staining the GeneCHIP array with detectable reagents, and  |    |                                                                            |
| CC | scanning GeneCHIP array. The amplification method is self-sustained        |    |                                                                            |
| CC | sequence reaction, ligase chain reaction, rapid amplification of cDNA      |    |                                                                            |
| CC | ends, PCR and ligase chain reaction, Q-beta phage amplification, strand    |    |                                                                            |
| CC | displacement amplification, or splice overlap extension PCR, preferably    |    |                                                                            |
| CC | PCR. The determination of the sequence of the alleles comprises            |    |                                                                            |
| CC | amplifying the locus of interest, fragmenting the amplicon, hybridising    |    |                                                                            |
| CC | fragmented amplicons to CodeLink Arrays, extension reaction to             |    |                                                                            |
| CC | incorporate a nucleotide and detecting incorporated nucleotides. The       |    |                                                                            |
| CC | amplicon fragmentation is by exonuclease digestion. Detecting a            |    |                                                                            |
| CC | chromosomal abnormality in a sample comprises determining the sequence of  |    |                                                                            |
| CC | alleles of a locus of interest from template DNA, where determining the    |    |                                                                            |
| CC | sequence of the alleles comprises using BeadArray Technology. The          |    |                                                                            |
| CC | determination of the sequence of the alleles may also be done by           |    |                                                                            |
| CC | amplifying the locus of interest, dephosphorylation of the unused          |    |                                                                            |
| CC | reagents, in vitro transcription reaction of the products, RNase A         |    |                                                                            |

CC determining the sequence of the alleles comprises amplifying the locus of  
CC interest, hybridising the amplified loci to GeneCHIP array, washing  
CC GeneCHIP array, staining the GeneCHIP array with detectable reagents, and  
CC scanning GeneCHIP array. The amplification method is self-sustained  
CC sequence reaction, ligase chain reaction, rapid amplification of cDNA  
CC ends, PCR and ligase chain reaction, Q-beta phage amplification, strand  
CC displacement amplification, or splice overlap extension PCR, preferably  
CC PCR. The determination of the sequence of the alleles comprises  
CC amplifying the locus of interest, fragmenting the amplicon, hybridising  
CC fragmented amplicons to CodeLink Arrays, extension reaction to  
CC incorporate a nucleotide and detecting incorporated nucleotides. The  
CC amplicon fragmentation is by exonuclease digestion. Detecting a  
CC chromosomal abnormality in a sample comprises determining the sequence of  
CC alleles of a locus of interest from template DNA, where determining the  
CC sequence of the alleles comprises using BeadArray Technology. The  
CC determination of the sequence of the alleles may also be done by  
CC amplifying the locus of interest, dephosphorylation of the unused  
CC reagents, in vitro transcription reaction of the products, RNase A  
CC cleavage of the products, mixing the products with CleanResin,  
CC transferring products to SpectroCHIP, and analysing the SpectroCHIP. The  
CC dephosphorylation reaction is with shrimp alkaline phosphatase.  
CC Alternatively, the determination of the sequence of the alleles comprises  
CC amplifying the locus of interest, dephosphorylation of the unused  
CC reagents, hybridising a primer to the locus of interest, incorporating a  
CC nucleotide, mixing the products with CleanResin, transferring products to  
CC SpectroCHIP, and analysing the SpectroCHIP. The hybridisation of primer  
CC is adjacent to the locus of interest. The determination of the sequence  
CC of the alleles may also comprise amplifying the locus of interest,  
CC treating the products with exonuclease, single stranded DNA is annealed  
CC to an oligonucleotide, incorporating a nucleotide using the annealed  
CC template and primer, and detecting the incorporated nucleotide. The  
CC method is useful for detecting a chromosomal abnormality in a sample.  
CC Specifically, the method is useful for detecting chromosomal  
CC abnormalities in a fetus including translocations, transversions,  
CC monosomies, trisomies, and other aneuploidies, deletions, additions,  
CC amplifications, and arrangements. The method of the invention can also be  
CC used for prenatal diagnosis. This sequence represents a multiplex PCR  
CC primer used to amplify the human SNP TSC0470003.

XX Sequence 12 BP; 4 A; 3 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ACCTGCTGTG 16  
||| |||||  
Db 10 ACCCGCTGTG 1

RESULT 442  
ADS08925/c  
ID ADS08925 standard; DNA; 12 BP.

XX ADS08925;

XX 02-DEC-2004 (first entry)

DE Human DNA PCR primer #262.

XX Human; PCR; primer; ss; nucleic acid detection; cell lysis;  
KW chromosomal abnormality; cancer; carcinoma; bladder; breast; bronchus;  
KW colon; kidney; liver; lung; oesophagus; gall bladder; ovary; pancreas;  
KW stomach; cervix; thyroid; prostate; skin; small cell lung cancer;  
KW squamous cell carcinoma; leukaemia; lymphoma; myelodysplastic syndrome;  
KW fibrosarcoma; rhabdomyosarcoma; astrocytoma; neuroblastoma; glioma;  
KW schwannoma; melanoma; seminoma; teratocarcinoma; osteosarcoma.

XX Homo sapiens.

OS WO2004078994-A2.

XX 16-SEP-2004.

XX 01-MAR-2004; 2004WO-US0006337.

XX 28-FEB-2003; 2003WO-US0006198.

XX (RAVG-) RAVGEN INC.

XX Dhallan R;

XX WPI; 2004-662434/64.

XX Detecting presence or absence of nucleic acid, containing mutation,  
PT involves isolating nucleic acid from sample containing cell lysis  
PT inhibitor, and detecting presence or absence of nucleic acid.

XX Example 12; Page 232; 440pp; English.

XX The invention relates to a method for detecting a nucleic acid, involving  
CC isolating a nucleic acid from a sample, where an agent that impedes cell  
CC lysis was added to the sample, and detecting the presence or absence of  
CC the nucleic acid. The invention also relates to a method for detecting  
CC chromosomal abnormalities in a DNA sample and determining the sequence of  
CC foetal DNA from a sample of a pregnant female. The nucleic acid contains  
CC at least one mutation chosen from a single point mutation, multiple point  
CC mutations, an insertion, a frameshift, a truncation, a deletion, a  
CC duplication and a transversion. The method is useful for detecting  
CC nucleic acid in a sample obtained from a source chosen from bacteria,  
CC viruses, fungi, mycobacteria, protozoa, molds, yeasts, plants, humans,  
CC non-humans, multi-cellular parasites, animals and archaeobacteria. The  
CC method is useful for detecting, diagnosing or monitoring a disease such  
CC as cancer chosen from carcinoma of the bladder, breast, bronchus, colon,  
CC kidney, liver, lung, oesophagus, gall bladder, ovary, pancreas, stomach,  
CC cervix, thyroid, prostate and skin, small cell lung cancer, squamous cell  
CC carcinoma, haematopoietic tumours of lymphoid lineage, leukaemia, acute  
CC lymphocytic leukaemia, acute lymphoblastic leukaemia, B-cell lymphoma, T-  
CC cell-lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma, hairy cell  
CC lymphoma, Burkett's lymphoma, haematopoietic tumours of myeloid lineage,  
CC acute and chronic myelogenous leukaemias, myelodysplastic syndrome and  
CC promyelocytic leukaemia, tumours of mesenchymal origin, fibrosarcoma and  
CC rhabdomyosarcoma, tumours of the central and peripheral nervous system,  
CC astrocytoma, neuroblastoma, glioma and schwannomas, melanoma, seminoma,  
CC teratocarcinoma and osteosarcoma. The method is also useful for  
CC monitoring response to treatment chosen from surgery, radiation,  
CC lifestyle change, dietary protocol and supplementation and administration  
CC of a drug. The drug is chosen from chemotherapeutic agents, anti-  
CC bacterial agents, anti-viral agents, anti-fungal agents, targeted-cancer  
CC drugs, cytotoxic agents, cytostatic agents and anti-proliferative agents.  
CC This sequence represents a PCR primer used in the scope of the invention.

XX Sequence 12 BP; 5 A; 5 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TGCTGTGTGA 19  
| |||||  
Db 12 TTCTGTGTGA 3

RESULT 443  
ADS08749/c  
ID ADS08749 standard; DNA; 12 BP.

XX ADS08749;

XX 02-DEC-2004 (first entry)

XX Human DNA PCR primer #86.

XX Human; PCR; primer; ss; nucleic acid detection; cell lysis;  
KW chromosomal abnormality; cancer; carcinoma; bladder; breast; bronchus;  
KW colon; kidney; liver; lung; oesophagus; gall bladder; ovary; pancreas;

KW stomach; cervix; thyroid; prostate; skin; small cell lung cancer;  
KW squamous cell carcinoma; leukaemia; lymphoma; myelodysplastic syndrome;  
KW fibrosarcoma; rhabdomyosarcoma; astrocytoma; neuroblastoma; glioma;  
KW schwannoma; melanoma; seminoma; teratocarcinoma; osteosarcoma.  
XX  
OS Homo sapiens.  
XX WO2004078994-A2.  
PN 16-SEP-2004.  
PD 01-MAR-2004; 2004WO-US006337.  
XX 28-FEB-2003; 2003WO-US006198.  
PF (RAVG-) RAVGEN INC.  
XX Dhallan R;  
PI WPI; 2004-662434/64.  
XX Detecting presence or absence of nucleic acid, containing mutation,  
PT involves isolating nucleic acid from sample containing cell lysis  
PT inhibitor, and detecting presence or absence of nucleic acid.  
XX  
PS Example 12; Page 209; 440pp; English.  
XX The invention relates to a method for detecting a nucleic acid, involving  
CC isolating a nucleic acid from a sample, where an agent that impedes cell  
CC lysis was added to the sample, and detecting the presence or absence of  
CC the nucleic acid. The invention also relates to a method for detecting  
CC chromosomal abnormalities in a DNA sample and determining the sequence of  
CC foetal DNA from a sample of a pregnant female. The nucleic acid contains  
CC at least one mutation chosen from a single point mutation, multiple point  
CC mutations, an insertion, a frameshift, a truncation, a deletion, a  
CC duplication and a transversion. The method is useful for detecting  
CC nucleic acid in a sample obtained from a source chosen from bacteria,  
CC viruses, fungi, mycobacteria, protozoa, molds, yeasts, plants, humans,  
CC non-humans, multi-cellular parasites, animals and archaeobacteria. The  
CC method is useful for detecting, diagnosing or monitoring a disease such  
CC as cancer chosen from carcinoma of the bladder, breast, bronchus, colon,  
CC kidney, liver, lung, oesophagus, gall bladder, ovary, pancreas, stomach,  
CC cervix, thyroid, prostate and skin, small cell lung cancer, squamous cell  
CC carcinoma, haematopoietic tumours of lymphoid lineage, leukaemia, acute  
CC lymphocytic leukaemia, acute lymphoblastic leukaemia, B-cell lymphoma, T-  
CC cell-lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma, hairy cell  
CC lymphoma, Burkett's lymphoma, haematopoietic tumours of myeloid lineage,  
CC acute and chronic myelogenous leukaemias, myelodysplastic syndrome and  
CC promyelocytic leukaemia, tumours of mesenchymal origin, fibrosarcoma and  
CC rhabdomyosarcoma, tumours of the central and peripheral nervous system,  
CC astrocytoma, neuroblastoma, glioma and schwannomas, melanoma, seminoma,  
CC teratocarcinoma and osteosarcoma. The method is also useful for  
CC monitoring response to treatment chosen from surgery, radiation,  
CC lifestyle change, dietary protocol and supplementation and administration  
CC of a drug. The drug is chosen from chemotherapeutic agents, anti-  
CC bacterial agents, anti-viral agents, anti-fungal agents, targeted-cancer  
CC drugs, cytotoxic agents, cytostatic agents and anti-proliferative agents.  
XX This sequence represents a PCR primer used in the scope of the invention.  
SQ Sequence 12 BP; 4 A; 3 C; 4 G; 1 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 7 ACCTGGCTGTG 16  
Db ||| |||||  
10 ACCCGCTGTG 1  
  
RESULT 444  
ADZ15183  
ID ADZ15183 standard; DNA; 12 BP.

XX ADZ15183;  
AC 16-JUN-2005 (first entry)  
DT PCR primer used to amplify microbial flora DNA - SEQ ID 45.  
XX microorganism identification; fertilizer; fermentation; PCR; primer; ss.  
KW Bacteria.  
OS JP2003274998-A.  
XX 30-SEP-2003.  
PN 25-MAR-2002; 2002JP-00084562.  
PD 25-MAR-2002; 2002JP-00084562.  
XX (SAOL ) SANYO ELECTRIC CO LTD.  
PA (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.  
XX WPI; 2004-137285/14.  
XX Simultaneous identification of two or more microorganisms in a population  
PT comprises PCR based methods and data base searching.  
PT  
PS Example 1; SEQ ID NO 45; 45pp; Japanese.  
XX The invention relates to a novel method for simultaneous identification  
CC of two or more microorganisms in a population, whereby the method is PCR-  
CC based and comprises database searching. Domestic organic waste may be  
CC converted into fertilizer via inclusion in compost. This conversion is  
CC governed by various bacteria and protozoa that are present within the  
CC compost material. Identification of the microbes present facilitates  
CC improved control of the fermentation temperature and the rate of refuse  
CC degradation, which in turn allows a fertilizer of improved quality to be  
CC produced. Is it also advantageous to identify microorganisms within the  
CC soil prior to applying fertilizer. The method of the invention may be  
CC useful to simultaneously identify multiple microorganisms. The current  
CC sequence is that of a PCR primer of the invention which was used to  
CC amplify and thus identify, microbial flora DNA.  
XX Sequence 12 BP; 0 A; 4 C; 3 G; 5 T; 0 U; 0 Other;  
SQ  
  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 6 CACCTGCTGT 15  
Db | || || || ||  
1 CTCCTGCTGT 10  
  
RESULT 445  
ADZ24372  
ID ADZ24372 standard; DNA; 12 BP.  
XX  
AC ADZ24372;  
XX 16-JUN-2005 (first entry)  
DT Human SNP detection related oligonucleotide #1339.  
XX ss; haplotype mapping; SNP detection; tumor; cytostatic; neoplasm;  
KW immune disorder; cardiovascular disease; metabolic disorder;  
KW respiratory disease; musculoskeletal disease; renal disease;  
KW nephrotropic; endocrine disease; genitourinary disease.  
XX  
OS Homo sapiens.  
XX WO2005030952-A1.  
PN  
XX



PD 07-APR-2005.  
XX  
PF 30-SEP-2004; 2004WO-JP014784.  
XX  
PN 30-SEP-2003; 2003JP-00342519.  
PR 28-MAY-2004; 2004JP-00158717.  
PR  
XX  
PA (RIKE ) RIKEN KK.  
PA (STAG-) STAGEN CO LTD.  
PA (SEKI/) SEKINE A.  
PA (IIDA/) IIDA A.  
PA (SAIT/) SAITO S.  
XX  
PI Sekine A, Iida A, Saito S, Nakamura Y, Kamatani N;  
XX  
XX WPI; 2005-305936/31.  
DR  
XX  
XX Analyzing haplotype, by detecting polymorphism in drug-related genes,  
PT electing common polymorphism (CP), building haplotype block using CP,  
PT specifying CP within block, specifying tag polymorphism from CP within  
PT block.  
XX  
PS Disclosure; SEQ ID NO 1339; 1290pp; Japanese.  
XX  
XX The invention relates to a method of analyzing haplotype, by detecting  
CC gene polymorphism in drug-related genes such as aryl acetylamide  
CC deacetylase, arylalkylamine N-acetyl transferase or ATP-binding cassette,  
CC sub-family A (ABCI), member 1. The method is useful for analyzing  
CC haplotype. The method is useful for estimating the sensitivity or disease  
CC of a medicine or a foreign material, for selecting the medicine for  
CC preventing or treating diseases, for determining appropriate dosage of  
CC medicine for preventing or treating a disease, for analyzing a drug  
CC interaction, and for determining the related polymorphism relative to the  
CC sensitivity of the medicine, foreign material or disease. The diseases  
CC include malignant tumor, immune disorder circulatory disease, metabolic  
CC disease, kidney disease, respiratory disease and muscle associated  
CC disease. The method enables analysis of the individual differences  
CC related to the sensitivity of a medicine, using a haplotype, without  
CC using each single nucleotide polymorphism. The present sequence  
CC represents a human SNP detection related oligonucleotide.  
XX  
SQ Sequence 12 BP; 1 A; 2 C; 6 G; 3 T; 0 U; 0 Other;  
  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 14 GTGTGACCTG 23  
||| |||  
Db 2 GTGTGGCCTG 11  
  
RESULT 446  
AEA50022  
ID AEA50022 standard; DNA; 12 BP.  
XX  
AC AEA50022;  
XX  
XX 25-AUG-2005 (first entry)  
XX  
XX Construct Fc-pcDNA3 DNA fragment #2.  
DE  
XX  
KW ds; immunoglobulin Fc receptor; autoimmune disease; multiple sclerosis;  
KW systemic lupus erythematosus; rheumatoid arthritis; scleroderma;  
KW Sjogrens syndrome; Behcets disease; inflammation;  
KW inflammatory bowel disease; ulcerative colitis; Crohns disease; uveitis;  
KW cancer; neoplasm; tumor; lung tumor; brain tumor; liver tumor; allergy;  
KW immune disorder; asthma; respiratory disease; atopic dermatitis;  
KW dermatological disease; drug delivery;  
KW endothelial immunoglobulin receptor; elgR; antiallergy;  
KW immunosuppressive; antiasthmatic; dermatological; antiinflammatory;  
KW vasotropic; gastrointestinal-Gen.; neuroprotective; antiarthritic;  
KW antirheumatic; antiulcer; ophthalmological.

XX  
OS Synthetic.  
XX  
PN WO2005056597-A1.  
XX  
PD 23-JUN-2005.  
XX  
PF 05-NOV-2004; 2004WO-JP016804.  
XX  
PR 09-DEC-2003; 2003JP-00410136.  
XX  
PA (RIKE ) RIKEN KK.  
XX  
PI Ohno H, Takatsu H;  
XX  
XX WPI; 2005-445145/45.  
DR  
XX  
XX Novel immunoglobulin Fc receptor protein having activity of binding to Fc  
PT of IgM and IgA, useful as medical agent for treatment of autoimmune  
PT disease e.g. multiple sclerosis, inflammatory disease, lung cancer and  
PT allergic disease.  
XX  
PS Example 3; Fig 5; 87pp; Japanese.  
XX  
XX This invention describes a novel immunoglobulin Fc receptor which can be  
CC used to screen for an agonist or antagonist for the treatment of  
CC autoimmune disease. the invention also describes 1) a protein consisting  
CC of partial amino acid sequence of the receptor; 2) a fusion protein  
CC comprising the receptor and another peptide; 3) a gene encoding the  
CC receptor; 4) a recombinant vector containing the gene; 5) transformed  
CC host transformed by the gene; 6) a method of preparing the receptor; 7)  
CC an antibody which specifically recognizes the Fc receptor; 8) a reagent  
CC for detecting the Fc receptor, comprising the antibody; 9) a method for  
CC screening an agonist or antagonist of the receptor, which involves  
CC reacting the Fc receptor with IgM or IgA in the presence of test sample  
CC and selecting the substance which promotes or inhibits binding of the  
CC receptor with IgM or IgA and 10) a pharmaceutical for controlling immune  
CC response, comprising the Fc receptor or its gene, or the agonist or  
CC antagonist obtained by the method in 9), as an active ingredient. The  
CC receptor is useful as a medical agent for treatment of autoimmune disease  
CC (e.g. multiple sclerosis, systemic lupus erythematosus, rheumatoid  
CC arthritis, scleroderma, multiple myositis, Sjogren's syndrome, Behcet's  
CC disease), inflammatory disease (e.g. inflammatory bowel disease,  
CC ulcerative colitis, Crohn's disease, uveitis), tumor (e.g. lung cancer,  
CC brain tumor, hepatic carcinoma), allergic disease (e.g. bronchial asthma,  
CC atopic dermatitis), etc. The receptor is useful for elucidating the  
CC immunological mechanism and for the development of drug delivery system.  
CC The isolated Fc receptor gene capable of binding with IgA/IgM was  
CC screened by BLAST program of National Center for Biotechnology  
CC information (NCBI). As a result, an Fc receptor gene having 36% homology  
CC to a known Fc receptor of human and mouse was identified. The identified  
CC gene was specific for endothelial cell and hence, the protein encoded by  
CC the gene was named as endothelial immunoglobulin receptor (elgR). This  
CC sequence represents a fragment of construct Fc-pcDNA3 which is used in  
CC the method of the invention.  
XX  
SQ Sequence 12 BP; 4 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 2e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 20 CCTGGTAAAT 29  
|| |||||  
Db 1 CCGGTTAAAT 10  
  
RESULT 447  
ABK09921  
ID ABK09921 standard; DNA; 10 BP.  
XX  
AC ABK09921;  
XX



DT 14-MAR-2002 (first entry)  
XX  
DE P2RY1 gene allele-specific oligonucleotide #72.  
XX  
KW Purinergic receptor P2Y, G-protein coupled 1; P2RY1; anticoagulant;  
KW coagulant; platelet aggregation; haplotyping; drug screening;  
KW transgenic animal; human; allele-specific oligonucleotide; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200190117-A2.  
XX  
PD 29-NOV-2001.  
XX  
PF 21-MAY-2001; 2001WO-US016432.  
XX  
PR 19-MAY-2000; 2000US-0205996P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Kazemi A, Koshy B, Tanguay DA;  
XX  
DR WPI; 2002-083074/11.  
XX  
PT New purinergic receptor P2Y G-protein coupled 1 (P2RY1) gene polymorphic  
PT variants, useful e.g. in studying the expression and function of P2RY1  
PT and screening candidate drugs for treating diseases related to P2RY1  
PT activity.  
XX  
PS Claim 18; Page 14; 79pp; English.  
XX  
CC The invention relates to a novel isolated polypeptide comprising a  
CC sequence which is a polymorphic variant of a reference sequence for the  
CC purinergic receptor P2Y, G-protein coupled, 1 (P2RY1) protein or its  
CC fragment. The polymorphic variant comprises one or more variant amino  
CC acids selected from valine at a position 34 and glycine at a position  
CC 262. The polymorphic variants are useful in studying the expression and  
CC function of P2RY1, in expressing P2RY1 protein for use in screening for  
CC candidate drugs to treat diseases related to P2RY1 activity, in studying  
CC the effect of the variation on the biological activity of P2RY1, and the  
CC binding affinity of candidate drugs targeting P2RY1 for the treatment of  
CC disorders related to platelet aggregation. The haplotyping methods are  
CC useful in validating P2RY1 as a candidate target for treating a specific  
CC condition or disease predicted to be associated with P2RY1 activity, or  
CC in the design of clinical trials of candidate drugs for treating a  
CC specific condition or disease associated with P2RY1 activity. The  
CC transgenic animals are useful for studying expression of the P2RY1  
CC isogenes in vivo, for in vivo screening and testing of drugs targeted  
CC against P2RY1 protein, and for testing the efficacy of therapeutic agents  
CC and compounds for disorders related to platelet aggregation in a  
CC biological system. ABK09950-ABK09924 represent human purinergic receptor  
CC P2Y, G-coupled protein 1 (P2RY1) gene allele-specific oligonucleotides of  
CC the invention  
XX  
SQ Sequence 10 BP; 1 A; 2 C; 2 G; 5 T; 0 U; 0 Other;  
  
Query Match 25.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 2.5e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 17 TGACCTGGT 25  
Db 2 TTACCTGGT 10  
  
RESULT 448  
ADU19159/c  
ID ADU19159 standard; DNA; 10 BP.  
XX  
AC ADU19159;  
XX  
DT 13-JAN-2005 (first entry)  
XX

DE Hypoxia-related tumorigenesis-related SAGE tag #950.  
XX  
KW screening; hypoxia-related tumorigenesis;  
KW hypoxia-induced gene regulation; tumour; SAGE tag; ds.  
XX  
OS Unidentified.  
XX  
PN WO2004092198-A2.  
XX  
PD 28-OCT-2004.  
XX  
PF 09-APR-2004; 2004WO-US011087.  
XX  
PR 09-APR-2003; 2003US-0461712P.  
XX  
PA (GENZ ) GENZYME CORP.  
XX  
PI Nacht M;  
XX  
DR WPI; 2004-758333/74.  
XX  
PT Identifying agents that alter biological activity of a polypeptide  
PT encoded by a polynucleotide involved in hypoxia-related tumorigenesis  
PT comprises contacting an agent with a target cell and monitoring activity  
PT of expressed product.  
XX  
PS Disclosure; Page 74; 100pp; English.  
XX  
CC The invention comprises a method of screening for candidate agents  
CC capable of altering the biological activity of a protein encoded by a  
CC nucleotide involved in hypoxia-related tumorigenesis. The method of the  
CC invention involves: contacting a test agent with a target cell expressing  
CC the nucleotide, and monitoring the activity of the expressed protein  
CC product; if the test agent modifies the activity of the expressed protein  
CC then this is a candidate agent. The method of the invention is useful for  
CC modifying hypoxia-induced gene regulation and for diagnosing, prognosing  
CC or treating tumours. The present DNA sequence represents a SAGE tag that  
CC was used in the exemplification of the invention.  
XX  
SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;  
  
Query Match 25.5%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 2.5e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 19 ACCTGGTAA 27  
Db 10 ACCTGGTCA 2  
  
Search completed: May 15, 2006, 15:03:40  
Job time : 2 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 15, 2006, 14:28:05 ; Search time 0.001 Seconds  
(without alignments)  
1.392 Million cell updates/sec

Title: US-09-904-968A-3-COPY  
Perfect score: 29  
Sequence: 1 ccattccacctgtgtgtgtgacctgtaaat 29

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 0.5

Searched: 2 seqs, 24 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 2 summaries

Database : estdb:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 9.4   | 32.4        | 13     | 1     | CW020522    |
| 2          | 9     | 31.0        | 11     | 1     | CZ171464    |

ALIGNMENTS

RESULT 1  
CW020522  
LOCUS  
DEFINITION GC0792 TIGEM gene trap library Mus musculus cDNA clone m4.E4.D08,  
mRNA sequence.  
ACCESSION CW020522  
VERSION CW020522.1 GI:52789782  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Cobellis,G., Nicolaus,G., Iovino,M., Romito,A., Marra,E.,  
Barbarisi,M., Sardiello,M., Di Giorgio,F.P., Iovino,N., Zollo,M.,  
Ballabio,A. and Cortese,R.  
TITLE Tagging genes with cassette-exchange sites  
JOURNAL Nucleic Acids Res. 33 (4), e44 (2005)  
PUBMED 15741177  
COMMENT Contact: TIGEM  
107  
TIGEM  
Via P. Castellino, 111, 80131 NAPOLI, ITALY  
Tel: +390816132205  
Fax: +390815790919

Email: cobellis@tigem.it  
Sequence tag generated by 5' RACE of total RNA from gene trap ES  
cell line. ES cell lines harboring insertion mutation of target  
gene are available upon request from TIGEM. Annotation information  
available from TIGEM  
Class: Gene Trap.

FEATURES  
source

Location/Qualifiers  
1..13  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129 Ola"  
/db\_xref="taxon:10090"  
/clone="m4.E4.D08"  
/sex="male"  
/cell\_type="Embryonic stem cell"  
/cell\_line="E14"  
/clone\_lib="TIGEM gene trap library"  
/note="Vector: pFLiP1"

Query Match 32.4%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 15 TGTGACCTGGT 25  
|||

Db 2 TGGGACCTGGT 12  
|||

RESULT 2

CZ171464

LOCUS

DEFINITION

CZ171464 11 bp DNA linear GSS 31-JAN-2005  
MIAA-10116b.b1 Meloidogyne incognita BAC end sequence library  
(MIAAGSS 001) Meloidogyne incognita genomic, genomic survey  
sequence.

ACCESSION

CZ171464

VERSION

CZ171464.1 GI:58339757

KEYWORDS

GSS.

SOURCE

Meloidogyne incognita (southern root-knot nematode)

ORGANISM

Meloidogyne incognita

Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;

Tylenchoidea; Meloidogynidae; Meloidogyninae; Meloidogyne.

REFERENCE 1 (bases 1 to 11)

AUTHORS

Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T.,  
Clifton,S., Budiman,A., Lakey,N., Opperman,C. and Bird,D.McK.

TITLE

Genome Survey sequences from the parasitic nematode Meloidogyne

incognita

JOURNAL

Unpublished (2005)

COMMENT

Contact: Mitreva M  
Washington University in St. Louis  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: nematode@watson.wustl.edu  
BAC ends sequenced by Washington University Genome Sequencing  
Center

Class: BAC ends.

FEATURES

source

Location/Qualifiers  
1..11  
/organism="Meloidogyne incognita"  
/mol\_type="genomic DNA"  
/strain="Race 1"  
/db\_xref="taxon:6306"  
/dev\_stage="L2"  
/clone\_lib="Meloidogyne incognita BAC end sequence library  
(MIAAGSS 001)"  
/note="Vector: pCUGI; Site 1: HindIII; Site 2: HindIII;  
BAC library constructed by Arief Budiman and Nathan Lakey  
at Orion Genomics, and David Bird and Charles Opperman at  
Center for the Biology of Nematode Parasitism at NCSU."

Query Match 31.0%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0;

Mon May 15 15:24:53 2006

|         |    |              |    |            |    |        |    |      |    |
|---------|----|--------------|----|------------|----|--------|----|------|----|
| Matches | 9; | Conservative | 0; | Mismatches | 0; | Indels | 0; | Gaps | 0; |
| Qy      | 1  | CCATCCACC    | 9  |            |    |        |    |      |    |
|         |    |              |    |            |    |        |    |      |    |
| Db      | 3  | CCATCCACC    | 11 |            |    |        |    |      |    |

Search completed: May 15, 2006, 14:28:05  
Job time : 0.001 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
  
OM nucleic - nucleic search, using sw model  
  
Run on: May 15, 2006, 14:55:23 ; Search time 0.001 Seconds  
(without alignments)  
288.028 Million cell updates/sec

Title: US-09-904-968A-3-COPY  
Perfect score: 29  
Sequence: 1 ccattccacctgtgtgtgaccttgtaaat 29

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 411 seqs, 4966 residues

Total number of hits satisfying chosen parameters: 822

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 412 summaries

Database : gedb:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 29    | 100.0       | 29     | 1     | AX440499    |
| 2          | 15.6  | 53.8        | 22     | 1     | AX684211    |
| 3          | 15.2  | 52.4        | 21     | 1     | AR299686    |
| 4          | 14.8  | 51.0        | 20     | 1     | AR297605    |
| 5          | 14.4  | 49.7        | 19     | 1     | CS050343    |
| 6          | 14.2  | 49.0        | 20     | 1     | AR099203    |
| 7          | 14.2  | 49.0        | 20     | 1     | AR154297    |
| 8          | 14.2  | 49.0        | 20     | 1     | BD136591    |
| 9          | 14.2  | 49.0        | 20     | 1     | AR361853    |
| 10         | 14.2  | 49.0        | 20     | 1     | AR432409    |
| 11         | 14.2  | 49.0        | 20     | 1     | AR475830    |
| 12         | 14.2  | 49.0        | 20     | 1     | AR679662    |
| 13         | 14.2  | 49.0        | 20     | 1     | AX591358    |
| 14         | 14.2  | 49.0        | 20     | 1     | AX591503    |
| 15         | 13.4  | 46.2        | 19     | 1     | AR294747    |
| 16         | 12.8  | 44.1        | 17     | 1     | E13312      |
| 17         | 12.8  | 44.1        | 17     | 1     | AX532129    |
| 18         | 12.8  | 44.1        | 17     | 1     | AX532130    |
| 19         | 12.8  | 44.1        | 18     | 1     | AR038733    |
| 20         | 12.8  | 44.1        | 18     | 1     | AR059619    |
| 21         | 12.8  | 44.1        | 18     | 1     | BD243945    |
| 22         | 12.8  | 44.1        | 18     | 1     | AR196740    |
| 23         | 12.8  | 44.1        | 18     | 1     | AR594350    |
| 24         | 12.4  | 42.8        | 17     | 1     | CQ617431    |
| 25         | 12.4  | 42.8        | 17     | 1     | CQ617432    |
| 26         | 12.4  | 42.8        | 17     | 1     | CQ617433    |
| 27         | 12.4  | 42.8        | 17     | 1     | CQ617434    |
| 28         | 12.4  | 42.8        | 17     | 1     | AR458494    |
| 29         | 12.4  | 42.8        | 17     | 1     | AR458495    |
| 30         | 12.4  | 42.8        | 17     | 1     | AR458496    |
| 31         | 12.4  | 42.8        | 17     | 1     | AR458497    |
| 32         | 12.4  | 42.8        | 17     | 1     | AX733424    |
| 33         | 12.4  | 42.8        | 17     | 1     | AX733431    |

|     |      |      |    |   |          |                    |
|-----|------|------|----|---|----------|--------------------|
| 34  | 12.4 | 42.8 | 17 | 1 | AX738031 | ACCESSION:AX738031 |
| 35  | 12.2 | 42.1 | 17 | 1 | AX532131 | ACCESSION:AX532131 |
| 36  | 12.2 | 42.1 | 17 | 1 | AX532132 | ACCESSION:AX532132 |
| 37  | 12.2 | 42.1 | 17 | 1 | AX532133 | ACCESSION:AX532133 |
| 38  | 12.2 | 42.1 | 17 | 1 | AX615973 | ACCESSION:AX615973 |
| 39  | 12   | 41.4 | 17 | 1 | CQ617429 | ACCESSION:CQ617429 |
| 40  | 12   | 41.4 | 17 | 1 | CQ617430 | ACCESSION:CQ617430 |
| 41  | 12   | 41.4 | 17 | 1 | AR458492 | ACCESSION:AR458492 |
| 42  | 12   | 41.4 | 17 | 1 | AR458493 | ACCESSION:AR458493 |
| 43  | 12   | 41.4 | 17 | 1 | AX671858 | ACCESSION:AX671858 |
| 44  | 12   | 41.4 | 17 | 1 | AX758887 | ACCESSION:AX758887 |
| 45  | 11.2 | 38.6 | 16 | 1 | AR134350 | ACCESSION:AR134350 |
| 46  | 11.2 | 38.6 | 16 | 1 | BD078236 | ACCESSION:BD078236 |
| 47  | 11.2 | 38.6 | 16 | 1 | CQ858631 | ACCESSION:CQ858631 |
| 48  | 11.2 | 38.6 | 16 | 1 | AR328258 | ACCESSION:AR328258 |
| 49  | 11   | 37.9 | 12 | 1 | I07726   | ACCESSION:I07726   |
| 50  | 11   | 37.9 | 15 | 1 | CQ828994 | ACCESSION:CQ828994 |
| 51  | 10.8 | 37.2 | 15 | 1 | A88223   | ACCESSION:A88223   |
| 52  | 10.8 | 37.2 | 15 | 1 | A90190   | ACCESSION:A90190   |
| 53  | 10.8 | 37.2 | 15 | 1 | AR033319 | ACCESSION:AR033319 |
| 54  | 10.8 | 37.2 | 15 | 1 | AR113141 | ACCESSION:AR113141 |
| 55  | 10.8 | 37.2 | 15 | 1 | BD065736 | ACCESSION:BD065736 |
| 56  | 10.8 | 37.2 | 15 | 1 | BD207052 | ACCESSION:BD207052 |
| 57  | 10.8 | 37.2 | 15 | 1 | I57548   | ACCESSION:I57548   |
| 58  | 10.4 | 35.9 | 13 | 1 | CQ794305 | ACCESSION:CQ794305 |
| 59  | 10.4 | 35.9 | 14 | 1 | A40464   | ACCESSION:A40464   |
| 60  | 10.4 | 35.9 | 14 | 1 | A88991   | ACCESSION:A88991   |
| 61  | 10.4 | 35.9 | 14 | 1 | BD066504 | ACCESSION:BD066504 |
| 62  | 10.4 | 35.9 | 14 | 1 | BD176783 | ACCESSION:BD176783 |
| 63  | 10.4 | 35.9 | 14 | 1 | AR232744 | ACCESSION:AR232744 |
| 64  | 10.4 | 35.9 | 14 | 1 | AR300215 | ACCESSION:AR300215 |
| 65  | 10.4 | 35.9 | 14 | 1 | AX316360 | ACCESSION:AX316360 |
| 66  | 10   | 34.5 | 11 | 1 | CQ828943 | ACCESSION:CQ828943 |
| 67  | 10   | 34.5 | 11 | 1 | AX394511 | ACCESSION:AX394511 |
| 68  | 10   | 34.5 | 11 | 1 | AX394518 | ACCESSION:AX394518 |
| 69  | 10   | 34.5 | 11 | 1 | AX471278 | ACCESSION:AX471278 |
| 70  | 10   | 34.5 | 11 | 1 | AX624482 | ACCESSION:AX624482 |
| 71  | 10   | 34.5 | 11 | 1 | AX625948 | ACCESSION:AX625948 |
| 72  | 10   | 34.5 | 11 | 1 | AX627058 | ACCESSION:AX627058 |
| 73  | 10   | 34.5 | 11 | 1 | AX631903 | ACCESSION:AX631903 |
| 74  | 10   | 34.5 | 12 | 1 | CQ828958 | ACCESSION:CQ828958 |
| 75  | 10   | 34.5 | 12 | 1 | CQ828995 | ACCESSION:CQ828995 |
| 76  | 10   | 34.5 | 12 | 1 | AX770861 | ACCESSION:AX770861 |
| 77  | 10   | 34.5 | 14 | 1 | A89161   | ACCESSION:A89161   |
| 78  | 10   | 34.5 | 14 | 1 | BD066674 | ACCESSION:BD066674 |
| 79  | 10   | 34.5 | 14 | 1 | BD209352 | ACCESSION:BD209352 |
| 80  | 10   | 34.5 | 14 | 1 | BD235127 | ACCESSION:BD235127 |
| 81  | 9.8  | 33.8 | 13 | 1 | AR175360 | ACCESSION:AR175360 |
| 82  | 9.8  | 33.8 | 13 | 1 | AX572357 | ACCESSION:AX572357 |
| 83  | 9.8  | 33.8 | 13 | 1 | AX572382 | ACCESSION:AX572382 |
| 84  | 9.8  | 33.8 | 14 | 1 | A40478   | ACCESSION:A40478   |
| 85  | 9.8  | 33.8 | 14 | 1 | A88219   | ACCESSION:A88219   |
| 86  | 9.8  | 33.8 | 14 | 1 | A89005   | ACCESSION:A89005   |
| 87  | 9.8  | 33.8 | 14 | 1 | A89321   | ACCESSION:A89321   |
| 88  | 9.8  | 33.8 | 14 | 1 | A90186   | ACCESSION:A90186   |
| 89  | 9.8  | 33.8 | 14 | 1 | BD065732 | ACCESSION:BD065732 |
| 90  | 9.8  | 33.8 | 14 | 1 | BD066518 | ACCESSION:BD066518 |
| 91  | 9.8  | 33.8 | 14 | 1 | BD066834 | ACCESSION:BD066834 |
| 92  | 9.8  | 33.8 | 14 | 1 | AR232758 | ACCESSION:AR232758 |
| 93  | 9.8  | 33.8 | 14 | 1 | AX316374 | ACCESSION:AX316374 |
| 94  | 9.8  | 33.8 | 14 | 1 | AX572354 | ACCESSION:AX572354 |
| 95  | 9.8  | 33.8 | 14 | 1 | AX572358 | ACCESSION:AX572358 |
| 96  | 9.8  | 33.8 | 14 | 1 | AX572372 | ACCESSION:AX572372 |
| 97  | 9.8  | 33.8 | 14 | 1 | AX572374 | ACCESSION:AX572374 |
| 98  | 9.8  | 33.8 | 14 | 1 | AX572377 | ACCESSION:AX572377 |
| 99  | 9.8  | 33.8 | 14 | 1 | AX572381 | ACCESSION:AX572381 |
| 100 | 9.4  | 32.4 | 11 | 1 | BD124223 | ACCESSION:BD124223 |
| 101 | 9.4  | 32.4 | 11 | 1 | BD124438 | ACCESSION:BD124438 |
| 102 | 9.4  | 32.4 | 11 | 1 | CQ836739 | ACCESSION:CQ836739 |
| 103 | 9.4  | 32.4 | 11 | 1 | CQ837792 | ACCESSION:CQ837792 |
| 104 | 9.4  | 32.4 | 11 | 1 | CS058325 | ACCESSION:CS058325 |
| 105 | 9.4  | 32.4 | 11 | 1 | AR301473 | ACCESSION:AR301473 |
| 106 | 9.4  | 32.4 | 11 | 1 | AR301688 | ACCESSION:AR301688 |



|       |     |      |    |   |          |                    |
|-------|-----|------|----|---|----------|--------------------|
| C 107 | 9.4 | 32.4 | 11 | 1 | AX036264 | ACCESSION:AX036264 |
| 108   | 9.4 | 32.4 | 11 | 1 | AX470508 | ACCESSION:AX470508 |
| 109   | 9.4 | 32.4 | 11 | 1 | AX623763 | ACCESSION:AX623763 |
| 110   | 9.4 | 32.4 | 11 | 1 | AX625616 | ACCESSION:AX625616 |
| 111   | 9.4 | 32.4 | 11 | 1 | AX625941 | ACCESSION:AX625941 |
| 112   | 9.4 | 32.4 | 11 | 1 | AX627200 | ACCESSION:AX627200 |
| 113   | 9.4 | 32.4 | 11 | 1 | AX627837 | ACCESSION:AX627837 |
| 114   | 9.4 | 32.4 | 11 | 1 | AX628604 | ACCESSION:AX628604 |
| 115   | 9.4 | 32.4 | 11 | 1 | AX631184 | ACCESSION:AX631184 |
| 116   | 9.4 | 32.4 | 12 | 1 | A91475   | ACCESSION:A91475   |
| 117   | 9.4 | 32.4 | 12 | 1 | BD248272 | ACCESSION:BD248272 |
| 118   | 9.4 | 32.4 | 12 | 1 | BD248273 | ACCESSION:BD248273 |
| 119   | 9.4 | 32.4 | 12 | 1 | I07725   | ACCESSION:I07725   |
| 120   | 9.4 | 32.4 | 12 | 1 | BD023257 | ACCESSION:BD023257 |
| 121   | 9.4 | 32.4 | 13 | 1 | I43005   | ACCESSION:I43005   |
| 122   | 9.4 | 32.4 | 13 | 1 | AR363773 | ACCESSION:AR363773 |
| 123   | 9   | 31.0 | 10 | 1 | BD239019 | ACCESSION:BD239019 |
| 124   | 9   | 31.0 | 10 | 1 | BD239139 | ACCESSION:BD239139 |
| 125   | 9   | 31.0 | 10 | 1 | BD240212 | ACCESSION:BD240212 |
| C 126 | 9   | 31.0 | 10 | 1 | CQ766709 | ACCESSION:CQ766709 |
| C 127 | 9   | 31.0 | 10 | 1 | CQ766752 | ACCESSION:CQ766752 |
| 128   | 9   | 31.0 | 10 | 1 | CQ828944 | ACCESSION:CQ828944 |
| C 129 | 9   | 31.0 | 10 | 1 | AX152110 | ACCESSION:AX152110 |
| C 130 | 9   | 31.0 | 10 | 1 | BD007825 | ACCESSION:BD007825 |
| C 131 | 9   | 31.0 | 11 | 1 | AR074494 | ACCESSION:AR074494 |
| C 132 | 9   | 31.0 | 11 | 1 | AR081174 | ACCESSION:AR081174 |
| C 133 | 9   | 31.0 | 11 | 1 | AR085371 | ACCESSION:AR085371 |
| C 134 | 9   | 31.0 | 11 | 1 | AR088119 | ACCESSION:AR088119 |
| C 135 | 9   | 31.0 | 11 | 1 | AR104278 | ACCESSION:AR104278 |
| C 136 | 9   | 31.0 | 11 | 1 | AR143540 | ACCESSION:AR143540 |
| C 137 | 9   | 31.0 | 11 | 1 | AR171446 | ACCESSION:AR171446 |
| C 138 | 9   | 31.0 | 11 | 1 | AR171617 | ACCESSION:AR171617 |
| C 139 | 9   | 31.0 | 11 | 1 | BD080109 | ACCESSION:BD080109 |
| C 140 | 9   | 31.0 | 11 | 1 | BD243207 | ACCESSION:BD243207 |
| 142   | 9   | 31.0 | 11 | 1 | CS058646 | ACCESSION:CS058646 |
| 143   | 9   | 31.0 | 11 | 1 | AR214824 | ACCESSION:AR214824 |
| C 144 | 9   | 31.0 | 11 | 1 | AR569645 | ACCESSION:AR569645 |
| C 145 | 9   | 31.0 | 11 | 1 | AX393112 | ACCESSION:AX393112 |
| C 146 | 9   | 31.0 | 11 | 1 | AX470507 | ACCESSION:AX470507 |
| 147   | 9   | 31.0 | 11 | 1 | AX623057 | ACCESSION:AX623057 |
| C 148 | 9   | 31.0 | 11 | 1 | AX630236 | ACCESSION:AX630236 |
| C 149 | 9   | 31.0 | 12 | 1 | AX630478 | ACCESSION:AX630478 |
| 150   | 8.8 | 30.3 | 12 | 1 | AR014245 | ACCESSION:AR014245 |
| C 151 | 8.8 | 30.3 | 12 | 1 | AR038696 | ACCESSION:AR038696 |
| 152   | 8.8 | 30.3 | 12 | 1 | AR058492 | ACCESSION:AR058492 |
| 153   | 8.8 | 30.3 | 12 | 1 | BD064895 | ACCESSION:BD064895 |
| 154   | 8.8 | 30.3 | 12 | 1 | BD271980 | ACCESSION:BD271980 |
| 155   | 8.8 | 30.3 | 12 | 1 | CQ766158 | ACCESSION:CQ766158 |
| C 156 | 8.8 | 30.3 | 12 | 1 | I23750   | ACCESSION:I23750   |
| 157   | 8.8 | 30.3 | 12 | 1 | I73177   | ACCESSION:I73177   |
| 158   | 8.8 | 30.3 | 12 | 1 | AR302271 | ACCESSION:AR302271 |
| 159   | 8.8 | 30.3 | 12 | 1 | AR308098 | ACCESSION:AR308098 |
| 160   | 8.8 | 30.3 | 12 | 1 | S55766   | ACCESSION:S55766   |
| 161   | 8.8 | 30.3 | 12 | 1 | S73118S2 | ACCESSION:S73119   |
| C 162 | 8.4 | 29.0 | 10 | 1 | AR164924 | ACCESSION:AR164924 |
| 163   | 8.4 | 29.0 | 10 | 1 | AR167603 | ACCESSION:AR167603 |
| 164   | 8.4 | 29.0 | 10 | 1 | BD083179 | ACCESSION:BD083179 |
| 165   | 8.4 | 29.0 | 10 | 1 | BD083230 | ACCESSION:BD083230 |
| 166   | 8.4 | 29.0 | 10 | 1 | BD083332 | ACCESSION:BD083332 |
| 167   | 8.4 | 29.0 | 10 | 1 | BD083352 | ACCESSION:BD083352 |
| C 168 | 8.4 | 29.0 | 10 | 1 | BD167115 | ACCESSION:BD167115 |
| 169   | 8.4 | 29.0 | 10 | 1 | BD195102 | ACCESSION:BD195102 |
| C 170 | 8.4 | 29.0 | 10 | 1 | BD238856 | ACCESSION:BD238856 |
| 171   | 8.4 | 29.0 | 10 | 1 | BD239707 | ACCESSION:BD239707 |
| 172   | 8.4 | 29.0 | 10 | 1 | BD240160 | ACCESSION:BD240160 |
| 173   | 8.4 | 29.0 | 10 | 1 | E06867   | ACCESSION:E06867   |
| C 174 | 8.4 | 29.0 | 10 | 1 | E39535   | ACCESSION:E39535   |
| 175   | 8.4 | 29.0 | 10 | 1 | E39641   | ACCESSION:E39641   |
| C 176 | 8.4 | 29.0 | 10 | 1 | E54734   | ACCESSION:E54734   |
| 177   | 8.4 | 29.0 | 10 | 1 | I43001   | ACCESSION:I43001   |
| C 178 | 8.4 | 29.0 | 10 | 1 | AR303393 | ACCESSION:AR303393 |
| 179   | 8.4 | 29.0 | 10 | 1 | AR306856 | ACCESSION:AR306856 |
| C 180 | 8.4 | 29.0 | 10 | 1 | AR490725 | ACCESSION:AR490725 |
| C 181 | 8.4 | 29.0 | 10 | 1 | AR532498 | ACCESSION:AR532498 |
| C 182 | 8.4 | 29.0 | 10 | 1 | AX018751 | ACCESSION:AX018751 |
| 183   | 8.4 | 29.0 | 10 | 1 | AX112967 | ACCESSION:AX112967 |
| 184   | 8.4 | 29.0 | 10 | 1 | AX152117 | ACCESSION:AX152117 |
| 185   | 8.4 | 29.0 | 10 | 1 | AX152126 | ACCESSION:AX152126 |
| 186   | 8.4 | 29.0 | 10 | 1 | AX152191 | ACCESSION:AX152191 |
| 187   | 8.4 | 29.0 | 10 | 1 | AX152676 | ACCESSION:AX152676 |
| 188   | 8.4 | 29.0 | 10 | 1 | BD007884 | ACCESSION:BD007884 |
| 189   | 8.4 | 29.0 | 11 | 1 | AR051278 | ACCESSION:AR051278 |
| C 190 | 8.4 | 29.0 | 11 | 1 | AR074507 | ACCESSION:AR074507 |
| C 191 | 8.4 | 29.0 | 11 | 1 | AR077230 | ACCESSION:AR077230 |
| C 192 | 8.4 | 29.0 | 11 | 1 | AR081187 | ACCESSION:AR081187 |
| C 193 | 8.4 | 29.0 | 11 | 1 | AR085384 | ACCESSION:AR085384 |
| C 194 | 8.4 | 29.0 | 11 | 1 | AR088132 | ACCESSION:AR088132 |
| C 195 | 8.4 | 29.0 | 11 | 1 | AR104291 | ACCESSION:AR104291 |
| C 196 | 8.4 | 29.0 | 11 | 1 | AR143553 | ACCESSION:AR143553 |
| C 197 | 8.4 | 29.0 | 11 | 1 | AR171459 | ACCESSION:AR171459 |
| C 198 | 8.4 | 29.0 | 11 | 1 | AR171630 | ACCESSION:AR171630 |
| 199   | 8.4 | 29.0 | 11 | 1 | BD057177 | ACCESSION:BD057177 |
| 200   | 8.4 | 29.0 | 11 | 1 | BD061634 | ACCESSION:BD061634 |
| 201   | 8.4 | 29.0 | 11 | 1 | BD124282 | ACCESSION:BD124282 |
| 202   | 8.4 | 29.0 | 11 | 1 | BD124454 | ACCESSION:BD124454 |
| C 203 | 8.4 | 29.0 | 11 | 1 | BD243220 | ACCESSION:BD243220 |
| C 204 | 8.4 | 29.0 | 11 | 1 | CQ766284 | ACCESSION:CQ766284 |
| C 205 | 8.4 | 29.0 | 11 | 1 | CQ833247 | ACCESSION:CQ833247 |
| C 206 | 8.4 | 29.0 | 11 | 1 | CQ833289 | ACCESSION:CQ833289 |
| 207   | 8.4 | 29.0 | 11 | 1 | CQ833356 | ACCESSION:CQ833356 |
| 208   | 8.4 | 29.0 | 11 | 1 | CQ835321 | ACCESSION:CQ835321 |
| C 209 | 8.4 | 29.0 | 11 | 1 | CQ835588 | ACCESSION:CQ835588 |
| 210   | 8.4 | 29.0 | 11 | 1 | CQ835701 | ACCESSION:CQ835701 |
| 211   | 8.4 | 29.0 | 11 | 1 | CQ836236 | ACCESSION:CQ836236 |
| C 212 | 8.4 | 29.0 | 11 | 1 | CQ836553 | ACCESSION:CQ836553 |
| 213   | 8.4 | 29.0 | 11 | 1 | CQ836684 | ACCESSION:CQ836684 |
| C 214 | 8.4 | 29.0 | 11 | 1 | CQ836692 | ACCESSION:CQ836692 |
| 215   | 8.4 | 29.0 | 11 | 1 | CQ836910 | ACCESSION:CQ836910 |
| C 216 | 8.4 | 29.0 | 11 | 1 | CQ837506 | ACCESSION:CQ837506 |
| C 217 | 8.4 | 29.0 | 11 | 1 | CQ837969 | ACCESSION:CQ837969 |
| 218   | 8.4 | 29.0 | 11 | 1 | CS058181 | ACCESSION:CS058181 |
| C 219 | 8.4 | 29.0 | 11 | 1 | CS058234 | ACCESSION:CS058234 |
| 220   | 8.4 | 29.0 | 11 | 1 | CS058596 | ACCESSION:CS058596 |
| 221   | 8.4 | 29.0 | 11 | 1 | AR301532 | ACCESSION:AR301532 |
| 222   | 8.4 | 29.0 | 11 | 1 | AR301704 | ACCESSION:AR301704 |
| C 223 | 8.4 | 29.0 | 11 | 1 | AR569658 | ACCESSION:AR569658 |
| 224   | 8.4 | 29.0 | 11 | 1 | AR085766 | ACCESSION:AR085766 |
| 225   | 8.4 | 29.0 | 11 | 1 | AX470852 | ACCESSION:AX470852 |
| C 226 | 8.4 | 29.0 | 11 | 1 | AX470941 | ACCESSION:AX470941 |
| C 227 | 8.4 | 29.0 | 11 | 1 | AX471016 | ACCESSION:AX471016 |
| 228   | 8.4 | 29.0 | 11 | 1 | AX471168 | ACCESSION:AX471168 |
| C 229 | 8.4 | 29.0 | 11 | 1 | AX471345 | ACCESSION:AX471345 |
| 230   | 8.4 | 29.0 | 11 | 1 | AX471608 | ACCESSION:AX471608 |
| C 231 | 8.4 | 29.0 | 11 | 1 | AX623509 | ACCESSION:AX623509 |
| C 232 | 8.4 | 29.0 | 11 | 1 | AX623560 | ACCESSION:AX623560 |
| 233   | 8.4 | 29.0 | 11 | 1 | AX624060 | ACCESSION:AX624060 |
| C 234 | 8.4 | 29.0 | 11 | 1 | AX624161 | ACCESSION:AX624161 |
| C 235 | 8.4 | 29.0 | 11 | 1 | AX624988 | ACCESSION:AX624988 |
| 236   | 8.4 | 29.0 | 11 | 1 | AX626149 | ACCESSION:AX626149 |
| C 237 | 8.4 | 29.0 | 11 | 1 | AX626748 | ACCESSION:AX626748 |
| C 238 | 8.4 | 29.0 | 11 | 1 | AX626997 | ACCESSION:AX626997 |
| 239   | 8.4 | 29.0 | 11 | 1 | AX627183 | ACCESSION:AX627183 |
| 240   | 8.4 | 29.0 | 11 | 1 | AX627753 | ACCESSION:AX627753 |
| C 241 | 8.4 | 29.0 | 11 | 1 | AX627875 | ACCESSION:AX627875 |
| 242   | 8.4 | 29.0 | 11 | 1 | AX627970 | ACCESSION:AX627970 |
| C 243 | 8.4 | 29.0 | 11 | 1 | AX628145 | ACCESSION:AX628145 |
| 244   | 8.4 | 29.0 | 11 | 1 | AX628168 | ACCESSION:AX628168 |
| C 245 | 8.4 | 29.0 | 11 | 1 | AX628220 | ACCESSION:AX628220 |
| 246   | 8.4 | 29.0 | 11 | 1 | AX628331 | ACCESSION:AX628331 |
| C 247 | 8.4 | 29.0 | 11 | 1 | AX628518 | ACCESSION:AX628518 |
| C 248 | 8.4 | 29.0 | 11 | 1 | AX629299 | ACCESSION:AX629299 |
| 249   | 8.4 | 29.0 | 11 | 1 | AX629728 | ACCESSION:AX629728 |
| 250   | 8.4 | 29.0 | 11 | 1 | AX629959 | ACCESSION:AX629959 |
| C 251 | 8.4 | 29.0 | 11 | 1 | AX630263 | ACCESSION:AX630263 |
| C 252 | 8.4 | 29.0 | 11 | 1 | AX630930 | ACCESSION:AX630930 |

|       |     |      |    |   |           |                    |
|-------|-----|------|----|---|-----------|--------------------|
| C 253 | 8.4 | 29.0 | 11 | 1 | AX630981  | ACCESSION:AX630981 |
| 254   | 8.4 | 29.0 | 11 | 1 | AX631481  | ACCESSION:AX631481 |
| C 255 | 8.4 | 29.0 | 11 | 1 | AX631582  | ACCESSION:AX631582 |
| C 256 | 8.4 | 29.0 | 11 | 1 | AX632409  | ACCESSION:AX632409 |
| 257   | 8.4 | 29.0 | 11 | 1 | HSPMLEX43 | ACCESSION:X63632   |
| C 258 | 8.4 | 29.0 | 12 | 1 | A71560    | ACCESSION:A71560   |
| 259   | 8.4 | 29.0 | 12 | 1 | AR167777  | ACCESSION:AR167777 |
| C 260 | 8.4 | 29.0 | 12 | 1 | AR167827  | ACCESSION:AR167827 |
| C 261 | 8.4 | 29.0 | 12 | 1 | BD143765  | ACCESSION:BD143765 |
| C 262 | 8.4 | 29.0 | 12 | 1 | BD168627  | ACCESSION:BD168627 |
| C 263 | 8.4 | 29.0 | 12 | 1 | CQ766277  | ACCESSION:CQ766277 |
| C 264 | 8.4 | 29.0 | 12 | 1 | CQ828759  | ACCESSION:CQ828759 |
| C 265 | 8.4 | 29.0 | 12 | 1 | CQ828760  | ACCESSION:CQ828760 |
| C 266 | 8.4 | 29.0 | 12 | 1 | CQ828918  | ACCESSION:CQ828918 |
| 267   | 8.4 | 29.0 | 12 | 1 | E29661    | ACCESSION:E29661   |
| C 268 | 8.4 | 29.0 | 12 | 1 | E29711    | ACCESSION:E29711   |
| 269   | 8.4 | 29.0 | 12 | 1 | E38767    | ACCESSION:E38767   |
| C 270 | 8.4 | 29.0 | 12 | 1 | E38817    | ACCESSION:E38817   |
| 271   | 8.4 | 29.0 | 12 | 1 | E64193    | ACCESSION:E64193   |
| C 272 | 8.4 | 29.0 | 12 | 1 | E64243    | ACCESSION:E64243   |
| C 273 | 8.4 | 29.0 | 12 | 1 | I34990    | ACCESSION:I34990   |
| 274   | 8.4 | 29.0 | 12 | 1 | AR408074  | ACCESSION:AR408074 |
| 275   | 8.4 | 29.0 | 12 | 1 | AR630023  | ACCESSION:AR630023 |
| C 276 | 8.4 | 29.0 | 12 | 1 | AX097958  | ACCESSION:AX097958 |
| C 277 | 8.4 | 29.0 | 12 | 1 | AX138534  | ACCESSION:AX138534 |
| 278   | 8.4 | 29.0 | 12 | 1 | AX351125  | ACCESSION:AX351125 |
| 279   | 8   | 27.6 | 10 | 1 | AR071511  | ACCESSION:AR071511 |
| C 280 | 8   | 27.6 | 10 | 1 | BD161300  | ACCESSION:BD161300 |
| C 281 | 8   | 27.6 | 10 | 1 | BD166593  | ACCESSION:BD166593 |
| 282   | 8   | 27.6 | 10 | 1 | BD238629  | ACCESSION:BD238629 |
| C 283 | 8   | 27.6 | 10 | 1 | BD238760  | ACCESSION:BD238760 |
| 284   | 8   | 27.6 | 10 | 1 | BD238881  | ACCESSION:BD238881 |
| 285   | 8   | 27.6 | 10 | 1 | BD239055  | ACCESSION:BD239055 |
| C 286 | 8   | 27.6 | 10 | 1 | BD239153  | ACCESSION:BD239153 |
| C 287 | 8   | 27.6 | 10 | 1 | BD239196  | ACCESSION:BD239196 |
| 288   | 8   | 27.6 | 10 | 1 | BD239212  | ACCESSION:BD239212 |
| 289   | 8   | 27.6 | 10 | 1 | BD239785  | ACCESSION:BD239785 |
| C 290 | 8   | 27.6 | 10 | 1 | BD240273  | ACCESSION:BD240273 |
| 291   | 8   | 27.6 | 10 | 1 | CQ766677  | ACCESSION:CQ766677 |
| C 292 | 8   | 27.6 | 10 | 1 | CQ766737  | ACCESSION:CQ766737 |
| 293   | 8   | 27.6 | 10 | 1 | CQ828565  | ACCESSION:CQ828565 |
| C 294 | 8   | 27.6 | 10 | 1 | CQ828675  | ACCESSION:CQ828675 |
| 295   | 8   | 27.6 | 10 | 1 | CQ828736  | ACCESSION:CQ828736 |
| C 296 | 8   | 27.6 | 10 | 1 | CQ828850  | ACCESSION:CQ828850 |
| C 297 | 8   | 27.6 | 10 | 1 | E16980    | ACCESSION:E16980   |
| 298   | 8   | 27.6 | 10 | 1 | E28643    | ACCESSION:E28643   |
| C 299 | 8   | 27.6 | 10 | 1 | E64716    | ACCESSION:E64716   |
| C 300 | 8   | 27.6 | 10 | 1 | AR241991  | ACCESSION:AR241991 |
| 301   | 8   | 27.6 | 10 | 1 | AR304497  | ACCESSION:AR304497 |
| C 302 | 8   | 27.6 | 10 | 1 | AR306871  | ACCESSION:AR306871 |
| 303   | 8   | 27.6 | 10 | 1 | AX152690  | ACCESSION:AX152690 |
| 304   | 8   | 27.6 | 10 | 1 | AX152728  | ACCESSION:AX152728 |
| C 306 | 8   | 27.6 | 10 | 1 | AX152911  | ACCESSION:AX152911 |
| C 307 | 8   | 27.6 | 10 | 1 | AX153356  | ACCESSION:AX153356 |
| 308   | 8   | 27.6 | 10 | 1 | AX301473  | ACCESSION:AX301473 |
| 309   | 8   | 27.6 | 10 | 1 | AX301553  | ACCESSION:AX301553 |
| 310   | 8   | 27.6 | 10 | 1 | AX512728  | ACCESSION:AX512728 |
| 311   | 8   | 27.6 | 11 | 1 | BD124275  | ACCESSION:BD124275 |
| 312   | 8   | 27.6 | 11 | 1 | CQ828564  | ACCESSION:CQ828564 |
| 313   | 8   | 27.6 | 11 | 1 | CQ828735  | ACCESSION:CQ828735 |
| 314   | 8   | 27.6 | 11 | 1 | CQ832674  | ACCESSION:CQ832674 |
| 315   | 8   | 27.6 | 11 | 1 | CQ832685  | ACCESSION:CQ832685 |
| C 316 | 8   | 27.6 | 11 | 1 | CQ832885  | ACCESSION:CQ832885 |
| C 317 | 8   | 27.6 | 11 | 1 | CQ833280  | ACCESSION:CQ833280 |
| 318   | 8   | 27.6 | 11 | 1 | CQ835128  | ACCESSION:CQ835128 |
| 319   | 8   | 27.6 | 11 | 1 | CQ835562  | ACCESSION:CQ835562 |
| C 320 | 8   | 27.6 | 11 | 1 | CQ835656  | ACCESSION:CQ835656 |
| 321   | 8   | 27.6 | 11 | 1 | CQ836490  | ACCESSION:CQ836490 |
| 322   | 8   | 27.6 | 11 | 1 | CQ836499  | ACCESSION:CQ836499 |
| C 323 | 8   | 27.6 | 11 | 1 | CQ836747  | ACCESSION:CQ836747 |
| 324   | 8   | 27.6 | 11 | 1 | CQ836833  | ACCESSION:CQ836833 |
| 325   | 8   | 27.6 | 11 | 1 | CQ837690  | ACCESSION:CQ837690 |

|       |     |      |    |   |          |                    |
|-------|-----|------|----|---|----------|--------------------|
| 326   | 8   | 27.6 | 11 | 1 | CQ837896 | ACCESSION:CQ837896 |
| 327   | 8   | 27.6 | 11 | 1 | CQ837956 | ACCESSION:CQ837956 |
| 328   | 8   | 27.6 | 11 | 1 | AR301525 | ACCESSION:AR301525 |
| C 329 | 8   | 27.6 | 11 | 1 | AR632418 | ACCESSION:AR632418 |
| 330   | 8   | 27.6 | 11 | 1 | AX470713 | ACCESSION:AX470713 |
| C 331 | 8   | 27.6 | 11 | 1 | AX470904 | ACCESSION:AX470904 |
| C 332 | 8   | 27.6 | 11 | 1 | AX470954 | ACCESSION:AX470954 |
| 333   | 8   | 27.6 | 11 | 1 | AX471035 | ACCESSION:AX471035 |
| 334   | 8   | 27.6 | 11 | 1 | AX471109 | ACCESSION:AX471109 |
| C 335 | 8   | 27.6 | 11 | 1 | AX471236 | ACCESSION:AX471236 |
| C 336 | 8   | 27.6 | 11 | 1 | AX471465 | ACCESSION:AX471465 |
| 337   | 8   | 27.6 | 11 | 1 | AX471492 | ACCESSION:AX471492 |
| 338   | 8   | 27.6 | 11 | 1 | AX482032 | ACCESSION:AX482032 |
| 339   | 8   | 27.6 | 11 | 1 | AX511271 | ACCESSION:AX511271 |
| 340   | 8   | 27.6 | 11 | 1 | AX622962 | ACCESSION:AX622962 |
| C 341 | 8   | 27.6 | 11 | 1 | AX623083 | ACCESSION:AX623083 |
| C 342 | 8   | 27.6 | 11 | 1 | AX623228 | ACCESSION:AX623228 |
| C 343 | 8   | 27.6 | 11 | 1 | AX624370 | ACCESSION:AX624370 |
| 344   | 8   | 27.6 | 11 | 1 | AX625507 | ACCESSION:AX625507 |
| C 345 | 8   | 27.6 | 11 | 1 | AX625837 | ACCESSION:AX625837 |
| C 346 | 8   | 27.6 | 11 | 1 | AX626039 | ACCESSION:AX626039 |
| C 347 | 8   | 27.6 | 11 | 1 | AX626143 | ACCESSION:AX626143 |
| 348   | 8   | 27.6 | 11 | 1 | AX626825 | ACCESSION:AX626825 |
| C 349 | 8   | 27.6 | 11 | 1 | AX627393 | ACCESSION:AX627393 |
| C 350 | 8   | 27.6 | 11 | 1 | AX627828 | ACCESSION:AX627828 |
| 351   | 8   | 27.6 | 11 | 1 | AX628284 | ACCESSION:AX628284 |
| C 352 | 8   | 27.6 | 11 | 1 | AX628336 | ACCESSION:AX628336 |
| 353   | 8   | 27.6 | 11 | 1 | AX628472 | ACCESSION:AX628472 |
| C 354 | 8   | 27.6 | 11 | 1 | AX628654 | ACCESSION:AX628654 |
| 355   | 8   | 27.6 | 11 | 1 | AX628766 | ACCESSION:AX628766 |
| C 356 | 8   | 27.6 | 11 | 1 | AX629030 | ACCESSION:AX629030 |
| C 357 | 8   | 27.6 | 11 | 1 | AX629150 | ACCESSION:AX629150 |
| 358   | 8   | 27.6 | 11 | 1 | AX629152 | ACCESSION:AX629152 |
| 359   | 8   | 27.6 | 11 | 1 | AX629352 | ACCESSION:AX629352 |
| 360   | 8   | 27.6 | 11 | 1 | AX629742 | ACCESSION:AX629742 |
| 361   | 8   | 27.6 | 11 | 1 | AX629813 | ACCESSION:AX629813 |
| C 362 | 8   | 27.6 | 11 | 1 | AX629849 | ACCESSION:AX629849 |
| 363   | 8   | 27.6 | 11 | 1 | AX630339 | ACCESSION:AX630339 |
| 364   | 8   | 27.6 | 11 | 1 | AX630383 | ACCESSION:AX630383 |
| C 365 | 8   | 27.6 | 11 | 1 | AX630504 | ACCESSION:AX630504 |
| C 366 | 8   | 27.6 | 11 | 1 | AX630649 | ACCESSION:AX630649 |
| C 367 | 8   | 27.6 | 11 | 1 | AX631791 | ACCESSION:AX631791 |
| 368   | 8   | 27.6 | 11 | 1 | AX924272 | ACCESSION:AX924272 |
| C 369 | 7.8 | 26.9 | 11 | 1 | A36701   | ACCESSION:A36701   |
| C 370 | 7.8 | 26.9 | 11 | 1 | BD095127 | ACCESSION:BD095127 |
| C 371 | 7.8 | 26.9 | 11 | 1 | CQ828950 | ACCESSION:CQ828950 |
| C 372 | 7.8 | 26.9 | 11 | 1 | CQ832704 | ACCESSION:CQ832704 |
| 373   | 7.8 | 26.9 | 11 | 1 | CQ832725 | ACCESSION:CQ832725 |
| 374   | 7.8 | 26.9 | 11 | 1 | CQ833139 | ACCESSION:CQ833139 |
| 375   | 7.8 | 26.9 | 11 | 1 | CQ833700 | ACCESSION:CQ833700 |
| C 376 | 7.8 | 26.9 | 11 | 1 | CQ833823 | ACCESSION:CQ833823 |
| 377   | 7.8 | 26.9 | 11 | 1 | CQ833936 | ACCESSION:CQ833936 |
| C 378 | 7.8 | 26.9 | 11 | 1 | CQ835054 | ACCESSION:CQ835054 |
| 379   | 7.8 | 26.9 | 11 | 1 | CQ836644 | ACCESSION:CQ836644 |
| 380   | 7.8 | 26.9 | 11 | 1 | CQ837342 | ACCESSION:CQ837342 |
| 381   | 7.8 | 26.9 | 11 | 1 | CQ837591 | ACCESSION:CQ837591 |
| C 382 | 7.8 | 26.9 | 11 | 1 | CQ837743 | ACCESSION:CQ837743 |
| 383   | 7.8 | 26.9 | 11 | 1 | CQ838096 | ACCESSION:CQ838096 |
| C 384 | 7.8 | 26.9 | 11 | 1 | CQ838096 | ACCESSION:CQ838096 |
| 385   | 7.8 | 26.9 | 11 | 1 | CS058269 | ACCESSION:CS058269 |
| C 386 | 7.8 | 26.9 | 11 | 1 | AR364168 | ACCESSION:AR364168 |
| 387   | 7.8 | 26.9 | 11 | 1 | AX470620 | ACCESSION:AX470620 |
| 388   | 7.8 | 26.9 | 11 | 1 | AX470911 | ACCESSION:AX470911 |
| 389   | 7.8 | 26.9 | 11 | 1 | AX471463 | ACCESSION:AX471463 |
| 390   | 7.8 | 26.9 | 11 | 1 | AX471815 | ACCESSION:AX471815 |
| 391   | 7.8 | 26.9 | 11 | 1 | AX623055 | ACCESSION:AX623055 |
| C 392 | 7.8 | 26.9 | 11 | 1 | AX623372 | ACCESSION:AX623372 |
| 393   | 7.8 | 26.9 | 11 | 1 | AX623975 | ACCESSION:AX623975 |
| 394   | 7.8 | 26.9 | 11 | 1 | AX624312 | ACCESSION:AX624312 |
| 395   | 7.8 | 26.9 | 11 | 1 | AX625384 | ACCESSION:AX625384 |
| C 396 | 7.8 | 26.9 | 11 | 1 | AX625836 | ACCESSION:AX625836 |
| C 397 | 7.8 | 26.9 | 11 | 1 | AX626289 | ACCESSION:AX626289 |
| C 398 | 7.8 | 26.9 | 11 | 1 | AX626533 | ACCESSION:AX626533 |

```
C 399      7.8 26.9 11 1 AX627698      ACCESSION:AX627698
400      7.8 26.9 11 1 AX627752      ACCESSION:AX627752
401      7.8 26.9 11 1 AX628274      ACCESSION:AX628274
402      7.8 26.9 11 1 AX628612      ACCESSION:AX628612
C 403      7.8 26.9 11 1 AX628674      ACCESSION:AX628674
C 404      7.8 26.9 11 1 AX629060      ACCESSION:AX629060
405      7.8 26.9 11 1 AX629446      ACCESSION:AX629446
406      7.8 26.9 11 1 AX629919      ACCESSION:AX629919
407      7.8 26.9 11 1 AX630160      ACCESSION:AX630160
408      7.8 26.9 11 1 AX630234      ACCESSION:AX630234
409      7.8 26.9 11 1 AX630476      ACCESSION:AX630476
C 410      7.8 26.9 11 1 AX630793      ACCESSION:AX630793
411      7.8 26.9 11 1 AX631396      ACCESSION:AX631396
412      7.8 26.9 11 1 AX631733      ACCESSION:AX631733
```

ALIGNMENTS

```
RESULT 1
AX440499
LOCUS      AX440499      29 bp      DNA      linear      PAT 29-JUN-2002
DEFINITION Sequence 3 from Patent WO0206529.
ACCESSION  AX440499
VERSION     AX440499.1  GI:21665302
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Germino,G.G., Watnick,T.J. and Phakdeekitcharoen,B.
TITLE       Detection and treatment of polycystic kidney disease
JOURNAL     Patent: WO 0206529-A 3 24-JAN-2002;
            The Johns Hopkins University School of Medicine (US)
FEATURES    Location/Qualifiers
            source
              1..29
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="PCR primer BPF14"
```

```
Query Match      100.0%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGTGACCTGGTAAAT 29
    |||||
DB 1 CCATCCACCTGCTGTGTGACCTGGTAAAT 29
```

```
RESULT 2
AX684211
LOCUS      AX684211      22 bp      DNA      linear      PAT 29-MAR-2003
DEFINITION Sequence 62 from Patent WO0246386.
ACCESSION  AX684211
VERSION     AX684211.1  GI:29371104
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS     Bolton,S., Clayton,R., Easton,A., Engel,L. and Messing,D.
TITLE       Aspergillus ochraceus 11 alpha hydroxylase and oxidoreductase
JOURNAL     Patent: WO 0246386-A 62 13-JUN-2002;
            Pharmacia Corporation (US) ; Bolton, Suzanne (US) ; Clayton, Robert
            (US) ; Easton, Alan (US) ; Engel, Leslie (US) ; Messing, Dean (US)
FEATURES    Location/Qualifiers
            source
              1..22
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
```

```
/note="human oxidoreductase primer 2C"
Query Match      53.8%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGTGACCTG 23
    |||||
DB 1 CATGACCACCTGTGTGAGCTG 22
```

```
RESULT 3
AR299686/c
LOCUS      AR299686      21 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION Sequence 11421 from patent US 6537751.
ACCESSION  AR299686
VERSION     AR299686.1  GI:31686970
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 21)
AUTHORS     Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE       Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
JOURNAL     Patent: US 6537751-A 11421 25-MAR-2003;
            Genset S.A.;;
FEATURES    Location/Qualifiers
            source
              1..21
                /organism="unknown"
                /mol_type="genomic DNA"
```

```
Query Match      52.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 21;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGTGACC 21
    |||
DB 21 CATTGACTTGCTGTGTGACC 2
```

```
RESULT 4
AR297605
LOCUS      AR297605      20 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION Sequence 9340 from patent US 6537751.
ACCESSION  AR297605
VERSION     AR297605.1  GI:31684889
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE       Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
JOURNAL     Patent: US 6537751-A 9340 25-MAR-2003;
            Genset S.A.;;
FEATURES    Location/Qualifiers
            source
              1..20
                /organism="unknown"
                /mol_type="genomic DNA"
```

```
Query Match      51.0%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TCCACCTGCTGTGTGACC 21
    |
DB 3 TGCACCTGCTCTGTGACC 20
```

RESULT 5  
CS050343  
LOCUS CS050343 19 bp DNA linear PAT 23-MAR-2005  
DEFINITION Sequence 127 from Patent WO2005021757.  
ACCESSION CS050343  
VERSION CS050343.1 GI:61889567  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Tomme,P.H. and van Rompaey,L.  
TITLE Polypeptides and polynucleotides for use as a medicament  
JOURNAL Patent: WO 2005021757-A 127 10-MAR-2005;  
Galapagos Genomics N.V. (BE)  
FEATURES  
source Location/Qualifiers  
1..19  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 49.7%; Score 14.4; DB 1; Length 19;  
Best Local Similarity 93.8%; Pred. No. 26;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 7 ACCTGCTGTGTGACCT 22  
||| ||||| ||||| |||||  
Db 3 ACTTGCTGTGTGACCT 18  
RESULT 6  
AR099203  
LOCUS AR099203 20 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 97 from patent US 6077692.  
ACCESSION AR099203  
VERSION AR099203.1 GI:12808969  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Ruben,S.M., Jimenez,P., Duan,D.Roxanne., Rampy,M.A., Mendrick,D., Zhang,J., Ni,J., Moore,P.A., Coleman,T.A., Gruber,J.R., Dillon,P.J. and Gentz,R.L.  
TITLE Keratinocyte growth factor-2  
JOURNAL Patent: US 6077692-A 97 20-JUN-2000;  
FEATURES  
source Location/Qualifiers  
1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 49.0%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 31;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 CATCCACCTGCTGTGTGAC 20  
||| ||||| ||||| |||||  
Db 1 CAACCACCTGCAGGGTGAC 19  
RESULT 7  
AR154297  
LOCUS AR154297 20 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 18 from patent US 623888.  
ACCESSION AR154297  
VERSION AR154297.1 GI:15122350  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 20)

AUTHORS Gentz,R.L., Chopra,A., Kaushal,P., Spitznagel,T., Unsworth,E. and Khan,F.  
TITLE Keratinocyte growth factor-2 formulations  
JOURNAL Patent: US 623888-A 18 29-MAY-2001;  
FEATURES  
source Location/Qualifiers  
1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 49.0%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 31;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 CATCCACCTGCTGTGTGAC 20  
||| ||||| ||||| |||||  
Db 1 CAACCACCTGCAGGGTGAC 19  
RESULT 8  
BD136591  
LOCUS BD136591 20 bp DNA linear PAT 18-SEP-2002  
DEFINITION Therapeutic utilization of horny cell growth factor-2.  
ACCESSION BD136591  
VERSION BD136591.1 GI:23231536  
KEYWORDS JP 2002507546-A/67.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Jimenez,P., Rampy,M.A., Mendrick,D., Russell,D. and Louie,A.  
TITLE Therapeutic utilization of horny cell growth factor-2  
JOURNAL Patent: JP 2002507546-A 67 12-MAR-2002;  
COMMENT HUMAN GENOME SCIENCES INC  
OS Homo sapiens (human)  
PN JP 2002507546-A/67  
PD 12-MAR-2002  
PF 12-FEB-1999 JP 2000531473  
PR 13-FEB-1998 US 60/074585,30-DEC-1998 US 60/114387 PI  
PABLO JIMENEZ,MARK A RAMPY,DONNA MENDRICK,DEBORAH RUSSELL, PI ARTHUR LOUIE  
PC A61K38/00,A61P1/00,A61P7/00,A61P7/04,A61P7/06,A61P11/00,A61P11/ PC 02,  
PC A61P13/08,A61P13/10,A61P27/02,A61P27/16,A61P35/02,C07K14/475, PC C07K14/50//  
PC A61K48/00,C12N15/09,A61K37/02,C12N15/00  
CC Therapeutic utilization of horny cell growth factor-2 FH Key Location/Qualifiers  
FT source 1..20  
FT /organism='Homo sapiens (human)'.  
FEATURES  
source Location/Qualifiers  
1..20  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
Query Match 49.0%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 31;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 CATCCACCTGCTGTGTGAC 20  
||| ||||| ||||| |||||  
Db 1 CAACCACCTGCAGGGTGAC 19  
RESULT 9  
AR361853  
LOCUS AR361853 20 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 97 from patent US 6599879.  
ACCESSION AR361853  
VERSION AR361853.1 GI:33769823



KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Jimenez,P., Rampy,M.A., Mendrick,D., Russell,D. and Louie,A.  
TITLE Therapeutic uses of Keratinocyte growth factor-2  
JOURNAL Patent: US 6599879-A 97 29-JUL-2003;  
Human Genome Sciences, Inc.; Rockville, MD  
FEATURES  
source  
1..20  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 49.0%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 31;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 2 CATCCACCTGCTGTGTGAC 20  
|| ||||| |||||  
Db 1 CAACCACCTGCAGGTGAC 19  
RESULT 10  
AR432409  
LOCUS AR432409 20 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 18 from patent US 6653284.  
ACCESSION AR432409  
VERSION AR432409.1 GI:40194731  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Gentz,R.L., Chopra,A., Kaushal,P., Spitznagel,T., Unsworth,E. and Khan,F.  
TITLE Keratinocyte growth factor-2 formulations  
JOURNAL Patent: US 6653284-A 18 25-NOV-2003;  
Human Genome Sciences, Inc.; Rockville, MD  
FEATURES  
source  
1..20  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 49.0%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 31;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 2 CATCCACCTGCTGTGTGAC 20  
|| ||||| |||||  
Db 1 CAACCACCTGCAGGTGAC 19  
RESULT 11  
AR475830  
LOCUS AR475830 20 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 97 from patent US 6693077.  
ACCESSION AR475830  
VERSION AR475830.1 GI:42715388  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Ruben,S.M., Jimenez,P., Duan,D.R., Rampy,M.A., Mendrick,D., Zhang,J., Ni,J., Moore,P.A., Coleman,T.A., Gruber,J.R., Dillon,P.J. and Gentz,R.L.  
TITLE Keratinocyte growth factor-2  
JOURNAL Patent: US 6693077-A 97 17-FEB-2004;  
Human Genome Sciences, Inc.; Rockville, MD  
FEATURES  
source  
1..20  
/organism="unknown"

/mol\_type="genomic DNA"  
Query Match 49.0%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 31;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 2 CATCCACCTGCTGTGTGAC 20  
|| ||||| |||||  
Db 1 CAACCACCTGCAGGTGAC 19  
RESULT 12  
AR679662  
LOCUS AR679662 20 bp mRNA linear PAT 13-JUN-2005  
DEFINITION Sequence 97 from patent US 6903072.  
ACCESSION AR679662  
VERSION AR679662.1 GI:67621396  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Ruben,S.M., Jimenez,P., Duan,D.R., Rampy,M.A., Mendrick,D., Zhang,J., Ni,J., Moore,P.A., Coleman,T.A., Gruber,J.R., Dillon,P.J. and Gentz,R.L.  
TITLE Keratinocyte growth factor-2  
JOURNAL Patent: US 6903072-A 97 07-JUN-2005;  
Human Genome Sciences, Inc.; Rockville, MD  
FEATURES  
source  
1..20  
/organism="unknown"  
/mol\_type="mRNA"  
Query Match 49.0%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 31;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 2 CATCCACCTGCTGTGTGAC 20  
|| ||||| |||||  
Db 1 CAACCACCTGCAGGTGAC 19  
RESULT 13  
AX591358  
LOCUS AX591358 20 bp DNA linear PAT 27-JAN-2003  
DEFINITION Sequence 96 from Patent EP1247530.  
ACCESSION AX591358  
VERSION AX591358.1 GI:27949814  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Duan,R.D., Ruben,S.M., Jimenez,P., Rampy,M.A., Mendrick,D., Zhang,J., Ni,J., Moore,P.A., Coleman,T.A. and Gentz,R.L.  
TITLE Keratinocyte growth factor-2 (kgf-2 or fibroblast growth factor-12, fgf-12)  
JOURNAL Patent: EP 1247530-A 96 09-OCT-2002;  
HUMAN GENOME SCIENCES, INC. (US)  
FEATURES  
source  
1..20  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 49.0%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 31;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 2 CATCCACCTGCTGTGTGAC 20  
|| ||||| |||||

Db 1 CAACCACCTGCAGGGTGAC 19

RESULT 14  
AX591503  
LOCUS AX591503 20 bp DNA linear PAT 27-JAN-2003  
DEFINITION Sequence 96 from Patent EP1247862.  
ACCESSION AX591503  
VERSION AX591503.1 GI:27949936  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Duan,R.D., Ruben,S.M., Jimenez,P., Rampy,M.A., Mendrick,D.,  
Zhang,J., Ni,J., Moore,P.A., Coleman,T.A. and Gentz,R.L.  
TITLE Keratinocyte growth factor-2 (kgf-2 or fibroblast growth factor-12,  
fgf-12)  
JOURNAL Patent: EP 1247862-A 96 09-OCT-2002;  
HUMAN GENOME SCIENCES, INC. (US)  
FEATURES  
source Location/Qualifiers  
1..20  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 49.0%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 31;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGTGAC 20  
|| ||||| | |||||  
Db 1 CAACCACCTGCAGGGTGAC 19

RESULT 15  
AR294747/c  
LOCUS AR294747 19 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 6482 from patent US 6537751.  
ACCESSION AR294747  
VERSION AR294747.1 GI:31682031  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 19)  
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.  
TITLE Biallelic markers for use in constructing a high density  
disequilibrium map of the human genome  
JOURNAL Patent: US 6537751-A 6482 25-MAR-2003;  
Genset S.A.;;  
FRX;

FEATURES  
source Location/Qualifiers  
1..19  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 46.2%; Score 13.4; DB 1; Length 19;  
Best Local Similarity 93.3%; Pred. No. 40;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTGA 19  
|| ||||| |||||  
Db 19 CCGCCTGCTGTGTGA 5

RESULT 16  
E13312/c  
LOCUS E13312 17 bp DNA linear PAT 27-APR-1998  
DEFINITION PCR primer for gaining 4-coumaric acid coenzyme A-ligase gene.  
ACCESSION E13312

VERSION E13312.1 GI:3252117  
KEYWORDS JP 1997173069-A/1.  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.

REFERENCE 1 (bases 1 to 17)  
AUTHORS Kajita,S. and Omori,S.  
TITLE 4-COUMARIC ACID : COENZYME A LIGASE GENE AND REDUCTION OF LIGNIN IN  
PLANT USING THE SAME GENE  
JOURNAL Patent: JP 1997173069-A 1 08-JUL-1997;  
MITSUBISHI PAPER MILLS LTD  
COMMENT OS None  
OC Artificial sequences.  
PN JP 1997173069-A/1  
PD 08-JUL-1997  
PF 22-DEC-1995 JP 1995334834  
PI KAJITA SHINYA, OMORI SHUNJI  
PC C12N15/09,A01H5/00,C07H21/04,C12N5/10,C12N9/00, PC  
D21C9/00//A01H1/00,C12N1/21,  
PC C12S3/08,(C12N1/21,C12R1:19);  
CC strandedness: Single;  
CC topology: Linear;  
CC hypothetical: No;  
CC anti-sense: No;  
FH Key  
FT source 1..17  
FT /organism='Artificial sequences'.

FEATURES  
source Location/Qualifiers  
1..17  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

Query Match 44.1%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 68.8%; Pred. No. 45;  
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTG 16  
||:||||:|:  
Db 17 CCRTCACYGTGTGNG 2

RESULT 17  
AX532129  
LOCUS AX532129 17 bp DNA linear PAT 22-NOV-2002  
DEFINITION Sequence 1638 from Patent EPI239051.  
ACCESSION AX532129  
VERSION AX532129.1 GI:25256043  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Shannon,M.  
TITLE Human posh-like protein 1  
JOURNAL Patent: EP 1239051-A 1638 11-SEP-2002;  
Aeomica, Inc. (US)

FEATURES  
source Location/Qualifiers  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 44.1%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 45;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATCCACCTGCTGTGTG 18  
||||| |||||  
Db 2 ATCCACCTCCTCTGTG 17

RESULT 18  
AX532130  
LOCUS AX532130 linear DNA 17 bp PAT 22-NOV-2002  
DEFINITION Sequence 1639 from Patent EP1239051.  
ACCESSION AX532130  
VERSION AX532130.1 GI:25256045  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Shannon,M.  
TITLE Human posh-like protein 1  
JOURNAL Patent: EP 1239051-A 1639 11-SEP-2002;  
Aeomica, Inc. (US)  
FEATURES  
source Location/Qualifiers  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 44.1%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 45;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3 ATCCACCTGCTGTGTG 18  
| | | | | | | | | | | | | | |  
Db 1 ATCCACCTCCTCTGTG 16  
| | | | | | | | | | | | | | |  
RESULT 19  
AR038733/c  
LOCUS AR038733 18 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 39 from patent US 5807681.  
ACCESSION AR038733  
VERSION AR038733.1 GI:5958096  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Giordano,A. and Baldi,A.  
TITLE Human retinoblastoma-related (pRb2/p130) genomic DNA and methods for detecting mutations therein  
JOURNAL Patent: US 5807681-A 39 15-SEP-1998;  
FEATURES  
source Location/Qualifiers  
1..18  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 44.1%; Score 12.8; DB 1; Length 18;  
Best Local Similarity 87.5%; Pred. No. 48;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 13 TGTGTGACCTGGTAAA 28  
| | | | | | | | | | | | | | |  
Db 17 TTTGTGACCTGGCAAA 2  
| | | | | | | | | | | | | | |  
RESULT 20  
AR059619/c  
LOCUS AR059619 18 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 39 from patent US 5840506.  
ACCESSION AR059619  
VERSION AR059619.1 GI:5986069  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 18)  
AUTHORS Giordano,A.  
TITLE Methods for the diagnosis and prognosis of cancer  
JOURNAL Patent: US 5840506-A 39 24-NOV-1998;  
FEATURES  
source Location/Qualifiers  
1..18  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 44.1%; Score 12.8; DB 1; Length 18;  
Best Local Similarity 87.5%; Pred. No. 48;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 13 TGTGTGACCTGGTAAA 28  
| | | | | | | | | | | | | | |  
Db 17 TTTGTGACCTGGCAAA 2  
| | | | | | | | | | | | | | |  
RESULT 21  
BD243945/c  
LOCUS BD243945 18 bp DNA linear PAT 17-JUL-2003  
DEFINITION TREX, a novel gene of TRAF-interacting EXT gene family and diagnostic and therapeutic uses thereof.  
ACCESSION BD243945  
VERSION BD243945.1 GI:33053715  
KEYWORDS JP 2002525126-A/21.  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Sato,T.  
TITLE TREX, a novel gene of TRAF-interacting EXT gene family and diagnostic and therapeutic uses thereof  
JOURNAL Patent: JP 2002525126-A 21 13-AUG-2002;  
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK  
COMMENT OS Linear  
PN JP 2002525126-A/21  
PD 13-AUG-2002  
PF 17-SEP-1999 JP 2000572406  
PR 17-SEP-1998 US 09/156191  
PI TAKAAKI SATO  
PC  
C12N15/09,A61K31/711,A61K39/395,A61K39/395,A61K45/00,A61K48/00, PC  
A61P35/00,  
PC A61P35/04,A61P37/02,C07K14/47,C07K16/18,C12P21/02,C12Q1/68, PC  
G01N33/15,  
PC  
G01N33/50,G01N33/566,G01N33/574//C12P21/08,(C12P21/02,C12R1:91) PC  
,C12N15/00  
CC TREX, a novel gene of TRAF-interacting EXT gene family and CC  
diagnostic and  
CC therapeutic uses thereof  
FH Key Location/Qualifiers  
FT source 1..18  
FT Location/Qualifiers  
/organism='Linear'.  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"  
Query Match 44.1%; Score 12.8; DB 1; Length 18;  
Best Local Similarity 87.5%; Pred. No. 48;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 5 CCACCTGCTGTGTGAC 20  
| | | | | | | | | | | | | | |  
Db 18 CCACATGCTGTGTTAC 3  
| | | | | | | | | | | | | | |  
RESULT 22  
AR196740  
LOCUS AR196740 18 bp DNA linear PAT 20-APR-2002

|                       |                                                                                                                            |                       |                                                                           |
|-----------------------|----------------------------------------------------------------------------------------------------------------------------|-----------------------|---------------------------------------------------------------------------|
| DEFINITION            | Sequence 1205 from patent US 6350934.                                                                                      | JOURNAL               | Patent: WO 0192524-A 2171 06-DEC-2001;                                    |
| ACCESSION             | AR196740                                                                                                                   | FEATURES              | Aeomica, Inc. (US)                                                        |
| VERSION               | AR196740.1 GI:20246177                                                                                                     | source                | 1. .17                                                                    |
| KEYWORDS              | .                                                                                                                          |                       | /organism="Homo sapiens"                                                  |
| SOURCE                | Unknown.                                                                                                                   |                       | /mol_type="unassigned DNA"                                                |
| ORGANISM              | Unknown.                                                                                                                   |                       | /db_xref="taxon:9606"                                                     |
| REFERENCE             | 1 (bases 1 to 18)                                                                                                          | Query Match           | 42.8%; Score 12.4; DB 1; Length 17;                                       |
| AUTHORS               | Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P.Ann.Owens., Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J. | Best Local Similarity | 92.9%; Pred. No. 54;                                                      |
| TITLE                 | Nucleic acid encoding delta-9 desaturase                                                                                   | Matches               | 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;                       |
| JOURNAL               | Patent: US 6350934-A 1205 26-FEB-2002;                                                                                     | Qy                    | 5 CCACCTGCTGTGTG 18                                                       |
| FEATURES              | Location/Qualifiers                                                                                                        | Db                    | 4 CCACCTGCTGTGAG 17                                                       |
| source                | 1. .18                                                                                                                     |                       |                                                                           |
|                       | /organism="unknown"                                                                                                        |                       |                                                                           |
|                       | /mol_type="unassigned DNA"                                                                                                 |                       |                                                                           |
| Query Match           | 44.1%; Score 12.8; DB 1; Length 18;                                                                                        | RESULT 25             |                                                                           |
| Best Local Similarity | 87.5%; Pred. No. 48;                                                                                                       | CQ617432              |                                                                           |
| Matches               | 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;                                                                        | LOCUS                 | CQ617432                                                                  |
| Qy                    | 5 CCACCTGCTGTGTGAC 20                                                                                                      | DEFINITION            | Sequence 2172 from Patent WO0192524.                                      |
| Db                    | 2 CCACCTGATGTTTGAC 17                                                                                                      | ACCESSION             | CQ617432                                                                  |
|                       |                                                                                                                            | VERSION               | CQ617432.1 GI:41667650                                                    |
|                       |                                                                                                                            | KEYWORDS              | .                                                                         |
|                       |                                                                                                                            | SOURCE                | Homo sapiens (human)                                                      |
|                       |                                                                                                                            | ORGANISM              | Homo sapiens                                                              |
| RESULT 23             |                                                                                                                            |                       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;         |
| AR594350/c            |                                                                                                                            |                       | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;               |
| LOCUS                 | AR594350                                                                                                                   |                       | Hominidae; Homo.                                                          |
| DEFINITION            | Sequence 34 from patent US 6812326.                                                                                        | REFERENCE             | 1                                                                         |
| ACCESSION             | AR594350                                                                                                                   | AUTHORS               | Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E. |
| VERSION               | AR594350.1 GI:56643986                                                                                                     | TITLE                 | Myosin-like gene expressed in human heart and muscle                      |
| KEYWORDS              | .                                                                                                                          | JOURNAL               | Patent: WO 0192524-A 2172 06-DEC-2001;                                    |
| SOURCE                | Unknown.                                                                                                                   |                       | Aeomica, Inc. (US)                                                        |
| ORGANISM              | Unknown.                                                                                                                   | FEATURES              | Location/Qualifiers                                                       |
| REFERENCE             | 1 (bases 1 to 18)                                                                                                          | source                | 1. .17                                                                    |
| AUTHORS               | Sato,T.-A.                                                                                                                 |                       | /organism="Homo sapiens"                                                  |
| TITLE                 | TREX, a novel gene of TRAF-interacting EXT gene family and diagnostic and therapeutic uses thereof                         |                       | /mol_type="unassigned DNA"                                                |
| JOURNAL               | Patent: US 6812326-A 34 02-NOV-2004;                                                                                       | Query Match           | 42.8%; Score 12.4; DB 1; Length 17;                                       |
|                       | The Trustees of Columbia University in the City of New York; New York, NY                                                  | Best Local Similarity | 92.9%; Pred. No. 54;                                                      |
| FEATURES              | Location/Qualifiers                                                                                                        | Matches               | 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;                       |
| source                | 1. .18                                                                                                                     | Qy                    | 5 CCACCTGCTGTGTG 18                                                       |
|                       | /organism="unknown"                                                                                                        | Db                    | 3 CCACCTGCTGTGAG 16                                                       |
|                       | /mol_type="genomic DNA"                                                                                                    |                       |                                                                           |
| Query Match           | 44.1%; Score 12.8; DB 1; Length 18;                                                                                        | RESULT 26             |                                                                           |
| Best Local Similarity | 87.5%; Pred. No. 48;                                                                                                       | CQ617433              |                                                                           |
| Matches               | 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;                                                                        | LOCUS                 | CQ617433                                                                  |
| Qy                    | 5 CCACCTGCTGTGTGAC 20                                                                                                      | DEFINITION            | Sequence 2173 from Patent WO0192524.                                      |
| Db                    | 18 CCACATGCTGTGTAC 3                                                                                                       | ACCESSION             | CQ617433                                                                  |
|                       |                                                                                                                            | VERSION               | CQ617433.1 GI:41667651                                                    |
|                       |                                                                                                                            | KEYWORDS              | .                                                                         |
|                       |                                                                                                                            | SOURCE                | Homo sapiens (human)                                                      |
|                       |                                                                                                                            | ORGANISM              | Homo sapiens                                                              |
| RESULT 24             |                                                                                                                            |                       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;         |
| CQ617431              |                                                                                                                            |                       | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;               |
| LOCUS                 | CQ617431                                                                                                                   |                       | Hominidae; Homo.                                                          |
| DEFINITION            | Sequence 2171 from Patent WO0192524.                                                                                       | REFERENCE             | 1                                                                         |
| ACCESSION             | CQ617431                                                                                                                   | AUTHORS               | Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E. |
| VERSION               | CQ617431.1 GI:41667649                                                                                                     | TITLE                 | Myosin-like gene expressed in human heart and muscle                      |
| KEYWORDS              | .                                                                                                                          | JOURNAL               | Patent: WO 0192524-A 2173 06-DEC-2001;                                    |
| SOURCE                | Homo sapiens (human)                                                                                                       |                       | Aeomica, Inc. (US)                                                        |
| ORGANISM              | Homo sapiens                                                                                                               | FEATURES              | Location/Qualifiers                                                       |
|                       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;                                                          | source                | 1. .17                                                                    |
|                       | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;                                                                |                       | /organism="Homo sapiens"                                                  |
|                       | Hominidae; Homo.                                                                                                           |                       | /mol_type="unassigned DNA"                                                |
| REFERENCE             | 1                                                                                                                          |                       | /db_xref="taxon:9606"                                                     |
| AUTHORS               | Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.                                                  |                       |                                                                           |
| TITLE                 | Myosin-like gene expressed in human heart and muscle                                                                       |                       |                                                                           |



Query Match 42.8%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 92.9%; Pred. No. 54;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTG 18  
| | | | | | | | | | |  
Db 2 CCACCTGCTGTGAG 15

RESULT 27  
CQ617434  
LOCUS  
DEFINITION Sequence 2174 from Patent WO0192524.  
ACCESSION CQ617434  
VERSION CQ617434.1 GI:41667652  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
TITLE Myosin-like gene expressed in human heart and muscle  
JOURNAL Patent: WO 0192524-A 2174 06-DEC-2001;  
Aeomica, Inc. (US)

FEATURES  
source Location/Qualifiers  
1 .17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 42.8%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 92.9%; Pred. No. 54;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTG 18  
| | | | | | | | | | |  
Db 1 CCACCTGCTGTGAG 14

RESULT 28  
AR458494  
LOCUS  
DEFINITION Sequence 2171 from patent US 6686188.  
ACCESSION AR458494  
VERSION AR458494.1 GI:42693551  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
JOURNAL Patent: US 6686188-A 2171 03-FEB-2004;  
Amersham PLC; Buckinghamshire;  
GBX;

FEATURES  
source Location/Qualifiers  
1 .17  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 42.8%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 92.9%; Pred. No. 54;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTG 18  
| | | | | | | | | | |  
Db 4 CCACCTGCTGTGAG 17

RESULT 29  
AR458495  
LOCUS  
DEFINITION Sequence 2172 from patent US 6686188.  
ACCESSION AR458495  
VERSION AR458495.1 GI:42693552  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
JOURNAL Patent: US 6686188-A 2172 03-FEB-2004;  
Amersham PLC; Buckinghamshire;  
GBX;

FEATURES  
source Location/Qualifiers  
1 .17  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 42.8%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 92.9%; Pred. No. 54;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTG 18  
| | | | | | | | | | |  
Db 3 CCACCTGCTGTGAG 16

RESULT 30  
AR458496  
LOCUS  
DEFINITION Sequence 2173 from patent US 6686188.  
ACCESSION AR458496  
VERSION AR458496.1 GI:42693553  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
JOURNAL Patent: US 6686188-A 2173 03-FEB-2004;  
Amersham PLC; Buckinghamshire;  
GBX;

FEATURES  
source Location/Qualifiers  
1 .17  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 42.8%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 92.9%; Pred. No. 54;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTG 18  
| | | | | | | | | | |  
Db 2 CCACCTGCTGTGAG 15

RESULT 31  
AR458497  
LOCUS  
DEFINITION Sequence 2174 from patent US 6686188.  
ACCESSION AR458497  
VERSION AR458497.1 GI:42693554  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
JOURNAL Patent: US 6686188-A 2174 03-FEB-2004;  
Amersham PLC; Buckinghamshire;  
GBX;  
FEATURES Location/Qualifiers  
source 1..17  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 42.8%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 92.9%; Pred. No. 54;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 5 CCACCTGCTGTGTG 18  
Db 1 CCACCTGCTGTGAG 14  
RESULT 32  
AX733424  
LOCUS AX733424 17 bp DNA linear PAT 08-MAY-2003  
DEFINITION Sequence 5058 from Patent WO03025175.  
ACCESSION AX733424  
VERSION AX733424.1 GI:30512767  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines  
JOURNAL Patent: WO 03025175-A 5058 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
FEATURES Location/Qualifiers  
source 1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 42.8%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 92.9%; Pred. No. 54;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 CATCCACCTGCTGT 15  
Db 4 CATCCTCCTGCTGT 17  
RESULT 33  
AX733431  
LOCUS AX733431 17 bp DNA linear PAT 08-MAY-2003  
DEFINITION Sequence 5065 from Patent WO03025175.  
ACCESSION AX733431  
VERSION AX733431.1 GI:30512774  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.

TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines  
JOURNAL Patent: WO 03025175-A 5065 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
FEATURES Location/Qualifiers  
source 1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 42.8%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 92.9%; Pred. No. 54;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 ATCCACCTGCTGTG 16  
Db 2 ATCCACCTGCTTTG 15  
RESULT 34  
AX738031  
LOCUS AX738031 17 bp DNA linear PAT 08-MAY-2003  
DEFINITION Sequence 3621 from Patent WO03025177.  
ACCESSION AX738031  
VERSION AX738031.1 GI:30517319  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments  
JOURNAL Patent: WO 03025177-A 3621 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
FEATURES Location/Qualifiers  
source 1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 42.8%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 92.9%; Pred. No. 54;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 ATCCACCTGCTGTG 16  
Db 2 ATCCACCTGCTGTG 15  
RESULT 35  
AX532131  
LOCUS AX532131 17 bp DNA linear PAT 22-NOV-2002  
DEFINITION Sequence 1640 from Patent EP1239051.  
ACCESSION AX532131  
VERSION AX532131.1 GI:25256047  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Shannon,M.  
TITLE Human posh-like protein 1  
JOURNAL Patent: EP 1239051-A 1640 11-SEP-2002;  
Aeomica, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..17



ACCESSION CQ617430  
VERSION CQ617430.1 GI:41667648  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
TITLE Myosin-like gene expressed in human heart and muscle  
JOURNAL Patent: WO 0192524-A 2170 06-DEC-2001;  
Aeomica, Inc. (US)  
FEATURES  
source Location/Qualifiers  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 41.4%; Score 12; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 CCACCTGCTGTG 16  
|||||  
Db 5 CCACCTGCTGTG 16  
RESULT 41  
AR458492  
LOCUS AR458492 Sequence 2169 from patent US 6686188. linear PAT 20-FEB-2004  
DEFINITION AR458492  
ACCESSION AR458492  
VERSION AR458492.1 GI:42693549  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
JOURNAL Patent: US 6686188-A 2169 03-FEB-2004;  
Amersham PLC; Buckinghamshire;  
GBX;  
FEATURES  
source Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 41.4%; Score 12; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 CCACCTGCTGTG 16  
|||||  
Db 6 CCACCTGCTGTG 17  
RESULT 42  
AR458493  
LOCUS AR458493 Sequence 2170 from patent US 6686188. linear PAT 20-FEB-2004  
DEFINITION AR458493  
ACCESSION AR458493  
VERSION AR458493.1 GI:42693550  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and

Shannon,M.E.  
Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
Patent: US 6686188-A 2170 03-FEB-2004;  
Amersham PLC; Buckinghamshire;  
GBX;  
FEATURES  
source Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 41.4%; Score 12; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 CCACCTGCTGTG 16  
|||||  
Db 5 CCACCTGCTGTG 16  
RESULT 43  
AX671858  
LOCUS AX671858 Sequence 303 from Patent WO03004526. linear PAT 27-MAR-2003  
DEFINITION AX671858  
ACCESSION AX671858  
VERSION AX671858.1 GI:29330206  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and their use as medicines  
JOURNAL Patent: WO 03004526-A 303 16-JAN-2003;  
Molecular Engines Laboratories (FR)  
FEATURES  
source Location/Qualifiers  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 41.4%; Score 12; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCATCCACCTGC 12  
|||||  
Db 6 CCATCCACCTGC 17  
RESULT 44  
AX758887  
LOCUS AX758887 Sequence 2208 from Patent WO03040369. linear PAT 25-JUN-2003  
DEFINITION AX758887  
ACCESSION AX758887  
VERSION AX758887.1 GI:32253503  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.  
TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines  
JOURNAL Patent: WO 03040369-A 2208 15-MAY-2003;  
Molecular Engines Laboratories (FR)



FEATURES source Location/Qualifiers  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 41.4%; Score 12; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCCACCTGC 12  
|||||  
Db 4 CCATCCACCTGC 15

RESULT 45  
AR134350/c  
LOCUS AR134350 16 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 13 from patent US 6194152.  
ACCESSION AR134350  
VERSION AR134350.1 GI:14123255  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Laus,R., Shapero,M.H. and Tsavaler,L.  
TITLE Prostate tumor polynucleotide compositions and methods of detection thereof  
JOURNAL Patent: US 6194152-A 13 27-FEB-2001;  
FEATURES Location/Qualifiers  
source 1..16  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 38.6%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 82;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 TGCTGTGTGACCTGGT 25  
|||||  
Db 16 TGCTGTGTGAAATTGT 1

RESULT 46  
BD078236/c  
LOCUS BD078236 16 bp DNA linear PAT 27-AUG-2002  
DEFINITION Prostatic tumor polynucleotide and antigen compositions.  
ACCESSION BD078236  
VERSION BD078236.1 GI:22623839  
KEYWORDS JP 2001514889-A/10.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Laus,R., Shapero,M.H. and Tsavaler,L.  
TITLE Prostatic tumor polynucleotide and antigen compositions  
JOURNAL Patent: JP 2001514889-A 10 18-SEP-2001;  
COMMENT DENDREON CORP  
OS Artificial Sequence  
PN JP 2001514889-A/10  
PD 18-SEP-2001  
PF 18-AUG-1998 JP 2000509830  
PR 20-AUG-1997 US 60/056110,09-JUL-1998 US 09/112096 PI  
REINER LAUS,MICHAEL H SHAPERO,LARISA TSAVALER PC  
C12N15/09,C07K14/705,C07K16/28,C07K19/00,C12N1/15,C12N1/19, PC  
C12N1/21.  
PC C12N5/10,C12P21/02,C12Q1/68,G01N33/53,G01N33/68//C12P21/08, PC  
C12N15/00,  
PC C12N5/00  
CC oligonucleotide primer  
FH Key Location/Qualifiers  
FT primer\_bind (1)..(16).

FEATURES source Location/Qualifiers  
1..16  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

Query Match 38.6%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 82;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 TGCTGTGTGACCTGGT 25  
|||||  
Db 16 TGCTGTGTGAAATTGT 1

RESULT 47  
CQ858631/c  
LOCUS CQ858631 16 bp DNA linear PAT 31-AUG-2004  
DEFINITION Sequence 93 from Patent WO2004069991.  
ACCESSION CQ858631  
VERSION CQ858631.1 GI:51852598  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Hansen,B., Thruue,C.A., Petersen,K.D., Westergaard,M. and Wissenbach,M.  
TITLE Oligomeric compounds for the modulation of survivin expression  
JOURNAL Patent: WO 2004069991-A 93 19-AUG-2004;  
Santaris Pharma A/S (DK)  
FEATURES Location/Qualifiers  
source 1..16  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 38.6%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 82;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TCCACCTGCTGTGTGA 19  
|||  
Db 16 TGCCACTGCTGTGTGA 1

RESULT 48  
AR328258  
LOCUS AR328258 16 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 5660 from patent US 6566127.  
ACCESSION AR328258  
VERSION AR328258.1 GI:33714066  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 5660 20-MAY-2003;  
Ribozyne Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO  
FEATURES Location/Qualifiers  
source 1..16  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 38.6%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 82;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 CCTGCTGTGTGACCTG 23  
Db 1 CCTGCTGTGCGCGCTG 16

RESULT 49  
I07726  
LOCUS I07726 12 bp DNA linear PAT 02-DEC-1994  
DEFINITION Sequence 31 from Patent EP 0364255.  
ACCESSION I07726  
VERSION I07726.1 GI:589733  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Caskey,C.T., Chamberlain,J.S., Gibbs,R.A., Rainer,J.E. and Nguyen,P.N.  
TITLE Multiplex genomic DNA amplification for deletion detection  
JOURNAL Patent: EP 0364255-A2 31 18-APR-1990;  
FEATURES Location/Qualifiers  
source 1. .12  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 37.9%; Score 11; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ACCTGGTAAAT 29  
Db 1 ACCTGGTAAAT 11

RESULT 50  
CQ828994/c  
LOCUS CQ828994 15 bp DNA linear PAT 05-JUL-2004  
DEFINITION Sequence 712 from Patent WO2004053120.  
ACCESSION CQ828994  
VERSION CQ828994.1 GI:49732477  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Weihe,E., Bieller,A. and Schaefer,M.K.  
TITLE Regulatory elements in the 5' region of the vrl gene  
JOURNAL Patent: WO 2004053120-A 712 24-JUN-2004;  
Gruenthal GmbH (DE)  
FEATURES Location/Qualifiers  
source 1. .15  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="V\$E47 01"

Query Match 37.9%; Score 11; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 82;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATCCACCTGC 12  
Db 14 CATCCACCTGC 4

RESULT 51  
A88223  
LOCUS A88223 15 bp DNA linear PAT 22-JAN-2000  
DEFINITION Sequence 371 from Patent WO9833904.  
ACCESSION A88223  
VERSION A88223.1 GI:6736793

KEYWORDS .  
SOURCE unidentified  
ORGANISM unidentified  
unclassified sequences.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Brysch,W. and Schlingensiepen,K.  
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD  
JOURNAL Patent: WO 9833904-A 371 06-AUG-1998;  
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)  
FEATURES Location/Qualifiers  
source 1. .15  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

Query Match 37.2%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 89;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTG 14  
Db 1 CCATCCACTTGATG 14

RESULT 52  
A90190  
LOCUS A90190 15 bp DNA linear PAT 22-JAN-2000  
DEFINITION Sequence 371 from Patent EP0856579.  
ACCESSION A90190  
VERSION A90190.1 GI:6738704  
KEYWORDS .  
SOURCE unidentified  
ORGANISM unidentified  
unclassified sequences.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.  
TITLE An antisense oligonucleotide preparation method  
JOURNAL Patent: EP 0856579-A 371 05-AUG-1998;  
BIOGNOSTIK GES (DE)  
FEATURES Location/Qualifiers  
source 1. .15  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

Query Match 37.2%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 89;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTG 14  
Db 1 CCATCCACTTGATG 14

RESULT 53  
AR033319/c  
LOCUS AR033319 15 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 85 from patent US 5869253.  
ACCESSION AR033319  
VERSION AR033319.1 GI:5948924  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Draper,K.G.  
TITLE Method and reagent for inhibiting hepatitis C virus replication  
JOURNAL Patent: US 5869253-A 85 09-FEB-1999;  
FEATURES Location/Qualifiers  
source 1. .15  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 37.2%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 89;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 GTGACCTGGTAAAT 29  
Db 15 GTGACCTGATACAT 2

RESULT 54  
AR113141/c  
LOCUS AR113141 15 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 85 from patent US 6132966.  
ACCESSION AR113141  
VERSION AR113141.1 GI:14093463  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Draper,K.G.  
TITLE Method and reagent for inhibiting hepatitis C virus replication  
JOURNAL Patent: US 6132966-A 85 17-OCT-2000;  
FEATURES  
source 1. .15  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 37.2%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 89;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 GTGACCTGGTAAAT 29  
Db 15 GTGACCTGATACAT 2

RESULT 55  
BD065736  
LOCUS BD065736 15 bp DNA linear PAT 27-AUG-2002  
DEFINITION An antisense oligonucleotide preparation method.  
ACCESSION BD065736  
VERSION BD065736.1 GI:22611339  
KEYWORDS JP 2001511000-A/371.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Schlingensiepen,K.H. and Brysch,W.  
TITLE An antisense oligonucleotide preparation method  
JOURNAL Patent: JP 2001511000-A 371 07-AUG-2001;  
COMMENT BIOGHOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH  
OS Unknown  
PN JP 2001511000-A/371  
PD 07-AUG-2001  
PR 30-JAN-1998 JP 1998532533  
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH  
PC C12N15/11,C07H21/04,A61K31/70  
CC An antisense oligonucleotide preparation method FH Key  
FT source 1. .15  
FT Location/Qualifiers  
/organism='Unknown'.  
1. .15  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

Query Match 37.2%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 89;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTG 14  
Db 1 CCATCCACCTTGATG 14

RESULT 56  
BD207052/c  
LOCUS BD207052 15 bp RNA linear PAT 17-JUL-2003  
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.  
ACCESSION BD207052  
VERSION BD207052.1 GI:33016822  
KEYWORDS JP 2002512791-A/642.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.  
TITLE Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection  
JOURNAL Patent: JP 2002512791-A 642 08-MAY-2002;  
COMMENT RIBOZYME PHARMACEUTICALS INC  
OS Hepatitis virus (hepatitis C virus)  
PN JP 2002512791-A/642  
PD 08-MAY-2002  
PF 26-APR-1999 JP 2000545991  
PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR  
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI  
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI  
PAVCO,  
PI DENNIS MACEJAK  
PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,  
PC A61K37/66,  
PC C12N15/00  
CC Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.  
FH Key Location/Qualifiers  
FT source 1. .15  
FT /organism='Hepatitis virus (hepatitis C virus)',  
Location/Qualifiers  
1. .15  
/organism="unidentified"  
/mol\_type="genomic RNA"  
/db\_xref="taxon:32644"

Query Match 37.2%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 89;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 GTGACCTGGTAAAT 29  
Db 15 GTGACCTGATACAT 2

RESULT 57  
I57548/c  
LOCUS I57548 15 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 85 from patent US 5610054.  
ACCESSION I57548  
VERSION I57548.1 GI:2482612  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Draper,K.G.  
TITLE Enzymatic RNA molecule targeted against Hepatitis C virus  
JOURNAL Patent: US 5610054-A 85 11-MAR-1997;  
FEATURES  
source 1. .15  
/organism="unknown"





```
RESULT 62
BD176783
LOCUS BD176783 14 bp DNA linear PAT 18-MAR-2003
DEFINITION Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression.
ACCESSION BD176783
VERSION BD176783.1 GI:29122495
KEYWORDS WO 02074951-A/30.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 14)
Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression
Patent: WO 02074951-A 30 26-SEP-2002;
KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
KUNITAKA HIROSE,JUN SAKAI
OS Homo sapiens (human)
PN WO 02074951-A/30
PD 26-SEP-2002
PF 13-MAR-2002 WO 2002JP002338
PR 15-MAR-2001 JP 01P 073959
PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
C12N15/09,C12Q1/68
CC Method of constructing cDNA tag for identifying expressed gene

CC and method
CC of analyzing gene expression
FH Key Location/Qualifiers
FT source 1..14
FT /organism='Homo sapiens (human)'.
FEATURES
source Location/Qualifiers
1..14
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 35.9%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 97;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 TGTGTGACCTGG 24
| | | | |
Db 2 TGTATGACCTGG 13

RESULT 63
AR232744/c
LOCUS AR232744 14 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 1 from patent US 6455689.
ACCESSION AR232744
VERSION AR232744.1 GI:27275082
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
1 (bases 1 to 14)
Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
Antisense-oligonucleotides for transforming growth factor-.beta.
(TGF-.beta.)
Patent: US 6455689-A 1 24-SEP-2002;
Biognostik Gesellschaft fur Biomolekulare Diagnostik mbH;
Gottingen;
EPX;
FEATURES
source Location/Qualifiers
1..14
/organism="unknown"
/mol_type="genomic DNA"

Query Match 35.9%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 97;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 TGTGTGACCTGG 24
| | | | |
Db 2 TGTATGACCTGG 13

RESULT 64
AR300215/c
LOCUS AR300215 14 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 17 from patent US 6537775.
ACCESSION AR300215
VERSION AR300215.1 GI:31687634
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
1 (bases 1 to 14)
Tournier-Lasserre,E., Joutel,A., Bousser,M.-G. and Bach,J.-F.
Gene involved in cadasil, method of diagnosis and therapeutic
application
Patent: US 6537775-A 17 25-MAR-2003;
Institut National de la Sante et de la Recherche (INSERM) and
Assistance Publique - Hopitaux de Paris; Paris;
FRX;
FEATURES
source Location/Qualifiers
1..14
/organism="unknown"
/mol_type="genomic DNA"

Query Match 35.9%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 97;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGC 12
| | | | |
Db 13 CTATCCACCTGC 2

RESULT 65
AX316360/c
LOCUS AX316360 14 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 1 from Patent EP1160319.
ACCESSION AX316360
VERSION AX316360.1 GI:17899533
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
Unclassified sequences.
1
Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
Patent: EP 1160319-A 1 05-DEC-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DB)
FEATURES
source Location/Qualifiers
1..14
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Description of unknown: unknown"

Query Match 35.9%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 97;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGC 12
| | | | |
Db 13 CTATCCACCTGC 2
```

```
Query Match 35.9%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 97;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGC 12
| | | | |
Db 13 CTATCCACCTGC 2

RESULT 64
AR300215/c
LOCUS AR300215 14 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 17 from patent US 6537775.
ACCESSION AR300215
VERSION AR300215.1 GI:31687634
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
1 (bases 1 to 14)
Tournier-Lasserre,E., Joutel,A., Bousser,M.-G. and Bach,J.-F.
Gene involved in cadasil, method of diagnosis and therapeutic
application
Patent: US 6537775-A 17 25-MAR-2003;
Institut National de la Sante et de la Recherche (INSERM) and
Assistance Publique - Hopitaux de Paris; Paris;
FRX;
FEATURES
source Location/Qualifiers
1..14
/organism="unknown"
/mol_type="genomic DNA"

Query Match 35.9%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 97;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGC 12
| | | | |
Db 14 CCACCCACCTGC 3

RESULT 65
AX316360/c
LOCUS AX316360 14 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 1 from Patent EP1160319.
ACCESSION AX316360
VERSION AX316360.1 GI:17899533
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
Unclassified sequences.
1
Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
Patent: EP 1160319-A 1 05-DEC-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DB)
FEATURES
source Location/Qualifiers
1..14
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Description of unknown: unknown"

Query Match 35.9%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 97;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGC 12
| | | | |
Db 13 CTATCCACCTGC 2
```

RESULT 66  
CQ828943  
LOCUS CQ828943 11 bp DNA linear PAT 05-JUL-2004  
DEFINITION Sequence 661 from Patent WO2004053120.  
ACCESSION CQ828943  
VERSION CQ828943.1 GI:49732426  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Weihe,E., Bieller,A. and Schaefer,M.K.  
TITLE Regulatory elements in the 5' region of the vrl gene  
JOURNAL Patent: WO 2004053120-A 661 24-JUN-2004;  
Gruenenthal GmbH (DE)  
FEATURES  
source Location/Qualifiers  
1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="V\$DELTAEF1 01"  
Query Match 34.5%; Score 10; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 87;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 ATCCACCTGC 12  
|||||  
Db 1 ATCCACCTGC 10  
RESULT 67  
AX394511/c  
LOCUS AX394511 11 bp DNA linear PAT 18-MAY-2002  
DEFINITION Sequence 56 from Patent WO0218638.  
ACCESSION AX394511  
VERSION AX394511.1 GI:21065649  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Risinger,C., Andersson,M.K., Lewander,T. and Oliasson,E.  
TITLE Detection of cyp2d6 polymorphisms  
JOURNAL Patent: WO 0218638-A 56 07-MAR-2002;  
Gemini Genomics PLC (GB)  
FEATURES  
source Location/Qualifiers  
1..11  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Synthetic oligonucleotide"  
Query Match 34.5%; Score 10; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 87;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCATCCACCT 10  
|||||  
Db 11 CCATCCACCT 2  
RESULT 68  
AX394518  
LOCUS AX394518 11 bp DNA linear PAT 18-MAY-2002  
DEFINITION Sequence 63 from Patent WO0218638.  
ACCESSION AX394518  
VERSION AX394518.1 GI:21065656  
KEYWORDS

SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Risinger,C., Andersson,M.K., Lewander,T. and Oliasson,E.  
TITLE Detection of cyp2d6 polymorphisms  
JOURNAL Patent: WO 0218638-A 63 07-MAR-2002;  
Gemini Genomics PLC (GB)  
FEATURES  
source Location/Qualifiers  
1..11  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Synthetic oligonucleotide"  
Query Match 34.5%; Score 10; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 87;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCATCCACCT 10  
|||||  
Db 1 CCATCCACCT 10  
RESULT 69  
AX471278  
LOCUS AX471278 11 bp DNA linear PAT 09-AUG-2002  
DEFINITION Sequence 855 from Patent WO02053773.  
ACCESSION AX471278  
VERSION AX471278.1 GI:22206403  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.  
TITLE Method for determining skin stress or skin ageing in vitro  
JOURNAL Patent: WO 02053773-A 855 11-JUL-2002;  
HENKEL KGAA (DE)  
FEATURES  
source Location/Qualifiers  
1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 34.5%; Score 10; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 87;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 ATCCACCTGC 12  
|||||  
Db 1 ATCCACCTGC 10  
RESULT 70  
AX624482  
LOCUS AX624482 11 bp DNA linear PAT 24-FEB-2003  
DEFINITION Sequence 1523 from Patent WO02053774.  
ACCESSION AX624482  
VERSION AX624482.1 GI:28452423  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 1523 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)

|                                                                   |                  |                                                     |  |  |  |  |  |  |  |  |  |
|-------------------------------------------------------------------|------------------|-----------------------------------------------------|--|--|--|--|--|--|--|--|--|
| FEATURES                                                          |                  | Location/Qualifiers                                 |  |  |  |  |  |  |  |  |  |
| source                                                            |                  | 1. .11                                              |  |  |  |  |  |  |  |  |  |
|                                                                   |                  | /organism="Homo sapiens"                            |  |  |  |  |  |  |  |  |  |
|                                                                   |                  | /mol_type="unassigned DNA"                          |  |  |  |  |  |  |  |  |  |
|                                                                   |                  | /db_xref="taxon:9606"                               |  |  |  |  |  |  |  |  |  |
| Query Match                                                       |                  | 34.5%; Score 10; DB 1; Length 11;                   |  |  |  |  |  |  |  |  |  |
| Best Local Similarity                                             |                  | 100.0%; Pred. No. 87;                               |  |  |  |  |  |  |  |  |  |
| Matches                                                           |                  | 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |  |  |  |  |  |  |  |  |  |
| QY                                                                | 3 ATCCACCTGC 12  |                                                     |  |  |  |  |  |  |  |  |  |
|                                                                   |                  |                                                     |  |  |  |  |  |  |  |  |  |
| Db                                                                | 1 ATCCACCTGC 10  |                                                     |  |  |  |  |  |  |  |  |  |
| RESULT 71                                                         |                  |                                                     |  |  |  |  |  |  |  |  |  |
| AX625948                                                          |                  |                                                     |  |  |  |  |  |  |  |  |  |
| LOCUS                                                             |                  |                                                     |  |  |  |  |  |  |  |  |  |
| AX625948                                                          |                  |                                                     |  |  |  |  |  |  |  |  |  |
| DEFINITION                                                        |                  |                                                     |  |  |  |  |  |  |  |  |  |
| Sequence 2989 from Patent WO02053774.                             |                  |                                                     |  |  |  |  |  |  |  |  |  |
| ACCESSION                                                         |                  |                                                     |  |  |  |  |  |  |  |  |  |
| AX625948                                                          |                  |                                                     |  |  |  |  |  |  |  |  |  |
| VERSION                                                           |                  |                                                     |  |  |  |  |  |  |  |  |  |
| AX625948.1 GI:28453986                                            |                  |                                                     |  |  |  |  |  |  |  |  |  |
| KEYWORDS                                                          |                  |                                                     |  |  |  |  |  |  |  |  |  |
| .                                                                 |                  |                                                     |  |  |  |  |  |  |  |  |  |
| SOURCE                                                            |                  |                                                     |  |  |  |  |  |  |  |  |  |
| Homo sapiens (human)                                              |                  |                                                     |  |  |  |  |  |  |  |  |  |
| ORGANISM                                                          |                  |                                                     |  |  |  |  |  |  |  |  |  |
| Homo sapiens                                                      |                  |                                                     |  |  |  |  |  |  |  |  |  |
| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |                  |                                                     |  |  |  |  |  |  |  |  |  |
| Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;       |                  |                                                     |  |  |  |  |  |  |  |  |  |
| Hominidae; Homo.                                                  |                  |                                                     |  |  |  |  |  |  |  |  |  |
| REFERENCE                                                         |                  |                                                     |  |  |  |  |  |  |  |  |  |
| 1                                                                 |                  |                                                     |  |  |  |  |  |  |  |  |  |
| AUTHORS                                                           |                  |                                                     |  |  |  |  |  |  |  |  |  |
| Petersohn,D., Conradt,M. and Hofmann,K.                           |                  |                                                     |  |  |  |  |  |  |  |  |  |
| TITLE                                                             |                  |                                                     |  |  |  |  |  |  |  |  |  |
| Method for determining homeostasis of the skin                    |                  |                                                     |  |  |  |  |  |  |  |  |  |
| JOURNAL                                                           |                  |                                                     |  |  |  |  |  |  |  |  |  |
| Patent: WO 02053774-A 2989 11-JUL-2002;                           |                  |                                                     |  |  |  |  |  |  |  |  |  |
| Henkel Kommanditgesellschaft auf Aktien (DE)                      |                  |                                                     |  |  |  |  |  |  |  |  |  |
| FEATURES                                                          |                  | Location/Qualifiers                                 |  |  |  |  |  |  |  |  |  |
| source                                                            |                  | 1. .11                                              |  |  |  |  |  |  |  |  |  |
|                                                                   |                  | /organism="Homo sapiens"                            |  |  |  |  |  |  |  |  |  |
|                                                                   |                  | /mol_type="unassigned DNA"                          |  |  |  |  |  |  |  |  |  |
|                                                                   |                  | /db_xref="taxon:9606"                               |  |  |  |  |  |  |  |  |  |
| Query Match                                                       |                  | 34.5%; Score 10; DB 1; Length 11;                   |  |  |  |  |  |  |  |  |  |
| Best Local Similarity                                             |                  | 100.0%; Pred. No. 87;                               |  |  |  |  |  |  |  |  |  |
| Matches                                                           |                  | 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |  |  |  |  |  |  |  |  |  |
| QY                                                                | 10 TGCTGTGTGA 19 |                                                     |  |  |  |  |  |  |  |  |  |
|                                                                   |                  |                                                     |  |  |  |  |  |  |  |  |  |
| Db                                                                | 2 TGCTGTGTGA 11  |                                                     |  |  |  |  |  |  |  |  |  |
| RESULT 72                                                         |                  |                                                     |  |  |  |  |  |  |  |  |  |
| AX627058                                                          |                  |                                                     |  |  |  |  |  |  |  |  |  |
| LOCUS                                                             |                  |                                                     |  |  |  |  |  |  |  |  |  |
| AX627058                                                          |                  |                                                     |  |  |  |  |  |  |  |  |  |
| DEFINITION                                                        |                  |                                                     |  |  |  |  |  |  |  |  |  |
| Sequence 4099 from Patent WO02053774.                             |                  |                                                     |  |  |  |  |  |  |  |  |  |
| ACCESSION                                                         |                  |                                                     |  |  |  |  |  |  |  |  |  |
| AX627058                                                          |                  |                                                     |  |  |  |  |  |  |  |  |  |
| VERSION                                                           |                  |                                                     |  |  |  |  |  |  |  |  |  |
| AX627058.1 GI:28455096                                            |                  |                                                     |  |  |  |  |  |  |  |  |  |
| KEYWORDS                                                          |                  |                                                     |  |  |  |  |  |  |  |  |  |
| .                                                                 |                  |                                                     |  |  |  |  |  |  |  |  |  |
| SOURCE                                                            |                  |                                                     |  |  |  |  |  |  |  |  |  |
| Homo sapiens (human)                                              |                  |                                                     |  |  |  |  |  |  |  |  |  |
| ORGANISM                                                          |                  |                                                     |  |  |  |  |  |  |  |  |  |
| Homo sapiens                                                      |                  |                                                     |  |  |  |  |  |  |  |  |  |
| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |                  |                                                     |  |  |  |  |  |  |  |  |  |
| Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;       |                  |                                                     |  |  |  |  |  |  |  |  |  |
| Hominidae; Homo.                                                  |                  |                                                     |  |  |  |  |  |  |  |  |  |
| REFERENCE                                                         |                  |                                                     |  |  |  |  |  |  |  |  |  |
| 1                                                                 |                  |                                                     |  |  |  |  |  |  |  |  |  |
| AUTHORS                                                           |                  |                                                     |  |  |  |  |  |  |  |  |  |
| Petersohn,D., Conradt,M. and Hofmann,K.                           |                  |                                                     |  |  |  |  |  |  |  |  |  |
| TITLE                                                             |                  |                                                     |  |  |  |  |  |  |  |  |  |
| Method for determining homeostasis of the skin                    |                  |                                                     |  |  |  |  |  |  |  |  |  |
| JOURNAL                                                           |                  |                                                     |  |  |  |  |  |  |  |  |  |
| Patent: WO 02053774-A 4099 11-JUL-2002;                           |                  |                                                     |  |  |  |  |  |  |  |  |  |
| Henkel Kommanditgesellschaft auf Aktien (DE)                      |                  |                                                     |  |  |  |  |  |  |  |  |  |
| FEATURES                                                          |                  | Location/Qualifiers                                 |  |  |  |  |  |  |  |  |  |
| source                                                            |                  | 1. .11                                              |  |  |  |  |  |  |  |  |  |
|                                                                   |                  | /organism="Homo sapiens"                            |  |  |  |  |  |  |  |  |  |
|                                                                   |                  | /mol_type="unassigned DNA"                          |  |  |  |  |  |  |  |  |  |
|                                                                   |                  | /db_xref="taxon:9606"                               |  |  |  |  |  |  |  |  |  |
| Query Match                                                       |                  | 34.5%; Score 10; DB 1; Length 11;                   |  |  |  |  |  |  |  |  |  |
| Best Local Similarity                                             |                  | 100.0%; Pred. No. 87;                               |  |  |  |  |  |  |  |  |  |
| Matches                                                           |                  | 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |  |  |  |  |  |  |  |  |  |
| QY                                                                | 3 ATCCACCTGC 12  |                                                     |  |  |  |  |  |  |  |  |  |
|                                                                   |                  |                                                     |  |  |  |  |  |  |  |  |  |
| Db                                                                | 12 ATCCACCTGC 3  |                                                     |  |  |  |  |  |  |  |  |  |
| RESULT 75                                                         |                  |                                                     |  |  |  |  |  |  |  |  |  |
| CQ828995/c                                                        |                  |                                                     |  |  |  |  |  |  |  |  |  |

|                                                                   |                 |                                                     |  |  |  |  |  |  |  |  |  |
|-------------------------------------------------------------------|-----------------|-----------------------------------------------------|--|--|--|--|--|--|--|--|--|
| QY                                                                | 2 CATCCACCTG 11 |                                                     |  |  |  |  |  |  |  |  |  |
|                                                                   |                 |                                                     |  |  |  |  |  |  |  |  |  |
| Db                                                                | 1 CATCCACCTG 10 |                                                     |  |  |  |  |  |  |  |  |  |
| RESULT 73                                                         |                 |                                                     |  |  |  |  |  |  |  |  |  |
| AX631903                                                          |                 |                                                     |  |  |  |  |  |  |  |  |  |
| LOCUS                                                             |                 |                                                     |  |  |  |  |  |  |  |  |  |
| AX631903                                                          |                 |                                                     |  |  |  |  |  |  |  |  |  |
| DEFINITION                                                        |                 |                                                     |  |  |  |  |  |  |  |  |  |
| Sequence 8945 from Patent WO02053774.                             |                 |                                                     |  |  |  |  |  |  |  |  |  |
| ACCESSION                                                         |                 |                                                     |  |  |  |  |  |  |  |  |  |
| AX631903                                                          |                 |                                                     |  |  |  |  |  |  |  |  |  |
| VERSION                                                           |                 |                                                     |  |  |  |  |  |  |  |  |  |
| AX631903.1 GI:28460041                                            |                 |                                                     |  |  |  |  |  |  |  |  |  |
| KEYWORDS                                                          |                 |                                                     |  |  |  |  |  |  |  |  |  |
| .                                                                 |                 |                                                     |  |  |  |  |  |  |  |  |  |
| SOURCE                                                            |                 |                                                     |  |  |  |  |  |  |  |  |  |
| Homo sapiens (human)                                              |                 |                                                     |  |  |  |  |  |  |  |  |  |
| ORGANISM                                                          |                 |                                                     |  |  |  |  |  |  |  |  |  |
| Homo sapiens                                                      |                 |                                                     |  |  |  |  |  |  |  |  |  |
| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |                 |                                                     |  |  |  |  |  |  |  |  |  |
| Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;       |                 |                                                     |  |  |  |  |  |  |  |  |  |
| Hominidae; Homo.                                                  |                 |                                                     |  |  |  |  |  |  |  |  |  |
| REFERENCE                                                         |                 |                                                     |  |  |  |  |  |  |  |  |  |
| 1                                                                 |                 |                                                     |  |  |  |  |  |  |  |  |  |
| AUTHORS                                                           |                 |                                                     |  |  |  |  |  |  |  |  |  |
| Petersohn,D., Conradt,M. and Hofmann,K.                           |                 |                                                     |  |  |  |  |  |  |  |  |  |
| TITLE                                                             |                 |                                                     |  |  |  |  |  |  |  |  |  |
| Method for determining homeostasis of the skin                    |                 |                                                     |  |  |  |  |  |  |  |  |  |
| JOURNAL                                                           |                 |                                                     |  |  |  |  |  |  |  |  |  |
| Patent: WO 02053774-A 8945 11-JUL-2002;                           |                 |                                                     |  |  |  |  |  |  |  |  |  |
| Henkel Kommanditgesellschaft auf Aktien (DE)                      |                 |                                                     |  |  |  |  |  |  |  |  |  |
| FEATURES                                                          |                 | Location/Qualifiers                                 |  |  |  |  |  |  |  |  |  |
| source                                                            |                 | 1. .11                                              |  |  |  |  |  |  |  |  |  |
|                                                                   |                 | /organism="Homo sapiens"                            |  |  |  |  |  |  |  |  |  |
|                                                                   |                 | /mol_type="unassigned DNA"                          |  |  |  |  |  |  |  |  |  |
|                                                                   |                 | /db_xref="taxon:9606"                               |  |  |  |  |  |  |  |  |  |
| Query Match                                                       |                 | 34.5%; Score 10; DB 1; Length 11;                   |  |  |  |  |  |  |  |  |  |
| Best Local Similarity                                             |                 | 100.0%; Pred. No. 87;                               |  |  |  |  |  |  |  |  |  |
| Matches                                                           |                 | 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |  |  |  |  |  |  |  |  |  |
| QY                                                                | 3 ATCCACCTGC 12 |                                                     |  |  |  |  |  |  |  |  |  |
|                                                                   |                 |                                                     |  |  |  |  |  |  |  |  |  |
| Db                                                                | 1 ATCCACCTGC 10 |                                                     |  |  |  |  |  |  |  |  |  |
| RESULT 74                                                         |                 |                                                     |  |  |  |  |  |  |  |  |  |
| CQ828958/c                                                        |                 |                                                     |  |  |  |  |  |  |  |  |  |
| LOCUS                                                             |                 |                                                     |  |  |  |  |  |  |  |  |  |
| CQ828958                                                          |                 |                                                     |  |  |  |  |  |  |  |  |  |
| DEFINITION                                                        |                 |                                                     |  |  |  |  |  |  |  |  |  |
| Sequence 676 from Patent WO2004053120.                            |                 |                                                     |  |  |  |  |  |  |  |  |  |
| ACCESSION                                                         |                 |                                                     |  |  |  |  |  |  |  |  |  |
| CQ828958                                                          |                 |                                                     |  |  |  |  |  |  |  |  |  |
| VERSION                                                           |                 |                                                     |  |  |  |  |  |  |  |  |  |
| CQ828958.1 GI:49732441                                            |                 |                                                     |  |  |  |  |  |  |  |  |  |
| KEYWORDS                                                          |                 |                                                     |  |  |  |  |  |  |  |  |  |
| .                                                                 |                 |                                                     |  |  |  |  |  |  |  |  |  |
| SOURCE                                                            |                 |                                                     |  |  |  |  |  |  |  |  |  |
| Homo sapiens (human)                                              |                 |                                                     |  |  |  |  |  |  |  |  |  |
| ORGANISM                                                          |                 |                                                     |  |  |  |  |  |  |  |  |  |
| Homo sapiens                                                      |                 |                                                     |  |  |  |  |  |  |  |  |  |
| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |                 |                                                     |  |  |  |  |  |  |  |  |  |
| Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;       |                 |                                                     |  |  |  |  |  |  |  |  |  |
| Hominidae; Homo.                                                  |                 |                                                     |  |  |  |  |  |  |  |  |  |
| REFERENCE                                                         |                 |                                                     |  |  |  |  |  |  |  |  |  |
| 1                                                                 |                 |                                                     |  |  |  |  |  |  |  |  |  |
| AUTHORS                                                           |                 |                                                     |  |  |  |  |  |  |  |  |  |
| Weihe,E., Bieller,A. and Schaefer,M.K.                            |                 |                                                     |  |  |  |  |  |  |  |  |  |
| TITLE                                                             |                 |                                                     |  |  |  |  |  |  |  |  |  |
| Regulatory elements in the 5' region of the vrl gene              |                 |                                                     |  |  |  |  |  |  |  |  |  |
| JOURNAL                                                           |                 |                                                     |  |  |  |  |  |  |  |  |  |
| Patent: WO 2004053120-A 676 24-JUN-2004;                          |                 |                                                     |  |  |  |  |  |  |  |  |  |
| Gruenenthal GmbH (DE)                                             |                 |                                                     |  |  |  |  |  |  |  |  |  |
| FEATURES                                                          |                 | Location/Qualifiers                                 |  |  |  |  |  |  |  |  |  |
| source                                                            |                 | 1. .12                                              |  |  |  |  |  |  |  |  |  |
|                                                                   |                 | /organism="Homo sapiens"                            |  |  |  |  |  |  |  |  |  |
|                                                                   |                 | /mol_type="unassigned DNA"                          |  |  |  |  |  |  |  |  |  |
|                                                                   |                 | /db_xref="taxon:9606"                               |  |  |  |  |  |  |  |  |  |
|                                                                   |                 | /note="V\$LMO2COM 01"                               |  |  |  |  |  |  |  |  |  |
| Query Match                                                       |                 | 34.5%; Score 10; DB 1; Length 12;                   |  |  |  |  |  |  |  |  |  |
| Best Local Similarity                                             |                 | 100.0%; Pred. No. 96;                               |  |  |  |  |  |  |  |  |  |
| Matches                                                           |                 | 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |  |  |  |  |  |  |  |  |  |
| QY                                                                | 3 ATCCACCTGC 12 |                                                     |  |  |  |  |  |  |  |  |  |
|                                                                   |                 |                                                     |  |  |  |  |  |  |  |  |  |
| Db                                                                | 12 ATCCACCTGC 3 |                                                     |  |  |  |  |  |  |  |  |  |
| RESULT 75                                                         |                 |                                                     |  |  |  |  |  |  |  |  |  |
| CQ828995/c                                                        |                 |                                                     |  |  |  |  |  |  |  |  |  |

LOCUS CQ828995 12 bp DNA linear PAT 05-JUL-2004  
DEFINITION Sequence 713 from Patent WO2004053120.  
ACCESSION CQ828995  
VERSION CQ828995.1 GI:49732478  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Weihe,E., Bieller,A. and Schaefer,M.K.  
TITLE Regulatory elements in the 5' region of the vrl gene  
JOURNAL Patent: WO 2004053120-A 713 24-JUN-2004;  
Gruenenthal GmbH (DE)  
FEATURES  
source Location/Qualifiers  
1..12  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="V\$LMO2COM 01"  
Query Match 34.5%; Score 10; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 96;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 ATCCACCTGC 12  
|||||  
Db 12 ATCCACCTGC 3  
RESULT 76  
AX770861/c  
LOCUS AX770861 12 bp DNA linear PAT 02-JUL-2003  
DEFINITION Sequence 50 from Patent WO03022875.  
ACCESSION AX770861  
VERSION AX770861.1 GI:32438026  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Alarcon-Riquelme,M. and Prokunina,L.  
TITLE Polymorphisms of pd-1  
JOURNAL Patent: WO 03022875-A 50 20-MAR-2003;  
Everygene AB (SE)  
FEATURES  
source Location/Qualifiers  
1..12  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 34.5%; Score 10; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 96;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CCATCCACT 10  
|||||  
Db 12 CCATCCACT 3  
RESULT 77  
A89161/c  
LOCUS A89161 14 bp DNA linear PAT 22-JAN-2000  
DEFINITION Sequence 1309 from Patent WO9833904.  
ACCESSION A89161  
VERSION A89161.1 GI:6737731  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
unclassified sequences.

REFERENCE 1 (bases 1 to 14)  
AUTHORS Brysch,W. and Schlingensiepen,K.  
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD  
JOURNAL Patent: WO 9833904-A 1309 06-AUG-1998;  
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)  
FEATURES  
source Location/Qualifiers  
1..14  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
Query Match 34.5%; Score 10; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 ATCCACCTGC 12  
|||||  
Db 10 ATCCACCTGC 1  
RESULT 78  
BD066674/c  
LOCUS BD066674 14 bp DNA linear PAT 27-AUG-2002  
DEFINITION An antisense oligonucleotide preparation method.  
ACCESSION BD066674  
VERSION BD066674.1 GI:22612277  
KEYWORDS JP 2001511000-A/1309.  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.  
1 (bases 1 to 14)  
REFERENCE  
AUTHORS Schlingensiepen,K.H. and Brysch,W.  
TITLE An antisense oligonucleotide preparation method  
JOURNAL Patent: JP 2001511000-A 1309 07-AUG-2001;  
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH  
COMMENT OS Unknown  
PN JP 2001511000-A/1309  
PD 07-AUG-2001  
PF 30-JAN-1998 JP 1998532533  
PR 31-JAN-1997 EP 97101531.8  
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH  
PC C12N15/11,C07H21/04,A61K31/70  
CC An antisense oligonucleotide preparation method FH Key  
FT source  
1..14  
/organism='Unknown'.  
FEATURES  
source Location/Qualifiers  
1..14  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"  
Query Match 34.5%; Score 10; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 ATCCACCTGC 12  
|||||  
Db 10 ATCCACCTGC 1  
RESULT 79  
BD209352  
LOCUS BD209352 14 bp RNA linear PAT 17-JUL-2003  
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related  
to hepatitis C virus infection.  
ACCESSION BD209352  
VERSION BD209352.1 GI:33019122  
KEYWORDS JP 2002512791-A/2942.  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.  
1 (bases 1 to 14)  
REFERENCE



AUTHORS Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.  
TITLE Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection  
JOURNAL Patent: JP 2002512791-A 2942 08-MAY-2002;  
COMMENT RIBOZYME PHARMACEUTICALS INC  
OS Hepatitis virus (hepatitis C virus)  
PN JP 2002512791-A/2942  
PD 08-MAY-2002  
PF 26-APR-1999 JP 2000545991  
PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR 25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI  
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI PAVCO,  
PI DENNIS MACEJAK  
PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,  
PC A61K37/66,  
PC C12N15/00  
CC Enzymatic nucleic acid treatment of diseases or conditions CC related to  
CC hepatitis C virus infection.  
FH Key Location/Qualifiers  
FT source 1..14 /organism='Hepatitis virus (hepatitis C FT virus)',  
FT Location/Qualifiers  
FEATURES  
source 1..14  
/organism="unidentified"  
/mol\_type="genomic RNA"  
/db\_xref="taxon:32644"  
Query Match 34.5%; Score 10; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 CTGCTGTGTG 18  
|||||  
Db 4 CTGCTGTGTG 13  
RESULT 80  
BD235127  
LOCUS Detection of non-viral organisms with SRP RNA. PAT 17-JUL-2003  
DEFINITION  
ACCESSION BD235127  
VERSION BD235127.1 GI:33044897  
KEYWORDS JP 2002518026-A/6.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Boles,C.T., Weir,L. and Stone,B.B.  
TITLE Detection of non-viral organisms with SRP RNA  
JOURNAL Patent: JP 2002518026-A 6 25-JUN-2002;  
COMMENT MOSAIC TECHNOLOGIES  
OS Artificial Sequence  
PN JP 2002518026-A/6  
PD 25-JUN-2002  
PF 18-JUN-1999 JP 2000554886  
PR 19-JUN-1998 US 60/090063  
PI CHRISTIAN T BOLES,LAWRENCE WEIR,BENJAMIN B STONE PC  
C12N15/09,C07H21/04,C12Q1/68,C12R1:93),C12N15/00 CC  
Description of Artificial Sequence:complement of conserved E. coli 4.5S  
CC RNA region nucleotides preferred shorter probe for detection  
CC of bacteria  
FH Key Location/Qualifiers  
FT source 1..14 /organism='Artificial Sequence'.  
FT Location/Qualifiers  
source 1..14  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

Query Match 34.5%; Score 10; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 17 TGACCTGGTA 26  
|||||  
Db 5 TGACCTGGTA 14  
RESULT 81  
AR175360  
LOCUS AR175360 13 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 83 from patent US 6309823.  
ACCESSION AR175360  
VERSION AR175360.1 GI:17916659  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Cronin,M.T., Miyada,C.G., Hubbell,E.A., Chee,M., Podor,S.P.A., Huang,X.C., Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.  
TITLE Arrays of nucleic acid probes for analyzing biotransformation genes and methods of using the same  
JOURNAL Patent: US 6309823-A 83 30-OCT-2001;  
FEATURES Location/Qualifiers  
source 1..13  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 33.8%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 1.1e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 10 TGCTGTGTGACCT 22  
|||  
Db 1 TGGTGTGTGCCCT 13  
RESULT 82  
AX572357/c  
LOCUS AX572357 13 bp DNA linear PAT 29-NOV-2002  
DEFINITION Sequence 397 from Patent WO02055741.  
ACCESSION AX572357  
VERSION AX572357.1 GI:26004447  
KEYWORDS  
SOURCE Human immunodeficiency virus  
ORGANISM Human immunodeficiency virus  
REFERENCE 1  
AUTHORS de Smet,K. and Stuyver,L.  
TITLE Method for detection of drug-induced mutations in the hiv reverse transcriptase gene  
JOURNAL Patent: WO 02055741-A 397 18-JUL-2002;  
FEATURES INNOGENETICS N.V. (BE)  
source Location/Qualifiers  
1..13  
/organism="Human immunodeficiency virus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:12721"  
Query Match 33.8%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 1.1e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 CATCCACCTGCTG 14  
|||||  
Db 13 CATCCACGTACTG 1

RESULT 83  
AX572382/c  
LOCUS AX572382 13 bp DNA linear PAT 29-NOV-2002  
DEFINITION Sequence 422 from Patent WO2055741.  
ACCESSION AX572382  
VERSION AX572382.1 GI:26004472  
KEYWORDS  
SOURCE Human immunodeficiency virus  
ORGANISM Human immunodeficiency virus  
Viruses; Retro-transcribing viruses; Retroviridae;  
Orthoretrovirinae; Lentivirus; Primate lentivirus group.  
REFERENCE 1  
AUTHORS de Smet,K. and Stuyver,L.  
TITLE Method for detection of drug-induced mutations in the hiv reverse transcriptase gene  
JOURNAL Patent: WO 02055741-A 422 18-JUL-2002;  
INNOGENETICS N.V. (BE)  
FEATURES  
source Location/Qualifiers  
1..13  
/organism="Human immunodeficiency virus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:12721"  
Query Match 33.8%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 1.1e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 CATCCACCTGCTG 14  
|||||||  
Db 13 CATCCACGTACTG 1  
RESULT 84  
A40478  
LOCUS A40478 14 bp DNA linear PAT 05-MAR-1997  
DEFINITION Sequence 15 from Patent WO9425578.  
ACCESSION A40478  
VERSION A40478.1 GI:2296513  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
unclassified sequences.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS  
TITLE ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))  
JOURNAL Patent: WO 9425578-A 15 10-NOV-1994;  
BIOGNOSTIK GES (DE)  
FEATURES  
source Location/Qualifiers  
1..14  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
Query Match 33.8%; Score 9.8; DB 1; Length 14;  
Best Local Similarity 84.6%; Pred. No. 1.2e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 10 TGCTGTGTGACCT 22  
|||||||  
Db 1 TGCTGTGTGTACT 13  
RESULT 85  
A88219  
LOCUS A88219 14 bp DNA linear PAT 22-JAN-2000  
DEFINITION Sequence 367 from Patent WO9833904.  
ACCESSION A88219  
VERSION A88219.1 GI:6736789  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
unclassified sequences.

REFERENCE 1 (bases 1 to 14)  
AUTHORS Brysch,W. and Schlingensiepen,K.  
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD  
JOURNAL Patent: WO 9833904-A 367 06-AUG-1998;  
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)  
FEATURES  
source Location/Qualifiers  
1..14  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
Query Match 33.8%; Score 9.8; DB 1; Length 14;  
Best Local Similarity 84.6%; Pred. No. 1.2e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 11 GCTGTGTGACCTG 23  
|||||||  
Db 1 GCTGTGTCAACAG 13  
RESULT 86  
A89005  
LOCUS A89005 14 bp DNA linear PAT 22-JAN-2000  
DEFINITION Sequence 1153 from Patent WO9833904.  
ACCESSION A89005  
VERSION A89005.1 GI:6737575  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
unclassified sequences.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Brysch,W. and Schlingensiepen,K.  
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD  
JOURNAL Patent: WO 9833904-A 1153 06-AUG-1998;  
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)  
FEATURES  
source Location/Qualifiers  
1..14  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
Query Match 33.8%; Score 9.8; DB 1; Length 14;  
Best Local Similarity 84.6%; Pred. No. 1.2e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 10 TGCTGTGTGACCT 22  
|||||||  
Db 1 TGCTGTGTGTACT 13  
RESULT 87  
A89321/c  
LOCUS A89321 14 bp DNA linear PAT 22-JAN-2000  
DEFINITION Sequence 1469 from Patent WO9833904.  
ACCESSION A89321  
VERSION A89321.1 GI:6737891  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
unclassified sequences.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Brysch,W. and Schlingensiepen,K.  
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD  
JOURNAL Patent: WO 9833904-A 1469 06-AUG-1998;  
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)  
FEATURES  
source Location/Qualifiers  
1..14  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
Query Match 33.8%; Score 9.8; DB 1; Length 14;  
Best Local Similarity 84.6%; Pred. No. 1.2e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 10 TGCTGTGTGACCT 22  
|||||||  
Db 1 TGCTGTGTGTACT 13



```

source      1..14
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match      33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 CTGTGTGACCTGG 24
    ||||| ||||| |||
Db 13 CTGCTGACATGG 1

RESULT 92
AR232758
LOCUS      AR232758              14 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 15 from patent US 6455689.
ACCESSION  AR232758
VERSION     AR232758.1 GI:27275096
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 14)
AUTHORS    Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
            Schlingensiepen,R. and Bogdahn,U.
TITLE      Antisense-oligonucleotides for transforming growth factor- .beta.
            (TGF- .beta.)
JOURNAL    Patent: US 6455689-A 15 24-SEP-2002;
            Biognostik Gesellschaft fur Biomolekulare Diagnostik mbH;
            Göttingen;
            EPX;
FEATURES    Location/Qualifiers
             source
              1..14
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match      33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 TGCTGTGTGACCT 22
    ||||| ||||| |||
Db 1 TGCTGTGTGTACT 13

RESULT 93
AX316374
LOCUS      AX316374              14 bp      DNA      linear      PAT 14-DEC-2001
DEFINITION Sequence 15 from Patent EP1160319.
ACCESSION  AX316374
VERSION     AX316374.1 GI:17899547
KEYWORDS    .
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1
AUTHORS     Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
            Schlingensiepen,R. and Bogdahn,U.
TITLE      Antisense-oligonucleotides for the treatment of immunosuppressive
            effects of transforming growth factor-beta (tgf-beta)
JOURNAL    Patent: EP 1160319-A 15 05-DEC-2001;
            BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
FEATURES    Location/Qualifiers
             source
              1..14
              /organism="unidentified"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32644"
              /note="Description of unknown: unknown"

Query Match      33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
```

```

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 TGCTGTGTGACCT 22
    ||||| ||||| |||
Db 1 TGCTGTGTGTACT 13

RESULT 94
AX572354/c
LOCUS      AX572354              14 bp      DNA      linear      PAT 29-NOV-2002
DEFINITION Sequence 394 from Patent WO02055741.
ACCESSION  AX572354
VERSION     AX572354.1 GI:26004444
KEYWORDS    .
SOURCE      Human immunodeficiency virus
ORGANISM    Human immunodeficiency virus
            Viruses; Retro-transcribing viruses; Retroviridae;
            Orthoretrovirinae; Lentivirus; Primate lentivirus group.
REFERENCE   1
AUTHORS     de Smet,K. and Stuyver,L.
TITLE      Method for detection of drug-induced mutations in the hiv reverse
            transcriptase gene
JOURNAL    Patent: WO 02055741-A 394 18-JUL-2002;
            INNOGENETICS N.V. (BE)
FEATURES    Location/Qualifiers
             source
              1..14
              /organism="Human immunodeficiency virus"
              /mol_type="unassigned DNA"
              /db_xref="taxon:12721"

Query Match      33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTG 14
    ||||| ||||| |||
Db 14 CATCCACGTACTG 2

RESULT 95
AX572358/c
LOCUS      AX572358              14 bp      DNA      linear      PAT 29-NOV-2002
DEFINITION Sequence 398 from Patent WO02055741.
ACCESSION  AX572358
VERSION     AX572358.1 GI:26004448
KEYWORDS    .
SOURCE      Human immunodeficiency virus
ORGANISM    Human immunodeficiency virus
            Viruses; Retro-transcribing viruses; Retroviridae;
            Orthoretrovirinae; Lentivirus; Primate lentivirus group.
REFERENCE   1
AUTHORS     de Smet,K. and Stuyver,L.
TITLE      Method for detection of drug-induced mutations in the hiv reverse
            transcriptase gene
JOURNAL    Patent: WO 02055741-A 398 18-JUL-2002;
            INNOGENETICS N.V. (BE)
FEATURES    Location/Qualifiers
             source
              1..14
              /organism="Human immunodeficiency virus"
              /mol_type="unassigned DNA"
              /db_xref="taxon:12721"

Query Match      33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTG 14
    ||||| ||||| |||
Db 14 CATCCACATACTG 2

RESULT 96
AX572372/c
```



LOCUS AX572372 14 bp DNA linear PAT 29-NOV-2002  
DEFINITION Sequence 412 from Patent WO02055741.  
ACCESSION AX572372  
VERSION AX572372.1 GI:26004462  
KEYWORDS  
SOURCE Human immunodeficiency virus  
ORGANISM Human immunodeficiency virus  
Viruses; Retro-transcribing viruses; Retroviridae;  
Orthoretrovirinae; Lentivirus; Primate lentivirus group.  
REFERENCE 1  
AUTHORS de Smet,K. and Stuyver,L.  
TITLE Method for detection of drug-induced mutations in the hiv reverse transcriptase gene  
JOURNAL Patent: WO 02055741-A 412 18-JUL-2002;  
INNOGENETICS N.V. (BE)  
FEATURES Location/Qualifiers  
source 1..14  
/organism="Human immunodeficiency virus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:12721"  
Query Match 33.8%; Score 9.8; DB 1; Length 14;  
Best Local Similarity 84.6%; Pred. No. 1.2e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 CATCCACCTGCTG 14  
|||||  
Db 14 CATCCACGTACTG 2  
RESULT 97  
AX572374/c  
LOCUS AX572374 14 bp DNA linear PAT 29-NOV-2002  
DEFINITION Sequence 414 from Patent WO02055741.  
ACCESSION AX572374  
VERSION AX572374.1 GI:26004464  
KEYWORDS  
SOURCE Human immunodeficiency virus  
ORGANISM Human immunodeficiency virus  
Viruses; Retro-transcribing viruses; Retroviridae;  
Orthoretrovirinae; Lentivirus; Primate lentivirus group.  
REFERENCE 1  
AUTHORS de Smet,K. and Stuyver,L.  
TITLE Method for detection of drug-induced mutations in the hiv reverse transcriptase gene  
JOURNAL Patent: WO 02055741-A 414 18-JUL-2002;  
INNOGENETICS N.V. (BE)  
FEATURES Location/Qualifiers  
source 1..14  
/organism="Human immunodeficiency virus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:12721"  
Query Match 33.8%; Score 9.8; DB 1; Length 14;  
Best Local Similarity 84.6%; Pred. No. 1.2e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 CATCCACCTGCTG 14  
|||||  
Db 14 CATCCACGTACTG 2  
RESULT 98  
AX572377/c  
LOCUS AX572377 14 bp DNA linear PAT 29-NOV-2002  
DEFINITION Sequence 417 from Patent WO02055741.  
ACCESSION AX572377  
VERSION AX572377.1 GI:26004467  
KEYWORDS  
SOURCE Human immunodeficiency virus  
ORGANISM Human immunodeficiency virus  
Viruses; Retro-transcribing viruses; Retroviridae;  
Orthoretrovirinae; Lentivirus; Primate lentivirus group.

REFERENCE 1  
AUTHORS de Smet,K. and Stuyver,L.  
TITLE Method for detection of drug-induced mutations in the hiv reverse transcriptase gene  
JOURNAL Patent: WO 02055741-A 417 18-JUL-2002;  
INNOGENETICS N.V. (BE)  
FEATURES Location/Qualifiers  
source 1..14  
/organism="Human immunodeficiency virus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:12721"  
Query Match 33.8%; Score 9.8; DB 1; Length 14;  
Best Local Similarity 84.6%; Pred. No. 1.2e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 CATCCACCTGCTG 14  
|||||  
Db 13 CATCCACATACTG 1  
RESULT 99  
AX572381/c  
LOCUS AX572381 14 bp DNA linear PAT 29-NOV-2002  
DEFINITION Sequence 421 from Patent WO02055741.  
ACCESSION AX572381  
VERSION AX572381.1 GI:26004471  
KEYWORDS  
SOURCE Human immunodeficiency virus  
ORGANISM Human immunodeficiency virus  
Viruses; Retro-transcribing viruses; Retroviridae;  
Orthoretrovirinae; Lentivirus; Primate lentivirus group.  
REFERENCE 1  
AUTHORS de Smet,K. and Stuyver,L.  
TITLE Method for detection of drug-induced mutations in the hiv reverse transcriptase gene  
JOURNAL Patent: WO 02055741-A 421 18-JUL-2002;  
INNOGENETICS N.V. (BE)  
FEATURES Location/Qualifiers  
source 1..14  
/organism="Human immunodeficiency virus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:12721"  
Query Match 33.8%; Score 9.8; DB 1; Length 14;  
Best Local Similarity 84.6%; Pred. No. 1.2e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 CATCCACCTGCTG 14  
|||||  
Db 13 CATCCACGTACTG 1  
RESULT 100  
BD124223/c  
LOCUS BD124223 11 bp DNA linear PAT 18-SEP-2002  
DEFINITION Compositions and method for healing wound.  
ACCESSION BD124223  
VERSION BD124223.1 GI:23219168  
KEYWORDS JP 2002503460-A/54.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchotheria; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 11)  
AUTHORS Katz,E.H.  
TITLE Compositions and method for healing wound  
JOURNAL Patent: JP 2002503460-A 54 05-FEB-2002;  
THE WISTAR INSTITUTE  
COMMENT OS Mus musculus (mouse)  
PN JP 2002503460-A/54  
PD 05-FEB-2002

PF 12-FEB-1999 JP 2000531545  
PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR  
28-SEP-1998 US 60/102051  
PI ELLEN HEBER KATZ  
PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC  
C12N5/00  
CC Compositions and method for healing wound  
FH Key Location/Qualifiers  
FT source 1. .11  
FT /organism='Mus musculus (mouse)'.  
  
FEATURES  
source  
Location/Qualifiers  
1. .11  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
  
Query Match 32.4%; Score 9.4; DB 1; Length 11;  
Best Local Similarity 90.9%; Pred. No. 1.1e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 13 TGTGTGACCTG 23  
|||||  
Db 11 TGTGTGGCCTG 1  
  
RESULT 101  
BD124438  
LOCUS BD124438 11 bp DNA linear PAT 18-SEP-2002  
DEFINITION Compositions and method for healing wound.  
ACCESSION BD124438  
VERSION BD124438.1 GI:23219383  
KEYWORDS JP 2002503460-A/269.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 11)  
Katz,E.H.  
REFERENCE  
AUTHORS Compositions and method for healing wound  
TITLE Patent: JP 2002503460-A 269 05-FEB-2002;  
JOURNAL THE WISTAR INSTITUTE  
COMMENT OS Mus musculus (mouse)  
PN JP 2002503460-A/269  
PD 05-FEB-2002  
PF 12-FEB-1999 JP 2000531545  
PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR  
28-SEP-1998 US 60/102051  
PI ELLEN HEBER KATZ  
PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC  
C12N5/00  
CC Compositions and method for healing wound  
FH Key Location/Qualifiers  
FT source 1. .11  
FT /organism='Mus musculus (mouse)'.  
  
FEATURES  
source  
Location/Qualifiers  
1. .11  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
  
Query Match 32.4%; Score 9.4; DB 1; Length 11;  
Best Local Similarity 90.9%; Pred. No. 1.1e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 CCACCTGCTGT 15  
|||||  
Db 1 CCACCTCCTGT 11  
  
RESULT 102  
CQ836739  
LOCUS CQ836739 11 bp DNA linear PAT 29-JUL-2004

DEFINITION Sequence 1797 from Patent WO2004059001.  
ACCESSION CQ836739  
VERSION CQ836739.1 GI:50836273  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
Conradt,M. and Hofmann,K.  
TITLE Method for determining markers of human facial skin  
JOURNAL Patent: WO 2004059001-A 1797 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source  
Location/Qualifiers  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
  
Query Match 32.4%; Score 9.4; DB 1; Length 11;  
Best Local Similarity 90.9%; Pred. No. 1.1e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 ATCCACCTGCT 13  
|||||  
Db 1 ATCCGCCTGCT 11  
  
RESULT 103  
CQ837792  
LOCUS CQ837792 11 bp DNA linear PAT 29-JUL-2004  
DEFINITION Sequence 2850 from Patent WO2004059001.  
ACCESSION CQ837792  
VERSION CQ837792.1 GI:50837326  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
Conradt,M. and Hofmann,K.  
TITLE Method for determining markers of human facial skin  
JOURNAL Patent: WO 2004059001-A 2850 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source  
Location/Qualifiers  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
  
Query Match 32.4%; Score 9.4; DB 1; Length 11;  
Best Local Similarity 90.9%; Pred. No. 1.1e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 CCACCTGCTGT 15  
|||||  
Db 1 CCACCTGCTTT 11  
  
RESULT 104  
CS058325  
LOCUS CS058325 11 bp DNA linear PAT 13-APR-2005  
DEFINITION Sequence 222 from Patent WO2005028671.  
ACCESSION CS058325  
VERSION CS058325.1 GI:62551508  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



```

RESULT 109
AX623763
LOCUS AX623763 11 bp DNA linear PAT 24-FEB-2003
DEFINITION Sequence 804 from Patent WO02053774.
ACCESSION AX623763
VERSION AX623763.1 GI:28451704
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 804 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 32.4%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 TGTGACCTGGT 25
|||||
Db 1 TGTTACCTGGT 11

RESULT 110
AX625616
LOCUS AX625616 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2657 from Patent WO02053774.
ACCESSION AX625616
VERSION AX625616.1 GI:28453557
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2657 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 32.4%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 TGTGACCTGGT 25
|||||
Db 1 TGTTACCTGGT 11

RESULT 111
AX625941
LOCUS AX625941 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2982 from Patent WO02053774.
ACCESSION AX625941
VERSION AX625941.1 GI:28453979
KEYWORDS
```

```

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2982 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 32.4%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATCCACCTGCT 13
|||||
Db 1 ATCCGCCTGCT 11

RESULT 112
AX627200
LOCUS AX627200 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 4241 from Patent WO02053774.
ACCESSION AX627200
VERSION AX627200.1 GI:28455238
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4241 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 32.4%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ACCTGCTGTGT 17
|||||
Db 1 ACTTGCTGTGT 11

RESULT 113
AX627837
LOCUS AX627837 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 4878 from Patent WO02053774.
ACCESSION AX627837
VERSION AX627837.1 GI:28455875
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4878 11-JUL-2002;
```





Best Local Simitarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 GTGTGACCTGG 24  
| | | | | | | | | |  
Db 1 GTGCGACCTGG 11

RESULT 118  
BD248273  
LOCUS BD248273 12 bp DNA linear PAT 17-JUL-2003  
DEFINITION Short-chain oligonucleotide for inhibiting VEGF expression.  
ACCESSION BD248273  
VERSION BD248273.1 GI:33058043  
KEYWORDS JP 2002524038-A/92.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Uhlmann,E., Peyman,A., Bitonti,A. and Woessner,R.  
TITLE Short-chain oligonucleotide for inhibiting VEGF expression  
JOURNAL Patent: JP 2002524038-A 92 06-AUG-2002;  
COMMENT AVENTIS PHARMA DEUTSCHLAND GMBH  
OS Artificial Sequence  
PN JP 2002524038-A/92  
PD 06-AUG-2002  
PF 29-JUL-1999 JP 2000563768  
PR 07-AUG-1998 EP 98114853.9  
PI EUGEN UHLMANN,ANUSCHIRWAN PEYMAN,ALAN BITONTI,RICHARD WOESSNER  
PC C12N15/09,A61K31/711,A61K31/7115,A61K31/712,A61K31/7125 PC  
A61K48/00,A61P9/00,  
PC A61P13/12,A61P17/16,A61P27/02,A61P29/00,A61P35/00,A61P43/00,  
PC C12N15/00  
CC Description of Artificial Sequence: Antisense FH Key  
Location/Qualifiers  
FT source  
FT 1. .12  
Location/Qualifiers  
/organism='Artificial Sequence'.  
1. .12  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

Query Match 32.4%; Score 9.4; DB 1; Length 12;  
Best Local Simitarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 GTGTGACCTGG 24  
| | | | | | | | | |  
Db 1 GTGTGACCCGG 11

RESULT 119  
I07725  
LOCUS I07725 12 bp DNA linear PAT 02-DEC-1994  
DEFINITION Sequence 30 from Patent EP 0364255.  
ACCESSION I07725  
VERSION I07725.1 GI:589732  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Caskey,C.T., Chamberlain,J.S., Gibbs,R.A., Rainer,J.E. and Nguyen,P.N.  
TITLE Multiplex genomic DNA amplification for deletion detection  
JOURNAL Patent: EP 0364255-A2 30 18-APR-1990;  
FEATURES Location/Qualifiers  
source 1. .12  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 32.4%; Score 9.4; DB 1; Length 12;

Best Local Simitarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 ACCTGGTAAAT 29  
| | | | | | | | | |  
Db 1 ACCTGGAAAT 11

RESULT 120  
BD023257  
LOCUS BD023257 12 bp DNA linear PAT 27-AUG-2002  
DEFINITION Method for detecting abnormality in chromosome.  
ACCESSION BD023257  
VERSION BD023257.1 GI:22564480  
KEYWORDS JP 2001505428-A/2.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Parisgard,N. and Hokurando,P.  
TITLE Method for detecting abnormality in chromosome  
JOURNAL Patent: JP 2001505428-A 2 24-APR-2001;  
COMMENT NEILLS PARISGARD  
PN JP 2001505428-A/2  
PD 24-APR-2001  
PF 08-DEC-1997 JP 1998525090  
PI NEILLS PARISGARD,PATER HOKURANDO  
PC C12N15/09,C12Q1/68,G01N33/50,C12N15/00  
CC Strandedness: Single;  
CC Topology: Linear;  
CC /desc = 'DNA (synthetic)'  
FH Key Location/Qualifiers  
1. .12  
Location/Qualifiers  
source  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

Query Match 32.4%; Score 9.4; DB 1; Length 12;  
Best Local Simitarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTGCTGTGTGA 19  
| | | | | | | | | |  
Db 1 CTGCTGGGTGA 11

RESULT 121  
I43005  
LOCUS I43005 13 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 27 from patent US 5631115.  
ACCESSION I43005  
VERSION I43005.1 GI:2468249  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Ohtsuka,E. and Koizumi,M.  
TITLE Looped, hairpin ribozyme  
JOURNAL Patent: US 5631115-A 27 20-MAY-1997;  
FEATURES Location/Qualifiers  
source 1. .13  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 32.4%; Score 9.4; DB 1; Length 13;  
Best Local Simitarity 90.9%; Pred. No. 1.3e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTGCTGTGTGA 19

Db

3 CTGTTGTGTGA 13

|||||

RESULT 122

AR363773

LOCUS AR363773 13 bp DNA linear PAT 03-SEP-2003

DEFINITION Sequence 13 from patent US 5225537.

AR363773

ACCESSION AR363773

VERSION AR363773.1 GI:34425778

KEYWORDS

SOURCE

Unknown.

ORGANISM

Unknown.

REFERENCE

1 (bases 1 to 13)

AUTHORS Foster,D.C.

TITLE Methods for producing hybrid phospholipid-binding proteins

JOURNAL Patent: US 522537-A 13 06-JUL-1993;

ZymoGenetics, Inc.; Seattle, WA

FEATURES

source

1. .13

/organism="unknown"

/mol\_type="genomic DNA"

Query Match 32.4%; Score 9.4; DB 1; Length 13;

Best Local Similarity 90.9%; Pred. No. 1.3e+02;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 17 TGACCTGGTAA 27

|||||

Db 3 TGACTTGGTAA 13

RESULT 123

BD239019

LOCUS BD239019 10 bp DNA linear PAT 17-JUL-2003

DEFINITION Preparation and use of superior vaccines.

BD239019

ACCESSION BD239019

VERSION BD239019.1 GI:33048789

KEYWORDS JP 2002534056-A/437.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 10)

Robertson,B.L. and Shankara,S.

Preparation and use of superior vaccines

Patent: JP 2002534056-A 437 15-OCT-2002;

GENZYME CORP

OS Homo sapiens (human)

PN JP 2002534056-A/437

PD 15-OCT-2002

PF 18-JUN-1999 JP 2000554749

PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR

19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR

19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR

19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR

19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR

19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR

19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR

19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR

19-JUN-1998 US 60/090044,19-JUN-1998 US 60/090036 PR

19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089844 PR

19-JUN-1998 US 60/089994,19-JUN-1998 US 60/089833 PR

19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR

19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR

19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR

08-DEC-1998 US 60/111715

PI BRUCE L ROBERTS,SRINIVAS SHANKARA

PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC C12N1/19,

PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC

G01N37/00,

PC C12N15/00,C12N5/00,C12N15/00

CC Preparation and use of superior vaccines

FH Key Location/Qualifiers

FT source 1. .10

/organism='Homo sapiens (human)'

FEATURES

source

1. .10

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

Query Match 31.0%; Score 9; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCTGCT 13

|||||

Db 1 CCACCTGCT 9

RESULT 124

BD239139

LOCUS BD239139 10 bp DNA linear PAT 17-JUL-2003

DEFINITION Preparation and use of superior vaccines.

BD239139

ACCESSION BD239139

VERSION BD239139.1 GI:33048909

KEYWORDS JP 2002534056-A/557.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 10)

Robertson,B.L. and Shankara,S.

Preparation and use of superior vaccines

Patent: JP 2002534056-A 557 15-OCT-2002;

GENZYME CORP

OS Homo sapiens (human)

PN JP 2002534056-A/557

PD 15-OCT-2002

PF 18-JUN-1999 JP 2000554749

PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR

19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR

19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR

19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR

19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR

19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR

19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR

19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR

19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR

19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR

19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR

19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR

19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR

19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR

08-DEC-1998 US 60/111715

PI BRUCE L ROBERTS,SRINIVAS SHANKARA

PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC C12N1/19,

PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC

Query Match 31.0%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TGCTGTGTG 18  
Db 1 TGCTGTGTG 9

RESULT 125  
BD240212  
LOCUS BD240212 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD240212  
VERSION BD240212.1 GI:33049982  
KEYWORDS JP 2002534056-A/1630.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.  
1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 1630 15-OCT-2002;  
GENZYME CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002534056-A/1630  
PD 15-OCT-2002  
PF 18-JUN-1999 JP 2000554749  
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR  
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR  
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR  
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR  
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR  
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR  
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR  
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR  
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR  
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR  
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR  
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR  
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR  
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR  
08-DEC-1998 US 60/111715  
PI BRUCE L ROBERTS,SRINIVAS SHANKARA  
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC  
C12N1/19,  
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC  
G01N37/00,  
PC C12N15/00,C12N5/00,C12N15/00  
CC Preparation and use of superior vaccines  
FT Key Location/Qualifiers  
FT source 1..10  
FT /organism='Homo sapiens (human)'.  
FEATURES  
source  
1..10  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

Query Match 31.0%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CTGTGTGAC 20  
Db 1 CTGTGTGAC 9

RESULT 126  
CQ766709/c  
LOCUS CQ766709 10 bp DNA linear PAT 03-MAR-2004

DEFINITION Sequence 65 from Patent WO2004005541.  
ACCESSION CQ766709  
VERSION CQ766709.1 GI:44908939  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS van Broeckhoven,C., de Jonghe,P., Timmerman,V. and Verhoeven,K.  
TITLE Diagnostic tests for the detection of peripheral neuropathy  
JOURNAL Patent: WO 2004005541-A 65 15-JAN-2004;  
Vlaams Interuniversitair Instituut voor Biotechnologie vz; w. (BE)  
FEATURES  
source  
1..10  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="3-intron/exon, exon 4, gene RAB7"

Query Match 31.0%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCACCTGCT 13  
Db 9 CCACCTGCT 1

RESULT 127  
CQ766752/c  
LOCUS CQ766752 10 bp DNA linear PAT 03-MAR-2004  
DEFINITION Sequence 108 from Patent WO2004005541.  
ACCESSION CQ766752  
VERSION CQ766752.1 GI:44908982  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS van Broeckhoven,C., de Jonghe,P., Timmerman,V. and Verhoeven,K.  
TITLE Diagnostic tests for the detection of peripheral neuropathy  
JOURNAL Patent: WO 2004005541-A 108 15-JAN-2004;  
Vlaams Interuniversitair Instituut voor Biotechnologie vz; w. (BE)  
FEATURES  
source  
1..10  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="5-intron/exon, exon 8"

Query Match 31.0%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCTGCTGTG 16  
Db 9 CCTGCTGTG 1

RESULT 128  
CQ828944  
LOCUS CQ828944 10 bp DNA linear PAT 05-JUL-2004  
DEFINITION Sequence 662 from Patent WO2004053120.  
ACCESSION CQ828944  
VERSION CQ828944.1 GI:49732427  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.  
REFERENCE 1  
AUTHORS Weihe,E., Bieller,A. and Schaefer,M.K.



TITLE  
 JOURNAL  
 Regulatory elements in the 5' region of the vr1 gene  
 Patent: WO 2004053120-A 662 24-JUN-2004;  
 Gruenenthal GmbH (DE)  
 FEATURES  
 source  
 1. .10  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 /note="V\$MYOD Q6"  
 Query Match  
 Best Local Similarity 31.0%; Score 9; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 TCCACCTGC 12  
 |||||  
 Db 1 TCCACCTGC 9  
 RESULT 129  
 AX152110/c  
 LOCUS AX152110 10 bp DNA linear PAT 22-JUN-2001  
 DEFINITION Sequence 25 from Patent WO0138577.  
 ACCESSION AX152110  
 VERSION AX152110.1 GI:14533761  
 KEYWORDS .  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.  
 TITLE Human transcriptomes  
 JOURNAL Patent: WO 0138577-A 25 31-MAY-2001;  
 The Johns Hopkins University (US)  
 FEATURES  
 source  
 1. .10  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 Query Match  
 Best Local Similarity 31.0%; Score 9; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 16 GTGACCTGG 24  
 |||||  
 Db 10 GTGACCTGG 2  
 RESULT 130  
 BD007825  
 LOCUS BD007825 10 bp DNA linear PAT 31-JAN-2002  
 DEFINITION LPS activated human monocyte expressing genes.  
 ACCESSION BD007825  
 VERSION BD007825.1 GI:18636198  
 KEYWORDS JP 2001069993-A/101.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 10)  
 AUTHORS Matsushima,K., Hashimoto,S. and Suzuki,T.  
 TITLE LPS activated human monocyte expressing genes  
 JOURNAL Patent: JP 2001069993-A 101 21-MAR-2001;  
 JAPAN SCIENCE AND TECHNOLOGY CORP  
 COMMENT OS Homo sapiens (human)  
 PN JP 2001069993-A/101  
 PD 21-MAR-2001  
 PF 28-APR-2000 JP 2000131079  
 PR

PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC  
 C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC  
 A61P29/00,  
 PC A61P31/00,C12P21/08,C12N15/00  
 CC  
 FH Key Location/Qualifiers  
 FT source 1. .10  
 FT /organism='Homo sapiens (human)'.  
 FEATURES  
 source  
 Location/Qualifiers  
 1. .10  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 Query Match  
 Best Local Similarity 31.0%; Score 9; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 14 GTGTGACCT 22  
 |||||  
 Db 2 GTGTGACCT 10  
 RESULT 131  
 AR074494/c  
 LOCUS AR074494 11 bp DNA linear PAT 28-AUG-2000  
 DEFINITION Sequence 73 from patent US 5955075.  
 ACCESSION AR074494  
 VERSION AR074494.1 GI:10001249  
 KEYWORDS .  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 REFERENCE 1 (bases 1 to 11)  
 AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
 TITLE Method of inhibiting tumor growth using antibodies to MN protein  
 JOURNAL Patent: US 5955075-A 73 21-SEP-1999;  
 FEATURES  
 source  
 1. .11  
 /organism="unknown"  
 /mol\_type="unassigned DNA"  
 Query Match  
 Best Local Similarity 31.0%; Score 9; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 CCACCTGCT 13  
 |||||  
 Db 9 CCACCTGCT 1  
 RESULT 132  
 AR081174/c  
 LOCUS AR081174 11 bp DNA linear PAT 31-AUG-2000  
 DEFINITION Sequence 73 from patent US 5972353.  
 ACCESSION AR081174  
 VERSION AR081174.1 GI:10007902  
 KEYWORDS .  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 REFERENCE 1 (bases 1 to 11)  
 AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
 TITLE MN proteins, polypeptides, fusion proteins and fusion polypeptides  
 JOURNAL Patent: US 5972353-A 73 26-OCT-1999;  
 FEATURES  
 source  
 Location/Qualifiers  
 1. .11  
 /organism="unknown"  
 /mol\_type="unassigned DNA"  
 Query Match  
 Best Local Similarity 31.0%; Score 9; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



RESULT 138  
AR171617/c  
LOCUS AR171617 11 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 73 from patent US 6297051.  
ACCESSION AR171617  
VERSION AR171617.1 GI:17910567  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 11)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE MN gene and protein  
JOURNAL Patent: US 6297051-A 73 02-OCT-2001;  
FEATURES  
    source  
        1..11  
            /organism="unknown"  
            /mol\_type="unassigned DNA"  
Query Match 31.0%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 CCACCTGCT 13  
    |||||  
Db 9 CCACCTGCT 1  
RESULT 139  
BD080109  
LOCUS BD080109 11 bp DNA linear PAT 27-AUG-2002  
DEFINITION Method of identifying cell- or tissue-specific artificial  
transcriptional regulatory region.  
ACCESSION BD080109  
VERSION BD080109.1 GI:22625712  
KEYWORDS JP 2001509395-A/3.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 11)  
AUTHORS Schwartz,R.J., Eastman,E.M., Li,X. and Nordstrom,J.  
TITLE Method of identifying cell- or tissue-specific artificial  
transcriptional regulatory region  
JOURNAL Patent: JP 2001509395-A 3 24-JUL-2001;  
VALENTIS INC  
COMMENT OS Artificial Sequence  
PN JP 2001509395-A/3  
PD 24-JUL-2001  
PF 14-JUL-1998 JP 2000502228  
PR 14-JUL-1997 US 60/052403  
PI ROBERT J SCHWARTZ,ERIC M EASTMAN,XUYANG LI,JEFF NORDSTROM PC  
C12Q1/68,C12N15/09,C12N15/00  
CC Method of identifying cell- or tissue-specific artificial CC  
transcriptional  
CC regulatory region  
FH Key Location/Qualifiers  
FT source 1..11  
    /organism='Artificial Sequence'.  
FEATURES  
    source  
        1..11  
            /organism="synthetic construct"  
            /mol\_type="genomic DNA"  
            /db\_xref="taxon:32630"  
Query Match 31.0%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CACCTGCTG 14  
    |||||  
Db 3 CACCTGCTG 11

RESULT 140  
BD243207/c  
LOCUS BD243207 11 bp DNA linear PAT 17-JUL-2003  
DEFINITION MN gene and protein.  
ACCESSION BD243207  
VERSION BD243207.1 GI:33052977  
KEYWORDS JP 2002528085-A/56.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 11)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE MN gene and protein  
JOURNAL Patent: JP 2002528085-A 56 03-SEP-2002;  
INSTITUTE OF VIROLOGY  
COMMENT OS Homo sapiens (human)  
PN JP 2002528085-A/56  
PD 03-SEP-2002  
PF 22-OCT-1999 JP 2000578465  
PR 23-OCT-1998 US 09/177776,23-OCT-1998 US 09/178115 PI  
JAN ZAVADA,SILVIA PASTOREKOVA,JAROMIR PASTOREK PC  
C12N15/09,A61K38/00,A61K39/395,A61K48/00,A61P35/00, PC  
C07K14/47,  
PC C12Q1/02,G01N33/566//(C12Q1/02,C12R1:91),C12N15/00,A61K37/02  
CC MN gene and protein  
FH Key Location/Qualifiers  
FT source 1..11  
    /organism='Homo sapiens (human)'.  
FEATURES  
    source  
        1..11  
            /organism="Homo sapiens"  
            /mol\_type="genomic DNA"  
            /db\_xref="taxon:9606"  
Query Match 31.0%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 CCACCTGCT 13  
    |||||  
Db 9 CCACCTGCT 1  
RESULT 141  
CS058646  
LOCUS CS058646 11 bp DNA linear PAT 13-APR-2005  
DEFINITION Sequence 543 from Patent WO2005028671.  
ACCESSION CS058646  
VERSION CS058646.1 GI:62551829  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and  
Kessler-Becker,D.  
TITLE Method for determining hair cycle markers  
JOURNAL Patent: WO 2005028671-A 543 31-MAR-2005;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
    source  
        1..11  
            /organism="Homo sapiens"  
            /mol\_type="unassigned DNA"  
            /db\_xref="taxon:9606"  
Query Match 31.0%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 TGCTGTGTG 18  
Db 1 TGCTGTGTG 9

RESULT 142  
AR214824

LOCUS AR214824 11 bp DNA linear PAT 25-SEP-2002  
DEFINITION Sequence 3 from patent US 6410228.  
ACCESSION AR214824  
VERSION AR214824.1 GI:23312758  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 11)  
AUTHORS Schwartz,R.J., Eastman,E.M., Li,X. and Nordstrom,J.  
TITLE Method for the identification of synthetic cell- or tissue-specific transcriptional regulatory regions  
JOURNAL Patent: US 6410228-A 3 25-JUN-2002;  
Baylor College of Medicine and Valentis, Inc.; Houston, TX

FEATURES  
source Location/Qualifiers  
1..11  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 31.0%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CACCTGCTG 14  
Db 3 CACCTGCTG 11

RESULT 143  
AR569645/c

LOCUS AR569645 11 bp DNA linear PAT 14-DEC-2004  
DEFINITION Sequence 73 from patent US 6770438.  
ACCESSION AR569645  
VERSION AR569645.1 GI:56570274  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 11)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE MN gene and protein  
JOURNAL Patent: US 6770438-A 73 03-AUG-2004;  
Institute of Virology, Slovak Academy of Sciences; Bratislava; CZX;

FEATURES  
source Location/Qualifiers  
1..11  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 31.0%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCTGCT 13  
Db 9 CCACCTGCT 1

RESULT 144  
AX393112/c

LOCUS AX393112 11 bp DNA linear PAT 23-MAR-2002  
DEFINITION Sequence 42 from Patent WO0210217.  
ACCESSION AX393112  
VERSION AX393112.1 GI:19701162  
KEYWORDS  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS St Croix,B., Kinzler,K.W. and Vogelstein,B.  
TITLE Endothelial cell expression patterns  
JOURNAL Patent: WO 0210217-A 42 07-FEB-2002;  
The Johns Hopkins University (US)

FEATURES  
source Location/Qualifiers  
1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 31.0%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GCTGTGTGA 19  
Db 10 GCTGTGTGA 2

RESULT 145  
AX470507/c

LOCUS AX470507 11 bp DNA linear PAT 09-AUG-2002  
DEFINITION Sequence 84 from Patent WO02053773.  
ACCESSION AX470507  
VERSION AX470507.1 GI:22205632  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1  
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.  
TITLE Method for determining skin stress or skin ageing in vitro  
JOURNAL Patent: WO 02053773-A 84 11-JUL-2002;  
HENKEL KGAA (DE)

FEATURES  
source Location/Qualifiers  
1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 31.0%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GCTGTGTGA 19  
Db 10 GCTGTGTGA 2

RESULT 146  
AX623057/c

LOCUS AX623057 11 bp DNA linear PAT 24-FEB-2003  
DEFINITION Sequence 98 from Patent WO02053774.  
ACCESSION AX623057  
VERSION AX623057.1 GI:28450998  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 98 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)



|                       |                                                                                                                                                |                                 |                                 |
|-----------------------|------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------|---------------------------------|
| FEATURES              |                                                                                                                                                | Location/Qualifiers             |                                 |
| source                | 1. .11                                                                                                                                         | /organism="Homo sapiens"        |                                 |
|                       |                                                                                                                                                | /mol_type="unassigned DNA"      |                                 |
|                       |                                                                                                                                                | /db_xref="taxon:9606"           |                                 |
| Query Match           |                                                                                                                                                |                                 |                                 |
| Best Local Similarity | 31.0%;                                                                                                                                         | Score 9;                        | DB 1; Length 11;                |
| Matches               | 9;                                                                                                                                             | Conservative 0;                 | Mismatches 0; Indels 0; Gaps 0; |
| QY 11 GCTGTGTGA 19    |                                                                                                                                                |                                 |                                 |
| Db 10 GCTGTGTGA 2     |                                                                                                                                                |                                 |                                 |
| RESULT 147            |                                                                                                                                                |                                 |                                 |
| AX630236              | LOCUS AX630236 11 bp DNA linear PAT 21-FEB-2003                                                                                                |                                 |                                 |
| DEFINITION            | Sequence 7277 from Patent WO02053774.                                                                                                          |                                 |                                 |
| ACCESSION             | AX630236                                                                                                                                       |                                 |                                 |
| VERSION               | AX630236.1 GI:28458274                                                                                                                         |                                 |                                 |
| KEYWORDS              | .                                                                                                                                              |                                 |                                 |
| SOURCE                | Homo sapiens (human)                                                                                                                           |                                 |                                 |
| ORGANISM              | Homo sapiens                                                                                                                                   |                                 |                                 |
|                       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. |                                 |                                 |
| REFERENCE             | 1                                                                                                                                              |                                 |                                 |
| AUTHORS               | Petersohn,D., Conradt,M. and Hofmann,K.                                                                                                        |                                 |                                 |
| TITLE                 | Method for determining homeostasis of the skin                                                                                                 |                                 |                                 |
| JOURNAL               | Patent: WO 02053774-A 7277 11-JUL-2002;                                                                                                        |                                 |                                 |
|                       | Henkel Kommanditgesellschaft auf Aktien (DE)                                                                                                   |                                 |                                 |
| FEATURES              | Location/Qualifiers                                                                                                                            |                                 |                                 |
| source                | 1. .11                                                                                                                                         | /organism="Homo sapiens"        |                                 |
|                       |                                                                                                                                                | /mol_type="unassigned DNA"      |                                 |
|                       |                                                                                                                                                | /db_xref="taxon:9606"           |                                 |
| Query Match           |                                                                                                                                                |                                 |                                 |
| Best Local Similarity | 31.0%;                                                                                                                                         | Score 9;                        | DB 1; Length 11;                |
| Matches               | 9;                                                                                                                                             | Conservative 0;                 | Mismatches 0; Indels 0; Gaps 0; |
| QY 10 TGCTGTGTG 18    |                                                                                                                                                |                                 |                                 |
| Db 1 TGCTGTGTG 9      |                                                                                                                                                |                                 |                                 |
| RESULT 148            |                                                                                                                                                |                                 |                                 |
| AX630478/c            | LOCUS AX630478 11 bp DNA linear PAT 21-FEB-2003                                                                                                |                                 |                                 |
| DEFINITION            | Sequence 7519 from Patent WO02053774.                                                                                                          |                                 |                                 |
| ACCESSION             | AX630478                                                                                                                                       |                                 |                                 |
| VERSION               | AX630478.1 GI:28458516                                                                                                                         |                                 |                                 |
| KEYWORDS              | .                                                                                                                                              |                                 |                                 |
| SOURCE                | Homo sapiens (human)                                                                                                                           |                                 |                                 |
| ORGANISM              | Homo sapiens                                                                                                                                   |                                 |                                 |
|                       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. |                                 |                                 |
| REFERENCE             | 1                                                                                                                                              |                                 |                                 |
| AUTHORS               | Petersohn,D., Conradt,M. and Hofmann,K.                                                                                                        |                                 |                                 |
| TITLE                 | Method for determining homeostasis of the skin                                                                                                 |                                 |                                 |
| JOURNAL               | Patent: WO 02053774-A 7519 11-JUL-2002;                                                                                                        |                                 |                                 |
|                       | Henkel Kommanditgesellschaft auf Aktien (DE)                                                                                                   |                                 |                                 |
| FEATURES              | Location/Qualifiers                                                                                                                            |                                 |                                 |
| source                | 1. .11                                                                                                                                         | /organism="Homo sapiens"        |                                 |
|                       |                                                                                                                                                | /mol_type="unassigned DNA"      |                                 |
|                       |                                                                                                                                                | /db_xref="taxon:9606"           |                                 |
| Query Match           |                                                                                                                                                |                                 |                                 |
| Best Local Similarity | 31.0%;                                                                                                                                         | Score 9;                        | DB 1; Length 11;                |
| Matches               | 9;                                                                                                                                             | Conservative 0;                 | Mismatches 0; Indels 0; Gaps 0; |
| QY 11 GCTGTGTGA 19    |                                                                                                                                                |                                 |                                 |
| Db 10 GCTGTGTGA 2     |                                                                                                                                                |                                 |                                 |
| RESULT 149            |                                                                                                                                                |                                 |                                 |
| AX395393              | LOCUS AX395393 12 bp DNA linear PAT 18-MAY-2002                                                                                                |                                 |                                 |
| DEFINITION            | Sequence 30 from Patent WO0206495.                                                                                                             |                                 |                                 |
| ACCESSION             | AX395393                                                                                                                                       |                                 |                                 |
| VERSION               | AX395393.1 GI:21066368                                                                                                                         |                                 |                                 |
| KEYWORDS              | .                                                                                                                                              |                                 |                                 |
| SOURCE                | synthetic construct                                                                                                                            |                                 |                                 |
| ORGANISM              | synthetic construct                                                                                                                            |                                 |                                 |
|                       | other sequences; artificial sequences.                                                                                                         |                                 |                                 |
| REFERENCE             | 1                                                                                                                                              |                                 |                                 |
| AUTHORS               | Chamberlain,J.S. and Hauschka,S.D.                                                                                                             |                                 |                                 |
| TITLE                 | Mutant muscle-specific enhancers                                                                                                               |                                 |                                 |
| JOURNAL               | Patent: WO 0206495-A 30 24-JAN-2002;                                                                                                           |                                 |                                 |
|                       | THE REGENTS OF THE UNIVERSITY OF MICHIGAN (US)                                                                                                 |                                 |                                 |
| FEATURES              | Location/Qualifiers                                                                                                                            |                                 |                                 |
| source                | 1. .12                                                                                                                                         | /organism="synthetic construct" |                                 |
|                       |                                                                                                                                                | /mol_type="unassigned DNA"      |                                 |
|                       |                                                                                                                                                | /db_xref="taxon:32630"          |                                 |
|                       |                                                                                                                                                | /note="Synthetic"               |                                 |
| Query Match           |                                                                                                                                                |                                 |                                 |
| Best Local Similarity | 31.0%;                                                                                                                                         | Score 9;                        | DB 1; Length 12;                |
| Matches               | 9;                                                                                                                                             | Conservative 0;                 | Mismatches 0; Indels 0; Gaps 0; |
| QY 6 CACCTGCTG 14     |                                                                                                                                                |                                 |                                 |
| Db 3 CACCTGCTG 11     |                                                                                                                                                |                                 |                                 |
| RESULT 150            |                                                                                                                                                |                                 |                                 |
| AR014245              | LOCUS AR014245 12 bp DNA linear PAT 05-DEC-1998                                                                                                |                                 |                                 |
| DEFINITION            | Sequence 9 from patent US 5773278.                                                                                                             |                                 |                                 |
| ACCESSION             | AR014245                                                                                                                                       |                                 |                                 |
| VERSION               | AR014245.1 GI:3971699                                                                                                                          |                                 |                                 |
| KEYWORDS              | .                                                                                                                                              |                                 |                                 |
| SOURCE                | Unknown.                                                                                                                                       |                                 |                                 |
| ORGANISM              | Unknown.                                                                                                                                       |                                 |                                 |
|                       | Unclassified.                                                                                                                                  |                                 |                                 |
| REFERENCE             | 1 (bases 1 to 12)                                                                                                                              |                                 |                                 |
| AUTHORS               | Schuchman,E.H. and Desnick,R.J.                                                                                                                |                                 |                                 |
| TITLE                 | Acid sphingomyelinase gene                                                                                                                     |                                 |                                 |
| JOURNAL               | Patent: US 5773278-A 9 30-JUN-1998;                                                                                                            |                                 |                                 |
| FEATURES              | Location/Qualifiers                                                                                                                            |                                 |                                 |
| source                | 1. .12                                                                                                                                         | /organism="unknown"             |                                 |
|                       |                                                                                                                                                | /mol_type="unassigned DNA"      |                                 |
| Query Match           |                                                                                                                                                |                                 |                                 |
| Best Local Similarity | 30.3%;                                                                                                                                         | Score 8.8;                      | DB 1; Length 12;                |
| Matches               | 10;                                                                                                                                            | Conservative 0;                 | Mismatches 2; Indels 0; Gaps 0; |
| QY 12 CTGTGTGACCTG 23 |                                                                                                                                                |                                 |                                 |
| Db 1 CTGTGCCACCTG 12  |                                                                                                                                                |                                 |                                 |
| RESULT 151            |                                                                                                                                                |                                 |                                 |
| AR038696/c            | LOCUS AR038696 12 bp DNA linear PAT 29-SEP-1999                                                                                                |                                 |                                 |
| DEFINITION            | Sequence 30 from patent US 5807678.                                                                                                            |                                 |                                 |
| ACCESSION             | AR038696                                                                                                                                       |                                 |                                 |
| VERSION               | AR038696.1 GI:5958059                                                                                                                          |                                 |                                 |
| KEYWORDS              | .                                                                                                                                              |                                 |                                 |
| SOURCE                | Unknown.                                                                                                                                       |                                 |                                 |

|                       |                                                                                                                        |  |  |  |  |  |  |  |  |  |
|-----------------------|------------------------------------------------------------------------------------------------------------------------|--|--|--|--|--|--|--|--|--|
| ORGANISM              | Unknown.                                                                                                               |  |  |  |  |  |  |  |  |  |
| REFERENCE             | Unclassified.                                                                                                          |  |  |  |  |  |  |  |  |  |
| AUTHORS               | 1 (bases 1 to 12)                                                                                                      |  |  |  |  |  |  |  |  |  |
| TITLE                 | Miller,W.L., Lin,D. and Strauss,J.F. III.                                                                              |  |  |  |  |  |  |  |  |  |
| JOURNAL               | Identification of gene mutations associated with congenital lipoid adrenal hyperplasia                                 |  |  |  |  |  |  |  |  |  |
| FEATURES              | Patent: US 5807678-A 30 15-SEP-1998;                                                                                   |  |  |  |  |  |  |  |  |  |
| source                | Location/Qualifiers                                                                                                    |  |  |  |  |  |  |  |  |  |
|                       | 1. .12                                                                                                                 |  |  |  |  |  |  |  |  |  |
|                       | /organism="unknown"                                                                                                    |  |  |  |  |  |  |  |  |  |
|                       | /mol_type="unassigned DNA"                                                                                             |  |  |  |  |  |  |  |  |  |
| Query Match           | 30.3%; Score 8.8; DB 1; Length 12;                                                                                     |  |  |  |  |  |  |  |  |  |
| Best Local Similarity | 83.3%; Pred. No. 1.5e+02;                                                                                              |  |  |  |  |  |  |  |  |  |
| Matches               | 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;                                                                    |  |  |  |  |  |  |  |  |  |
| QY                    | 18 GACCTGGTAAAT 29                                                                                                     |  |  |  |  |  |  |  |  |  |
| Db                    | 12 GACCTGGTTGAT 1                                                                                                      |  |  |  |  |  |  |  |  |  |
| RESULT 152            | AR058492                                                                                                               |  |  |  |  |  |  |  |  |  |
| LOCUS                 | AR058492                                                                                                               |  |  |  |  |  |  |  |  |  |
| DEFINITION            | Sequence 69 from patent US 5837832.                                                                                    |  |  |  |  |  |  |  |  |  |
| ACCESSION             | AR058492                                                                                                               |  |  |  |  |  |  |  |  |  |
| VERSION               | AR058492.1 GI:5984069                                                                                                  |  |  |  |  |  |  |  |  |  |
| KEYWORDS              |                                                                                                                        |  |  |  |  |  |  |  |  |  |
| SOURCE                | Unknown.                                                                                                               |  |  |  |  |  |  |  |  |  |
| ORGANISM              | Unknown.                                                                                                               |  |  |  |  |  |  |  |  |  |
| REFERENCE             | 1 (bases 1 to 12)                                                                                                      |  |  |  |  |  |  |  |  |  |
| AUTHORS               | Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A., Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L. |  |  |  |  |  |  |  |  |  |
| TITLE                 | Arrays of nucleic acid probes on biological chips                                                                      |  |  |  |  |  |  |  |  |  |
| JOURNAL               | Patent: US 5837832-A 69 17-NOV-1998;                                                                                   |  |  |  |  |  |  |  |  |  |
| FEATURES              | Location/Qualifiers                                                                                                    |  |  |  |  |  |  |  |  |  |
| source                | 1. .12                                                                                                                 |  |  |  |  |  |  |  |  |  |
|                       | /organism="unknown"                                                                                                    |  |  |  |  |  |  |  |  |  |
|                       | /mol_type="unassigned DNA"                                                                                             |  |  |  |  |  |  |  |  |  |
| Query Match           | 30.3%; Score 8.8; DB 1; Length 12;                                                                                     |  |  |  |  |  |  |  |  |  |
| Best Local Similarity | 83.3%; Pred. No. 1.5e+02;                                                                                              |  |  |  |  |  |  |  |  |  |
| Matches               | 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;                                                                    |  |  |  |  |  |  |  |  |  |
| QY                    | 13 TGTGTGACCTGG 24                                                                                                     |  |  |  |  |  |  |  |  |  |
| Db                    | 1 TGTGTGTGCTGG 12                                                                                                      |  |  |  |  |  |  |  |  |  |
| RESULT 153            | BD064895                                                                                                               |  |  |  |  |  |  |  |  |  |
| LOCUS                 | BD064895                                                                                                               |  |  |  |  |  |  |  |  |  |
| DEFINITION            | Method for detecting the extent of binding of transcriptional regulatory protein to oligoDNA.                          |  |  |  |  |  |  |  |  |  |
| ACCESSION             | BD064895                                                                                                               |  |  |  |  |  |  |  |  |  |
| VERSION               | BD064895.1 GI:22610498                                                                                                 |  |  |  |  |  |  |  |  |  |
| KEYWORDS              | JP 2001275678-A/107.                                                                                                   |  |  |  |  |  |  |  |  |  |
| SOURCE                | synthetic construct                                                                                                    |  |  |  |  |  |  |  |  |  |
| ORGANISM              | synthetic construct                                                                                                    |  |  |  |  |  |  |  |  |  |
| REFERENCE             | other sequences; artificial sequences.                                                                                 |  |  |  |  |  |  |  |  |  |
| AUTHORS               | 1 (bases 1 to 12)                                                                                                      |  |  |  |  |  |  |  |  |  |
| TITLE                 | Kishimoto,T., Niwa,S., Mori,Y., Sachiyo, Mimaki, Fukushima,R. and Nishikawa,K.                                         |  |  |  |  |  |  |  |  |  |
| JOURNAL               | Method for detecting the extent of binding of transcriptional regulatory protein to oligoDNA                           |  |  |  |  |  |  |  |  |  |
| COMMENT               | Patent: JP 2001275678-A 107 09-OCT-2001; SUMITOMO ELECTRIC INDUSTRIES LTD                                              |  |  |  |  |  |  |  |  |  |
|                       | OS Artificial Sequence                                                                                                 |  |  |  |  |  |  |  |  |  |
|                       | PN JP 2001275678-A/107                                                                                                 |  |  |  |  |  |  |  |  |  |
|                       | PD 09-OCT-2001                                                                                                         |  |  |  |  |  |  |  |  |  |
|                       | PF 31-MAR-2000 JP 2000096306                                                                                           |  |  |  |  |  |  |  |  |  |
|                       | PI TOSHIHIKO KISHIMOTO,SHINICHIRO NIWA,YUKO MORI,SACHIYO PI                                                            |  |  |  |  |  |  |  |  |  |

|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                                                                           |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| MIMAKI,REI FUKUSHIMA,<br>PI KAZUKO NISHIKAWA<br>PC C12N15/09,C12N5/10,C12Q1/00,C12N15/68,C12N15/00,C12N5/00 CC<br>Synthetic DNA<br>FH Key Location/Qualifiers<br>FT source 1. .12<br>FT /organism='Artificial Sequence'.<br>FEATURES<br>source<br>1. .12<br>/organism="synthetic construct"<br>/mol_type="genomic DNA"<br>/db_xref="taxon:32630"<br>Query Match 30.3%; Score 8.8; DB 1; Length 12;<br>Best Local Similarity 83.3%; Pred. No. 1.5e+02;<br>Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;<br>QY 9 CTGCTGTGTGAC 20<br>     <br>Db 1 CTGCTGAGTCAC 12 | BD271980 12 bp DNA linear PAT 17-JUL-2003<br>Methods and for mutations for the separation of biological macromolecules.<br>BD271980<br>BD271980.1 GI:33081748<br>JP 2002529734-A/3.<br>Bacteriophage M13mp18<br>Bacteriophage M13mp18<br>Viruses.<br>1 (bases 1 to 12)<br>Martinez,M.C.R.<br>Methods and for mutations for the separation of biological macromolecules<br>Patent: JP 2002529734-A 3 10-SEP-2002;<br>CURAGEN CORP<br>OS Bacteriophage M13mp18<br>PN JP 2002529734-A/3<br>PD 10-SEP-2002<br>PF 10-NOV-1999 JP 2000581443<br>PR 10-NOV-1998 US 60/107798,13-AUG-1999 US 09/374174 PI<br>MARIE C RUIZ MARTINEZ<br>PC G01N27/447,G01N27/447,B01D57/02,B03C5/00,C08K5/20,C08K5/21, PC C08K5/3415,<br>PC C08L33/26,C12N15/09//C12Q1/68,G01N33/483,G01N27/26,G01N27/26,<br>PC C12N15/00<br>CC Methods and for mutations for the separation of biological macromolecules<br>FH Key Location/Qualifiers<br>FT source 1. .12<br>FT /organism='Bacteriophage M13mp18'.<br>FEATURES<br>source<br>1. .12<br>/organism="Bacteriophage M13mp18"<br>/mol_type="genomic DNA"<br>/db_xref="taxon:28360"<br>Query Match 30.3%; Score 8.8; DB 1; Length 12;<br>Best Local Similarity 83.3%; Pred. No. 1.5e+02;<br>Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;<br>QY 4 TCCACCTGCTGT 15<br>     <br>Db 1 TCCACCTGGTTT 12 | BD271980 12 bp DNA linear PAT 17-JUL-2003<br>Methods and for mutations for the separation of biological macromolecules.<br>BD271980<br>BD271980.1 GI:33081748<br>JP 2002529734-A/3.<br>Bacteriophage M13mp18<br>Bacteriophage M13mp18<br>Viruses.<br>1 (bases 1 to 12)<br>Martinez,M.C.R.<br>Methods and for mutations for the separation of biological macromolecules<br>Patent: JP 2002529734-A 3 10-SEP-2002;<br>CURAGEN CORP<br>OS Bacteriophage M13mp18<br>PN JP 2002529734-A/3<br>PD 10-SEP-2002<br>PF 10-NOV-1999 JP 2000581443<br>PR 10-NOV-1998 US 60/107798,13-AUG-1999 US 09/374174 PI<br>MARIE C RUIZ MARTINEZ<br>PC G01N27/447,G01N27/447,B01D57/02,B03C5/00,C08K5/20,C08K5/21, PC C08K5/3415,<br>PC C08L33/26,C12N15/09//C12Q1/68,G01N33/483,G01N27/26,G01N27/26,<br>PC C12N15/00<br>CC Methods and for mutations for the separation of biological macromolecules<br>FH Key Location/Qualifiers<br>FT source 1. .12<br>FT /organism='Bacteriophage M13mp18'.<br>FEATURES<br>source<br>1. .12<br>/organism="Bacteriophage M13mp18"<br>/mol_type="genomic DNA"<br>/db_xref="taxon:28360"<br>Query Match 30.3%; Score 8.8; DB 1; Length 12;<br>Best Local Similarity 83.3%; Pred. No. 1.5e+02;<br>Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;<br>QY 4 TCCACCTGCTGT 15<br>     <br>Db 1 TCCACCTGGTTT 12 | BD271980 12 bp DNA linear PAT 17-JUL-2003<br>Methods and for mutations for the separation of biological macromolecules.<br>BD271980<br>BD271980.1 GI:33081748<br>JP 2002529734-A/3.<br>Bacteriophage M13mp18<br>Bacteriophage M13mp18<br>Viruses.<br>1 (bases 1 to 12)<br>Martinez,M.C.R.<br>Methods and for mutations for the separation of biological macromolecules<br>Patent: JP 2002529734-A 3 10-SEP-2002;<br>CURAGEN CORP<br>OS Bacteriophage M13mp18<br>PN JP 2002529734-A/3<br>PD 10-SEP-2002<br>PF 10-NOV-1999 JP 2000581443<br>PR 10-NOV-1998 US 60/107798,13-AUG-1999 US 09/374174 PI<br>MARIE C RUIZ MARTINEZ<br>PC G01N27/447,G01N27/447,B01D57/02,B03C5/00,C08K5/20,C08K5/21, PC C08K5/3415,<br>PC C08L33/26,C12N15/09//C12Q1/68,G01N33/483,G01N27/26,G01N27/26,<br>PC C12N15/00<br>CC Methods and for mutations for the separation of biological macromolecules<br>FH Key Location/Qualifiers<br>FT source 1. .12<br>FT /organism='Bacteriophage M13mp18'.<br>FEATURES<br>source<br>1. .12<br>/organism="Bacteriophage M13mp18"<br>/mol_type="genomic DNA"<br>/db_xref="taxon:28360"<br>Query Match 30.3%; Score 8.8; DB 1; Length 12;<br>Best Local Similarity 83.3%; Pred. No. 1.5e+02;<br>Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;<br>QY 4 TCCACCTGCTGT 15<br>     <br>Db 1 TCCACCTGGTTT 12 | BD271980 12 bp DNA linear PAT 17-JUL-2003<br>Methods and for mutations for the separation of biological macromolecules.<br>BD271980<br>BD271980.1 GI:33081748<br>JP 2002529734-A/3.<br>Bacteriophage M13mp18<br>Bacteriophage M13mp18<br>Viruses.<br>1 (bases 1 to 12)<br>Martinez,M.C.R.<br>Methods and for mutations for the separation of biological macromolecules<br>Patent: JP 2002529734-A 3 10-SEP-2002;<br>CURAGEN CORP<br>OS Bacteriophage M13mp18<br>PN JP 2002529734-A/3<br>PD 10-SEP-2002<br>PF 10-NOV-1999 JP 2000581443<br>PR 10-NOV-1998 US 60/107798,13-AUG-1999 US 09/374174 PI<br>MARIE C RUIZ MARTINEZ<br>PC G01N27/447,G01N27/447,B01D57/02,B03C5/00,C08K5/20,C08K5/21, PC C08K5/3415,<br>PC C08L33/26,C12N15/09//C12Q1/68,G01N33/483,G01N27/26,G01N27/26,<br>PC C12N15/00<br>CC Methods and for mutations for the separation of biological macromolecules<br>FH Key Location/Qualifiers<br>FT source 1. .12<br>FT /organism='Bacteriophage M13mp18'.<br>FEATURES<br>source<br>1. .12<br>/organism="Bacteriophage M13mp18"<br>/mol_type="genomic DNA"<br>/db_xref="taxon:28360"<br>Query Match 30.3%; Score 8.8; DB 1; Length 12;<br>Best Local Similarity 83.3%; Pred. No. 1.5e+02;<br>Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;<br>QY 4 TCCACCTGCTGT 15<br>     <br>Db 1 TCCACCTGGTTT 12 | BD271980 12 bp DNA linear PAT 17-JUL-2003<br>Methods and for mutations for the separation of biological macromolecules.<br>BD271980<br>BD271980.1 GI:33081748<br>JP 2002529734-A/3.<br>Bacteriophage M13mp18<br>Bacteriophage M13mp18<br>Viruses.<br>1 (bases 1 to 12)<br>Martinez,M.C.R.<br>Methods and for mutations for the separation of biological macromolecules<br>Patent: JP 2002529734-A 3 10-SEP-2002;<br>CURAGEN CORP<br>OS Bacteriophage M13mp18<br>PN JP 2002529734-A/3<br>PD 10-SEP-2002<br>PF 10-NOV-1999 JP 2000581443<br>PR 10-NOV-1998 US 60/107798,13-AUG-1999 US 09/374174 PI<br>MARIE C RUIZ MARTINEZ<br>PC G01N27/447,G01N27/447,B01D57/02,B03C5/00,C08K5/20,C08K5/21, PC C08K5/3415,<br>PC C08L33/26,C12N15/09//C12Q1/68,G01N33/483,G01N27/26,G01N27/26,<br>PC C12N15/00<br>CC Methods and for mutations for the separation of biological macromolecules<br>FH Key Location/Qualifiers<br>FT source 1. .12<br>FT /organism='Bacteriophage M13mp18'.<br>FEATURES<br>source<br>1. .12<br>/organism="Bacteriophage M13mp18"<br>/mol_type="genomic DNA"<br>/db_xref="taxon:28360"<br>Query Match 30.3%; Score 8.8; DB 1; Length 12;<br>Best Local Similarity 83.3%; Pred. No. 1.5e+02;<br>Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;<br>QY 4 TCCACCTGCTGT 15<br>     <br>Db 1 TCCACCTGGTTT 12 | BD271980 12 bp DNA linear PAT 17-JUL-2003<br>Methods and for mutations for the separation of biological macromolecules.<br>BD271980<br>BD271980.1 GI:33081748<br>JP 2002529734-A/3.<br>Bacteriophage M13mp18<br>Bacteriophage M13mp18<br>Viruses.<br>1 (bases 1 to 12)<br>Martinez,M.C.R.<br>Methods and for mutations for the separation of biological macromolecules<br>Patent: JP 2002529734-A 3 10-SEP-2002;<br>CURAGEN CORP<br>OS Bacteriophage M13mp18<br>PN JP 2002529734-A/3<br>PD 10-SEP-2002<br>PF 10-NOV-1999 JP 2000581443<br>PR 10-NOV-1998 US 60/107798,13-AUG-1999 US 09/374174 PI<br>MARIE C RUIZ MARTINEZ<br>PC G01N27/447,G01N27/447,B01D57/02,B03C5/00,C08K5/20,C08K5/21, PC C08K5/3415,<br>PC C08L33/26,C12N15/09//C12Q1/68,G01N33/483,G01N27/26,G01N27/26,<br>PC C12N15/00<br>CC Methods and for mutations for the separation of biological macromolecules<br>FH Key Location/Qualifiers<br>FT source 1. .12<br>FT /organism='Bacteriophage M13mp18'.<br>FEATURES<br>source<br>1. .12<br>/organism="Bacteriophage M13mp18"<br>/mol_type="genomic DNA"<br>/db_xref="taxon:28360"<br>Query Match 30.3%; Score 8.8; DB 1; Length 12;<br>Best Local Similarity 83.3%; Pred. No. 1.5e+02;<br>Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;<br>QY 4 TCCACCTGCTGT 15<br>     <br>Db 1 TCCACCTGGTTT 12 | BD271980 12 bp DNA linear PAT 17-JUL-2003<br>Methods and for mutations for the separation of biological macromolecules.<br>BD271980<br>BD271980.1 GI:33081748<br>JP 2002529734-A/3.<br>Bacteriophage M13mp18<br>Bacteriophage M13mp18<br>Viruses.<br>1 (bases 1 to 12)<br>Martinez,M.C.R.<br>Methods and for mutations for the separation of biological macromolecules<br>Patent: JP 2002529734-A 3 10-SEP-2002;<br>CURAGEN CORP<br>OS Bacteriophage M13mp18<br>PN JP 2002529734-A/3<br>PD 10-SEP-2002<br>PF 10-NOV-1999 JP 2000581443<br>PR 10-NOV-1998 US 60/107798,13-AUG-1999 US 09/374174 PI<br>MARIE C RUIZ MARTINEZ<br>PC G01N27/447,G01N27/447,B01D57/02,B03C5/00,C08K5/20,C08K5/21, PC C08K5/3415,<br>PC C08L33/26,C12N15/09//C12Q1/68,G01N33/483,G01N27/26,G01N27/26,<br>PC C12N15/00<br>CC Methods and for mutations for the separation of biological macromolecules<br>FH Key Location/Qualifiers<br>FT source 1. .12<br>FT /organism='Bacteriophage M13mp18'.<br>FEATURES<br>source<br>1. .12<br>/organism="Bacteriophage M13mp18"<br>/mol_type="genomic DNA"<br>/db_xref="taxon:28360"<br>Query Match 30.3%; Score 8.8; DB 1; Length 12;<br>Best Local Similarity 83.3%; Pred. No. 1.5e+02;<br>Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;<br>QY 4 TCCACCTGCTGT 15<br>     <br>Db 1 TCCACCTGGTTT 12 | BD271980 12 bp DNA linear PAT 17-JUL-2003<br>Methods and for mutations for the separation of biological macromolecules.<br>BD271980<br>BD271980.1 GI:33081748<br>JP 2002529734-A/3.<br>Bacteriophage M13mp18<br>Bacteriophage M13mp18<br>Viruses.<br>1 (bases 1 to 12)<br>Martinez,M.C.R.<br>Methods and for mutations for the separation of biological macromolecules<br>Patent: JP 2002529734-A 3 10-SEP-2002;<br>CURAGEN CORP<br>OS Bacteriophage M13mp18<br>PN JP 2002529734-A/3<br>PD 10-SEP-2002<br>PF 10-NOV-1999 JP 2000581443<br>PR 10-NOV-1998 US 60/107798,13-AUG-1999 US 09/374174 PI<br>MARIE C RUIZ MARTINEZ<br>PC G01N27/447,G01N27/447,B01D57/02,B03C5/00,C08K5/20,C08K5/21, PC C08K5/3415,<br>PC C08L33/26,C12N15/09//C12Q1/68,G01N33/483,G01N27/26,G01N27/26,<br>PC C12N15/00<br>CC Methods and for mutations for the separation of biological macromolecules<br>FH Key Location/Qualifiers<br>FT source 1. .12<br>FT /organism='Bacteriophage M13mp18'.<br>FEATURES<br>source<br>1. .12<br>/organism="Bacteriophage M13mp18"<br>/mol_type="genomic DNA"<br>/db_xref="taxon:28360"<br>Query Match 30.3%; Score 8.8; DB 1; Length 12;<br>Best Local Similarity 83.3%; Pred. No. 1.5e+02;<br>Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;<br>QY 4 TCCACCTGCTGT 15<br>     <br>Db 1 TCCACCTGGTTT 12 | BD271980 12 bp DNA linear PAT 17-JUL-2003<br>Methods and for mutations for the separation of biological macromolecules.<br>BD271980<br>BD271980.1 GI:33081748<br>JP 2002529734-A/3.<br>Bacteriophage M13mp18<br>Bacteriophage M13mp18<br>Viruses.<br>1 (bases 1 to 12)<br>Martinez,M.C.R.<br>Methods and for mutations for the separation of biological macromolecules<br>Patent: JP 2002529734-A 3 10-SEP-2002;<br>CURAGEN CORP<br>OS Bacteriophage M13mp18<br>PN JP 2002529734-A/3<br>PD 10-SEP-2002<br>PF 10-NOV-1999 JP 2000581443<br>PR 10-NOV-1998 US 60/107798,13-AUG-1999 US 09/374174 PI<br>MARIE C RUIZ MARTINEZ<br>PC G01N27/447,G01N27/447,B01D57/02,B03C5/00,C08K5/20,C08K5/21, PC C08K5/3415,<br>PC C08L33/26,C12N15/09//C12Q1/68,G01N33/483,G01N27/26,G01N27/26,<br>PC C12N15/00<br>CC Methods and for mutations for the separation of biological macromolecules<br>FH Key Location/Qualifiers<br>FT source 1. .12<br>FT /organism='Bacteriophage M13mp18'.<br>FEATURES<br>source<br>1. .12<br>/organism="Bacteriophage M13mp18"<br>/mol_type="genomic DNA"<br>/db_xref="taxon:28360"<br>Query Match 30.3%; Score 8.8; DB 1; Length 12;<br>Best Local Similarity 83.3%; Pred. No. 1.5e+02;<br>Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;<br>QY 4 TCCACCTGCTGT 15<br>     <br>Db 1 TCCACCTGGTTT 12 | BD271980 12 bp DNA linear PAT 17-JUL-2003<br>Methods and for mutations for the separation of biological macromolecules.<br>BD271980<br>BD271980.1 GI:33081748<br>JP 2002529734-A/3.<br>Bacteriophage M13mp18<br>Bacteriophage M13mp18<br>Viruses.<br>1 (bases 1 to 12)<br>Martinez,M.C.R.<br>Methods and for mutations for the separation of biological macromolecules<br>Patent: JP 2002529734-A 3 10-SEP-2002;<br>CURAGEN CORP<br>OS Bacteriophage M13mp18<br>PN JP 2002529734-A/3<br>PD 10-SEP-2002<br>PF 10-NOV-1999 JP 2000581443<br>PR 10-NOV-1998 US 60/107798,13-AUG-1999 US 09/374174 PI<br>MARIE C RUIZ MARTINEZ<br>PC G01N27/447,G01N27/447,B01D57/02,B03C5/00,C08K5/20,C08K5/21, PC C08K5/3415,<br>PC C08L33/26,C12N15/09//C12Q1/68,G01N33/483,G01N27/26,G01N27/26,<br>PC C12N15/00<br>CC Methods and for mutations for the separation of biological macromolecules<br>FH Key Location/Qualifiers<br>FT source 1. .12<br>FT /organism='Bacteriophage M13mp18'.<br>FEATURES<br>source<br>1. .12<br>/organism="Bacteriophage M13mp18"<br>/mol_type="genomic DNA"<br>/db_xref="taxon:28360"<br>Query Match 30.3%; Score 8.8; DB 1; Length 12;<br>Best Local Similarity 83.3%; Pred. No. 1.5e+02;<br>Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;<br>QY 4 TCCACCTGCTGT 15<br>     <br>Db 1 TCCACCTGGTTT 12 | BD271980 12 bp DNA linear PAT 17-JUL-2003<br>Methods and for mutations for the separation of biological macromolecules.<br>BD271980<br>BD271980.1 GI:33081748<br>JP 2002529734-A/3.<br>Bacteriophage M13mp18<br>Bacteriophage M13mp18<br>Viruses.<br>1 (bases 1 to 12)<br>Martinez,M.C.R.<br>Methods and for mutations for the separation of biological macromolecules<br>Patent: JP 2002529734-A 3 10-SEP-2002;<br>CURAGEN CORP<br>OS Bacteriophage M13mp18<br>PN JP 2002529734-A/3<br>PD 10-SEP-2002<br>PF 10-NOV-1999 JP 2000581443<br>PR 10-NOV-1998 US 60/107798,13-AUG-1999 US 09/374174 PI<br>MARIE C RUIZ MARTINEZ<br>PC G01N27/447,G01N27/447,B01D57/02,B03C5/00,C08K5/20,C08K5/21, PC C08K5/3415,<br>PC C08L33/26,C12N15/09//C12Q1/68,G01N33/483,G01N27/26,G01N27/26,<br>PC C12N15/00<br>CC Methods and for mutations for the separation of biological macromolecules<br>FH Key Location/Qualifiers<br>FT source 1. .12<br>FT /organism='Bacteriophage M13mp18'.<br>FEATURES<br>source<br>1. .12<br>/organism="Bacteriophage M13mp18"<br>/mol_type="genomic DNA"<br>/db_xref="taxon:28360"<br>Query Match 30.3%; Score 8.8; DB 1; Length 12;<br>Best Local Similarity 83.3%; Pred. No. 1.5e+02;<br>Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;<br>QY 4 TCCACCTGCTGT 15<br>     <br>Db 1 TCCACCTGGTTT 12 | BD271980 12 bp DNA linear PAT 17-JUL-2003<br>Methods and for mutations for the separation of biological macromolecules.<br>BD271980<br>BD271980.1 GI:33081748<br>JP 2002529734-A/3.<br>Bacteriophage M13mp18<br>Bacteriophage M13mp18<br>Viruses.<br>1 (bases 1 to 12)<br>Martinez,M.C.R.<br>Methods and for mutations for the separation of biological macromolecules<br>Patent: JP 2002529734-A 3 10-SEP-2002;<br>CURAGEN CORP<br>OS Bacteriophage M13mp18<br>PN JP 2002529734-A/3<br>PD 10-SEP-2002<br>PF 10-NOV-1999 JP 2000581443<br>PR 10-NOV-1998 US 60/107798,13-AUG-1999 US 09/374174 PI<br>MARIE C RUIZ MARTINEZ<br>PC G01N27/447,G01N27/447,B01D57/02,B03C5/00,C08K5/20,C08K5/21, PC C08K5/3415,<br>PC C08L33/26,C12N15/09//C12Q1/68,G01N33/483,G01N27/26,G01N27/26,<br>PC C12N15/00<br>CC Methods and for mutations for the separation of biological macromolecules<br>FH Key Location/Qualifiers<br>FT source 1. .12<br>FT /organism='Bacteriophage M13mp18'.<br>FEATURES<br>source<br>1. .12<br>/organism="Bacteriophage M13mp18"<br>/mol_type="genomic DNA"<br>/db_xref="taxon:28360"<br>Query Match 30.3%; Score 8.8; DB 1; Length 12;<br>Best Local Similarity 83.3%; Pred. No. 1.5e+02;<br>Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;<br>QY 4 TCCACCTGCTGT 15<br>     <br>Db 1 TCCACCTGGTTT 12 | BD271980 12 bp DNA linear PAT 17-JUL-2003<br>Methods and for mutations for the separation of biological macromolecules.<br>BD271980<br>BD271980.1 GI:33081748<br>JP 2002529734-A/3.<br>Bacteriophage M13mp18<br>Bacteriophage M13mp18<br>Viruses.<br>1 (bases 1 to 12)<br>Martinez,M.C.R.<br>Methods and for mutations for the separation of biological macromolecules<br>Patent: JP 2002529734-A 3 10-SEP-2002;<br>CURAGEN CORP<br>OS Bacteriophage M13mp18<br>PN JP 2002529734-A/3<br>PD 10-SEP-2002<br>PF 10-NOV-1999 JP 2000581443<br>PR 10-NOV-1998 US 60/107798,13-AUG-1999 US 09/374174 PI<br>MARIE C RUIZ MARTINEZ<br>PC G01N27/447,G01N27/447,B01D57/02,B03C5/00,C08K5/20,C08K5/21, PC C08K5/3415,<br>PC C08L33/26,C12N15/09//C12Q1/68,G01N33/483,G01N27/26,G01N27/26,<br>PC C12N15/00<br>CC Methods and for mutations for the separation of biological macromolecules<br>FH Key Location/Qualifiers<br>FT source 1. .12<br>FT /organism='Bacteriophage M13mp18'.<br>FEATURES<br>source<br>1. .12<br>/organism="Bacteriophage M13mp18"<br>/mol_type="genomic DNA"<br>/db_xref="taxon:28360"<br>Query Match 30.3%; Score 8.8; DB 1; Length 12;<br>Best Local Similarity 83.3%; Pred. No. 1.5e+02;<br>Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;<br>QY 4 TCCACCTGCTGT 15<br>     <br>Db 1 TCCACCTGGTTT 12 | BD271980 12 bp DNA linear PAT 17-JUL-2003<br>Methods and for mutations for the separation of biological macromolecules.<br>BD271980<br>BD271980.1 GI:33081748<br>JP 2002529734-A/3.<br>Bacteriophage M13mp18<br>Bacteriophage M13mp18<br>Viruses.<br>1 (bases 1 to 12)<br>Martinez,M.C.R.<br>Methods and for mutations for the separation of biological macromolecules<br>Patent: JP 2002529734-A 3 10-SEP-2002;<br>CURAGEN CORP<br>OS Bacteriophage M13mp18<br>PN JP 2002529734-A/3<br>PD 10-SEP-2002<br>PF 10-NOV-1999 JP 2000581443<br>PR 10-NOV-1998 US 60/107798,13-AUG-1999 US 09/374174 PI<br>MARIE C RUIZ MARTINEZ<br>PC G01N27/447,G01N27/447,B01D57/02,B03C5/00,C08K5/20,C08K5/21, PC C08K5/3415,<br>PC C08L33/26,C12N15/09//C12Q1/68,G01N33/483,G01N27/26,G01N27/26,<br>PC C12N15/00<br>CC Methods and for mutations for the separation of biological macromolecules<br>FH Key Location/Qualifiers<br>FT source 1. .12<br>FT /organism='Bacteriophage M13mp18'.<br>FEATURES<br>source<br>1. .12<br>/organism="Bacteriophage M13mp18"<br>/mol_type="genomic DNA"<br>/db_xref="taxon:28360"<br>Query Match 30.3%; Score 8.8; DB 1; Length 12;<br>Best Local Similarity 83.3%; Pred. No. 1.5e+02;<br>Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;<br>QY 4 TCCACCTGCTGT 15<br>     <br>Db 1 TCCACCTGGTTT 12 | BD271980 12 bp DNA linear PAT 17-JUL-2003<br>Methods and for mutations for the separation of biological macromolecules.<br>BD271980<br>BD271980.1 GI:33081748<br>JP 2002529734-A/3.<br>Bacteriophage M13mp18<br>Bacteriophage M13mp18<br>Viruses.<br>1 (bases 1 to 12)<br>Martinez,M.C.R.<br>Methods and for mutations for the separation of biological macromolecules<br>Patent: JP 2002529734-A 3 10-SEP-2002;<br>CURAGEN CORP<br>OS Bacteriophage M13mp18<br>PN JP 2002529734-A/3<br>PD 10-SEP-2002<br>PF 10-NOV-1999 JP 2000581443<br>PR 10-NOV-1998 US 60/107798,13-AUG-1999 US 09/374174 PI<br>MARIE C RUIZ MARTINEZ<br>PC G01N27/447,G01N27/447,B01D57/02,B03C5/00,C08K5/20,C08K5/21, PC C08K5/3415,<br>PC C08L33/26,C12N15/09//C12Q1/68,G01N33/483,G01N27/26,G01N27/26,<br>PC C12N15/00<br>CC Methods and for mutations for the separation of biological macromolecules<br>FH Key Location/Qualifiers<br>FT source 1. .12<br>FT /organism='Bacteriophage M13mp18'.<br>FEATURES<br>source<br>1. .12<br>/organism="Bacteriophage M13mp18"<br>/mol_type="genomic DNA"<br>/db_xref="taxon:28360"<br>Query Match 30.3%; Score 8.8; DB 1; Length 12;<br>Best Local Similarity 83.3%; Pred. No. 1.5e+02;<br>Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;<br>QY 4 TCCACCTGCTGT 15<br>     <br>Db 1 TCCACCTGGTTT 12 | BD271980 12 bp DNA linear PAT 17-JUL-2003<br>Methods and for mutations for the separation of biological macromolecules.<br>BD271980<br>BD271980.1 GI:33081748<br>JP 2002529734-A/3.<br>Bacteriophage M13mp18<br>Bacteriophage M13mp18<br>Viruses.<br>1 (bases 1 to 12)<br>Martinez,M.C.R.<br>Methods and for mutations for the separation |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|

```
ACCESSION      CQ766158
VERSION        CQ766158.1  GI:44908418
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Weinzierl,R.
TITLE          Method
JOURNAL        Patent: WO 2004005547-A 119 15-JAN-2004;
IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES
  source
    1. .12
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="HS consensus sequence"

  Query Match      30.3%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity 83.3%;  Pred. No. 1.5e+02;
  Matches 10;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

QY      1  CCATCCACCTGC 12
      ||||| |||||
Db      1  CCACCCATCTGC 12

RESULT 156
I23750/c
LOCUS      I23750              12 bp      DNA      linear      PAT 07-OCT-1996
DEFINITION Sequence 15 from patent US 5538844.
ACCESSION  I23750
VERSION    I23750.1  GI:1603620
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1  (bases 1 to 12)
AUTHORS    Duyao,M.P., MacDonald,M.E. and Gusella,J.F.
TITLE      Transport protein gene from the Huntington's disease region
JOURNAL    Patent: US 5538844-A 15 23-JUL-1996;
FEATURES
  source
    1. .12
      /organism="unknown"
      /mol_type="unassigned DNA"

  Query Match      30.3%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity 83.3%;  Pred. No. 1.5e+02;
  Matches 10;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

QY      3  ATCCACCTGCTG 14
      | ||||| |||
Db      12  ACCCACCTACTG 1

RESULT 157
I73177
LOCUS      I73177              12 bp      DNA      linear      PAT 03-APR-1998
DEFINITION Sequence 29 from patent US 5686240.
ACCESSION  I73177
VERSION    I73177.1  GI:3009316
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1  (bases 1 to 12)
AUTHORS    Schuchman,E.H. and Desnick,R.J.
TITLE      Acid sphingomyelinase gene and diagnosis of Niemann-Pick disease
JOURNAL    Patent: US 5686240-A 29 11-NOV-1997;
FEATURES
  source
    1. .12
      /organism="unknown"
      /mol_type="unassigned DNA"
```

```
Query Match      30.3%;  Score 8.8;  DB 1;  Length 12;
Best Local Similarity 83.3%;  Pred. No. 1.5e+02;
Matches 10;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

QY      12  CTGTGTGACCTG 23
      ||||| |||||
Db      1  CTGTGCCACCTG 12

RESULT 158
AR302271
LOCUS      AR302271              12 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION Sequence 9 from patent US 6541218.
ACCESSION  AR302271
VERSION    AR302271.1  GI:31690510
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1  (bases 1 to 12)
AUTHORS    Schuchman,E.H. and Desnick,R.J.
TITLE      Acid sphingomyelinase protein and methods of treating type B
          Niemann-Pick disease
JOURNAL    Patent: US 6541218-A 9 01-APR-2003;
          The Mount Sinai School of Medicine of the city University of New
          York; New York, NY
FEATURES
  source
    1. .12
      /organism="unknown"
      /mol_type="genomic DNA"

  Query Match      30.3%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity 83.3%;  Pred. No. 1.5e+02;
  Matches 10;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

QY      12  CTGTGTGACCTG 23
      ||||| |||||
Db      1  CTGTGCCACCTG 12

RESULT 159
AR308098
LOCUS      AR308098              12 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION Sequence 3 from patent US 6554985.
ACCESSION  AR308098
VERSION    AR308098.1  GI:31699106
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1  (bases 1 to 12)
AUTHORS    Ruiz-Martinez,M.C., Berka,J. and Simpson,J.W.
TITLE      Methods and formulations for the separation of biological
          macromolecules
JOURNAL    Patent: US 6554985-A 3 29-APR-2003;
          CuraGen Corporation; New Haven, CT
FEATURES
  source
    1. .12
      /organism="unknown"
      /mol_type="genomic DNA"

  Query Match      30.3%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity 83.3%;  Pred. No. 1.5e+02;
  Matches 10;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

QY      4  TCCACCTGCTGT 15
      ||||| |||
Db      1  TCCACCTGGTTT 12

RESULT 160
S55766
```

LOCUS S55766 12 bp DNA linear PRI 04-MAY-2000  
DEFINITION Homo sapiens acid sphingomyelinase gene, partial cds.  
ACCESSION S55766  
VERSION S55766.1 GI:234719  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Levran,O., Desnick,R.J. and Schuchman,E.H.  
TITLE Niemann-Pick type B disease. Identification of a single codon deletion in the acid sphingomyelinase gene and genotype/phenotype correlations in type A and B patients  
J. Clin. Invest. 88 (3), 806-810 (1991)  
JOURNAL 1885770  
PUBMED  
REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 55766] from the original journal article.  
COMMENT 3 bp deletion.  
FEATURES  
source location/Qualifiers  
1..12  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
<1..>12  
/product="acid sphingomyelinase"  
<1..>12  
/note="lysosomal hydrolase"  
/codon\_start=1  
/product="acid sphingomyelinase"  
/protein\_id="AAB19680.1"  
/db\_xref="GI:234720"  
/translation="LCHL"  
mRNA  
CDS  
Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 12 CTGTGTGACCTG 23  
| | | | |  
Db 1 CTGTGCCACCTG 12  
RESULT 161  
S73118S2  
LOCUS S73118S2 12 bp DNA linear PRI 07-MAY-1993  
DEFINITION dystrophin {intragenic deletion} [human, Genomic Mutant, 12 nt, segment 2 of 2].  
ACCESSION S73119  
VERSION S73119.1 GI:241101  
KEYWORDS  
SEGMENT 2 of 2  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Love,D.R., Flint,T.J., Genet,S.A., Middleton-Price,H.R. and Davies,K.E.  
TITLE Becker muscular dystrophy patient with a large intragenic dystrophin deletion: implications for functional minigenes and gene therapy  
J. Med. Genet. 28 (12), 860-864 (1991)  
JOURNAL 1757963  
PUBMED  
REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 73119] from the original journal article.  
FEATURES  
source location/Qualifiers  
1..12  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

gene order(S73118.1:1..12,1..12)  
/gene="dystrophin"  
CDS join(S73118.1:1..12,1..12)  
/gene="dystrophin"  
/codon\_start=1  
/product="dystrophin"  
/protein\_id="AAB20694.1"  
/db\_xref="GI:241102"  
/translation="QQITCVNL"  
Query Match 30.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 13 TGTGTGACCTGG 24  
| | | | |  
Db 1 TGTGTGAACCTG 12  
RESULT 162  
AR164924/c  
LOCUS AR164924 10 bp DNA linear PAT 17-OCT-2001  
DEFINITION Sequence 129 from patent US 6274339.  
ACCESSION AR164924  
VERSION AR164924.1 GI:16238232  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Moore,K. and Nagle,D.Lynn.  
TITLE Methods and compositions for the diagnosis and treatment of body weight disorders, including obesity  
JOURNAL Patent: US 6274339-A 129 14-AUG-2001;  
FEATURES  
source location/Qualifiers  
1..10  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.5e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 12 CTGTGTGACC 21  
| | | | |  
Db 10 CTGTGTGTCC 1  
RESULT 163  
AR167603  
LOCUS AR167603 10 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 13 from patent US 6287763.  
ACCESSION AR167603  
VERSION AR167603.1 GI:17903393  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Lee,F., Huszar,D. and Gu,W.  
TITLE Screening methods for compounds useful in the regulation of body weight  
JOURNAL Patent: US 6287763-A 13 11-SEP-2001;  
FEATURES  
source location/Qualifiers  
1..10  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.5e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 3 ATCCACCTGC 12





PD 27-NOV-2001  
PF 22-MAY-2000 JP 2000150562  
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI PI  
NAGAI  
PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00  
CC  
FH Key Location/Qualifiers.  
FEATURES  
source  
1. .10  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.5e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 13 TGTGTGACCT 22  
| | | | | | | |  
Db 1 TGTGTGAGCT 10  
RESULT 168  
BD167115/c  
LOCUS BD167115 10 bp DNA linear PAT 17-JAN-2003  
DEFINITION Human liver disease-expressing genes.  
ACCESSION BD167115  
VERSION BD167115.1 GI:27872927  
KEYWORDS JP 2002209591-A/660.  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.  
TITLE Human liver disease-expressing genes  
JOURNAL Patent: JP 2002209591-A 660 30-JUL-2002;  
JAPAN SCIENCE AND TECHNOLOGY CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002209591-A/660  
PD 30-JUL-2002  
PF 19-JAN-2001 JP 2001012328  
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI  
YAMASHITA  
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,  
C12P21/08,  
PC C12N15/00  
CC Human liver disease-expressing genes  
FH Key Location/Qualifiers  
FT source 1. .10  
/organism='Homo sapiens (human)'.  
FEATURES  
source  
Location/Qualifiers  
1. .10  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.5e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 8 CCTGCTGTGT 17  
| | | | | | | |  
Db 10 CTTGCTGTGT 1  
RESULT 169  
BD195102  
LOCUS BD195102 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Screening methods for compounds useful in the regulation of body weight.  
ACCESSION BD195102  
VERSION BD195102.1 GI:33004861  
KEYWORDS JP 2002514041-A/5.

SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Lee,F., Huszar,D. and Gu,W.  
TITLE Screening methods for compounds useful in the regulation of body  
JOURNAL Patent: JP 2002514041-A 5 14-MAY-2002;  
MILLENNIUM PHARMACEUTICALS INC  
COMMENT OS Artificial Sequence  
PN JP 2002514041-A/5  
PD 14-MAY-2002  
PF 09-JUN-1997 JP 1998501745  
PR 10-JUN-1996 US 08/662560,08-JAN-1997 US 08/780749 PR  
06-JUN-1997 US 08/870511  
PI FRANK LEE,DENNIS HUSZAR,WEI GU  
PC A61K38/16,A61K39/395,A61K48/00,C07H21/04,C12N15/11,C12Q1/68,  
G01N33/53,  
PC C12Q1/25,C12Q1/66,C12Q1/68  
CC Description of artificial sequence: primer  
FH Key Location/Qualifiers  
FT source 1. .10  
/organism='Artificial Sequence'.  
FEATURES  
source  
Location/Qualifiers  
1. .10  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.5e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 ATCCACCTGC 12  
| | | | | | | |  
Db 1 ATCCACTTGC 10  
RESULT 170  
BD238856/c  
LOCUS BD238856 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD238856  
VERSION BD238856.1 GI:33048626  
KEYWORDS JP 2002534056-A/274.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 274 15-OCT-2002;  
GENZYME CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002534056-A/274  
PD 15-OCT-2002  
PF 18-JUN-1999 JP 2000554749  
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR  
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/089853 PR  
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/090079 PR  
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR  
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR  
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR  
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR  
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR  
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR  
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR  
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR  
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR  
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR  
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR  
08-DEC-1998 US 60/111715

```

PI      BRUCE L ROBERTS, SRINIVAS SHANKARA
PC      C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC      C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC      C12N15/00,C12N5/00,C12N15/00
CC      Preparation and use of superior vaccines
FH      Key      Location/Qualifiers
FT      source      1..10
FT      Location/Qualifiers
FEATURES
    source
    1..10
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

    Query Match      29.0%; Score 8.4; DB 1; Length 10;
    Best Local Similarity 90.0%; Pred. No. 1.5e+02;
    Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 CCTGCTGTGT 17
      ||||||
Db      10 CTGCTGTGT 1

RESULT 171
BD239707
LOCUS      BD239707 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239707
VERSION    BD239707.1 GI:33049477
KEYWORDS   JP 2002534056-A/1125.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Roberts,B.L. and Shankara,S.
TITLE      Preparation and use of superior vaccines
JOURNAL    Patent: JP 2002534056-A 1125 15-OCT-2002;
            GENZYME CORP
COMMENT     OS Homo sapiens (human)
            PN JP 2002534056-A/1125
            PD 15-OCT-2002
            PF 18-JUN-1999 JP 2000554749
            PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
            19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
            19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
            19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
            19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
            19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
            19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
            19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
            19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
            19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
            19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
            19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
            19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
            19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
            08-DEC-1998 US 60/111715
            PI BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
            C12N1/19,
            G01N37/00,
            CC Preparation and use of superior vaccines
            FH Key      Location/Qualifiers
            FT source      1..10
            FT      Location/Qualifiers
            FT      /organism='Homo sapiens (human)'.

PI      BRUCE L ROBERTS, SRINIVAS SHANKARA
PC      C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC      C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC      C12N15/00,C12N5/00,C12N15/00
CC      Preparation and use of superior vaccines
FH      Key      Location/Qualifiers
FT      source      1..10
FT      Location/Qualifiers
FEATURES
    source
    1..10
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

    Query Match      29.0%; Score 8.4; DB 1; Length 10;
    Best Local Similarity 90.0%; Pred. No. 1.5e+02;
    Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 CCTGCTGTGT 17
      ||||||
Db      10 CTGCTGTGT 1

RESULT 172
BD240160
LOCUS      BD240160 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240160
VERSION    BD240160.1 GI:33049930
KEYWORDS   JP 2002534056-A/1578.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Roberts,B.L. and Shankara,S.
TITLE      Preparation and use of superior vaccines
JOURNAL    Patent: JP 2002534056-A 1578 15-OCT-2002;
            GENZYME CORP
COMMENT     OS Homo sapiens (human)
            PN JP 2002534056-A/1578
            PD 15-OCT-2002
            PF 18-JUN-1999 JP 2000554749
            PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
            19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
            19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
            19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
            19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
            19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
            19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
            19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
            19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
            19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
            19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
            19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
            19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
            19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
            08-DEC-1998 US 60/111715
            PI BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
            C12N1/19,
            G01N37/00,
            CC Preparation and use of superior vaccines
            FH Key      Location/Qualifiers
            FT source      1..10
            FT      Location/Qualifiers
            FT      /organism='Homo sapiens (human)'.

PI      BRUCE L ROBERTS, SRINIVAS SHANKARA
PC      C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC      C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC      C12N15/00,C12N5/00,C12N15/00
CC      Preparation and use of superior vaccines
FH      Key      Location/Qualifiers
FT      source      1..10
FT      Location/Qualifiers
FEATURES
    source
    1..10
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

    Query Match      29.0%; Score 8.4; DB 1; Length 10;
    Best Local Similarity 90.0%; Pred. No. 1.5e+02;
    Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9 CTGCTGTGTG 18
      ||||||
Db      1 CTGCTATGTG 10
```

```

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

    Query Match      29.0%; Score 8.4; DB 1; Length 10;
    Best Local Similarity 90.0%; Pred. No. 1.5e+02;
    Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 ATCCACCTGC 12
      |||||
Db      1 ATCCGCCTGC 10

RESULT 172
BD240160
LOCUS      BD240160 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240160
VERSION    BD240160.1 GI:33049930
KEYWORDS   JP 2002534056-A/1578.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Roberts,B.L. and Shankara,S.
TITLE      Preparation and use of superior vaccines
JOURNAL    Patent: JP 2002534056-A 1578 15-OCT-2002;
            GENZYME CORP
COMMENT     OS Homo sapiens (human)
            PN JP 2002534056-A/1578
            PD 15-OCT-2002
            PF 18-JUN-1999 JP 2000554749
            PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
            19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
            19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
            19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
            19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
            19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
            19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
            19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
            19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
            19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
            19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
            19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
            19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
            19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
            08-DEC-1998 US 60/111715
            PI BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
            C12N1/19,
            G01N37/00,
            CC Preparation and use of superior vaccines
            FH Key      Location/Qualifiers
            FT source      1..10
            FT      Location/Qualifiers
            FT      /organism='Homo sapiens (human)'.

FEATURES
    source
    1..10
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

    Query Match      29.0%; Score 8.4; DB 1; Length 10;
    Best Local Similarity 90.0%; Pred. No. 1.5e+02;
    Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9 CTGCTGTGTG 18
      ||||||
Db      1 CTGCTATGTG 10
```

```
RESULT 173
E06867
LOCUS       E06867               10 bp      RNA          linear      PAT 29-SEP-1997
DEFINITION   Substrate of ribozyme.
ACCESSION   E06867
VERSION     E06867.1  GI:5708532
KEYWORDS    JP 1994070774-A/15.
SOURCE      synthetic construct
ORGANISM    synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 10)
AUTHORS     Otsuka,E. and Koizumi,M.
TITLE       RIBOZYME HAVING THERMODYNAMICALLY STABLE LOOP STRUCTURE
JOURNAL     Patent: JP 1994070774-A 15 15-MAR-1994;
            SANKYO CO LTD
COMMENT     OS Artificial gene
            OC Artificial sequence; Genes.
            PN JP 1994070774-A/15
            PD 15-MAR-1994
            PF 01-JUL-1993 JP 1993163530
            PR 02-JUL-1992 JP 92P 175706
            PI OTSUKA EIKO, KOIZUMI MAKOTO
            PC C12N15/11,C12N1/21,C12N9/00,C12N15/10,(C12N1/21,C12R1:19); CC
            strandedness: Single;
            CC topology: Linear;
            CC hypothetical: No;
            CC anti-sense: No;
            FH Key
            FH Key
            FT misc_feature 1..10
            FT /note=Substrate of ribozyme'.
FEATURES     source
            Location/Qualifiers
                1..10
                /organism="synthetic construct"
                /mol_type="genomic RNA"
                /db_xref="taxon:32630"
Query Match      29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TGCTGTGTGA 19
    |||||||
Db 1 TGTGTGTGCA 10

RESULT 174
E39535/c
LOCUS       E39535               10 bp      DNA          linear      PAT 31-JAN-2002
DEFINITION   Genes with human dendritic cell expression.
ACCESSION   E39535
VERSION     E39535.1  GI:18621626
KEYWORDS    JP 2000279181-A/68.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
AUTHORS     Hashimoto,S., Matsushima,K. and Suzuki,T.
TITLE       Genes with human dendritic cell expression
JOURNAL     Patent: JP 2000279181-A 68 10-OCT-2000;
            SCIENCE & TECH AGENCY
COMMENT     OS Homo sapiens (human)
            PN JP 2000279181-A/68
            PD 10-OCT-2000
            PF 01-APR-1999 JP 1999095481
            PR SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
            C12N15/09,C07K14/475,C07K16/18,C12N15/00
            CC

Qy 10 TGCTGTGTGA 19
    |||||||
Db 1 TGTGTGTGCA 10

RESULT 175
E54734/c
LOCUS       E54734               10 bp      DNA          linear      PAT 27-AUG-2002
DEFINITION   Human normal liver cell expression genes.
ACCESSION   E54734
VERSION     E54734.1  GI:22556217
KEYWORDS    JP 2001211883-A/86.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
AUTHORS     Hashimoto,S., Matsushima,K. and Suzuki,T.
TITLE       Genes with human dendritic cell expression
JOURNAL     Patent: JP 2000279181-A 68 10-OCT-2000;
            SCIENCE & TECH AGENCY
COMMENT     OS Homo sapiens (human)
            PN JP 2000279181-A/68
            PD 10-OCT-2000
            PF 01-APR-1999 JP 1999095481
            PR SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
            C12N15/09,C07K14/475,C07K16/18,C12N15/00
            CC

Qy 10 TGCTGTGTGA 19
    |||||||
Db 1 TGTGTGTGCA 10
```

```
FT source 1..10
FT /organism='Homo sapiens (human)'.
FEATURES     source
            Location/Qualifiers
                1..10
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
Query Match      29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGT 17
    |||||||
Db 10 CTGCTGTGT 1

RESULT 175
E39641
LOCUS       E39641               10 bp      DNA          linear      PAT 31-JAN-2002
DEFINITION   Genes with human dendritic cell expression.
ACCESSION   E39641
VERSION     E39641.1  GI:18621732
KEYWORDS    JP 2000279181-A/174.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
AUTHORS     Hashimoto,S., Matsushima,K. and Suzuki,T.
TITLE       Genes with human dendritic cell expression
JOURNAL     Patent: JP 2000279181-A 174 10-OCT-2000;
            SCIENCE & TECH AGENCY
COMMENT     OS Homo sapiens (human)
            PN JP 2000279181-A/174
            PD 10-OCT-2000
            PF 01-APR-1999 JP 1999095481
            PR SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
            C12N15/09,C07K14/475,C07K16/18,C12N15/00
            CC

FT Key
FT source 1..10
FT /organism='Homo sapiens (human)'.
FEATURES     source
            Location/Qualifiers
                1..10
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
Query Match      29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 TGTGTGACCT 22
    |||||||
Db 1 TGTGTGAGCT 10

RESULT 176
E54734/c
LOCUS       E54734               10 bp      DNA          linear      PAT 27-AUG-2002
DEFINITION   Human normal liver cell expression genes.
ACCESSION   E54734
VERSION     E54734.1  GI:22556217
KEYWORDS    JP 2001211883-A/86.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
```

AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.  
TITLE Human normal liver cell expression genes  
JOURNAL Patent: JP 2001211883-A 86 07-AUG-2001;  
SCIENCE & TECH AGENCY  
COMMENT OS Homo sapiens (human)  
PN JP 2001211883-A/86  
PD 07-AUG-2001  
PF 31-JAN-2000 JP 2000023170  
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI  
YAMASHITA  
PC C12N15/09,C07K16/18,C12P21/02,C12N15/00  
CC  
FH Key Location/Qualifiers.  
FEATURES  
source  
1..10  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.5e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 8 CCTGCTGTGT 17  
Db 10 CTTGCTGTGT 1  
RESULT 177  
I43001  
LOCUS I43001 10 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 23 from patent US 5631115.  
ACCESSION I43001  
VERSION I43001.1 GI:2468245  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Ohtsuka,E. and Koizumi,M.  
TITLE Looped, hairpin ribozyme  
JOURNAL Patent: US 5631115-A 23 20-MAY-1997;  
FEATURES  
source  
1..10  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.5e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 10 TGCTGTGTGA 19  
Db 1 TGTGTGTGA 10  
RESULT 178  
AR303393/c  
LOCUS AR303393 10 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 118 from patent US 6544736.  
ACCESSION AR303393  
VERSION AR303393.1 GI:31692169  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.  
TITLE Method for synthesizing cDNA from mRNA sample  
JOURNAL Patent: US 6544736-A 118 08-APR-2003;  
Nippon Gene Co., Ltd. and Agene Research Institute Co., Ltd.; Tokyo;

JPX; Location/Qualifiers  
FEATURES  
source  
1..10  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.5e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 16 GTGACCTGGT 25  
Db 10 GTGACCTTGT 1  
RESULT 179  
AR306856  
LOCUS AR306856 10 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 8 from patent US 6551476.  
ACCESSION AR306856  
VERSION AR306856.1 GI:31697256  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Scherba,E.S.  
TITLE Noble-metal coated inert anode for aluminum production  
JOURNAL Patent: US 6551476-A 8 22-APR-2003;  
FEATURES  
source  
1..10  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.5e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 CATCCACCTG 11  
Db 1 CATCCCCCTG 10  
RESULT 180  
AR490725/c  
LOCUS AR490725 10 bp DNA linear PAT 15-MAY-2004  
DEFINITION Sequence 130 from patent US 6713277.  
ACCESSION AR490725  
VERSION AR490725.1 GI:47258124  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Moore,K. and Nagle,D.L.  
TITLE Methods and composition for the diagnosis and treatment of body weight disorders, including obesity  
JOURNAL Patent: US 6713277-A 130 30-MAR-2004;  
Millennium Pharmaceuticals, Inc.; Cambridge, MA  
FEATURES  
source  
1..10  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 29.0%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1.5e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 12 CTGTGTGACC 21  
Db 10 CTGTGTGTCC 1



```
RESULT 181
AR532498/c
LOCUS AR532498 10 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 129 from patent US 6727348.
ACCESSION AR532498
VERSION AR532498.1 GI:53921716
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 10)
AUTHORS Moore,K. and Nagle,D.L.
TITLE Compositions and methods for the diagnosis and treatment of body
weight disorders, including obesity
JOURNAL Patent: US 6727348-A 129 27-APR-2004;
Millennium Pharmaceuticals, Inc.; Cambridge, MA
FEATURES
source
1. .10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CTGTGTGACC 21
|||||
Db 10 CTGTGTGTCC 1

RESULT 182
AX018751/c
LOCUS AX018751 10 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 9 from Patent WO9943848.
ACCESSION AX018751
VERSION AX018751.1 GI:10042874
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Ong,C.J. and Jirik,F.R.
TITLE Protein interaction and transcription factor trap
JOURNAL Patent: WO 9943848-A 9 02-SEP-1999;
ONG CHRISTOPHER J (CA); UNIV BRITISH COLUMBIA (CA); JIRIK FRANK R
(CA)
FEATURES
source
Location/Qualifiers
1. .10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligomer containing a splice acceptor sequence"

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 15 TGTGACCTGG 24
||
Db 10 TGCGACCTGG 1

RESULT 183
AX112967
LOCUS AX112967 10 bp DNA linear PAT 01-MAY-2001
DEFINITION Sequence 14 from Patent WO0127267.
ACCESSION AX112967
VERSION AX112967.1 GI:13939402
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
```

```
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1
AUTHORS Adams,E., Waldmann,H., Cobbold,S. and Zelenika,D.
TITLE Genes differentially expressed in tr1 cells and their use in the
manufacture of immunoregulatory compositions
JOURNAL Patent: WO 0127267-A 14 19-APR-2001;
ISIS INNOVATION LIMITED (GB)
FEATURES
source
Location/Qualifiers
1. .10
/organism="Mus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:10095"

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTG 18
|||||
Db 1 CTGCTTTGTG 10

RESULT 184
AX152117
LOCUS AX152117 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 32 from Patent WO0138577.
ACCESSION AX152117
VERSION AX152117.1 GI:14533768
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 32 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
Location/Qualifiers
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CTGTGTGACC 21
|||||
Db 1 CTGTGTGCC 10

RESULT 185
AX152126
LOCUS AX152126 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 41 from Patent WO0138577.
ACCESSION AX152126
VERSION AX152126.1 GI:14533777
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 41 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
Location/Qualifiers
1. .10
```

/organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 Query Match 29.0%; Score 8.4; DB 1; Length 10;  
 Best Local Similarity 90.0%; Pred. No. 1.5e+02;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 12 CTGTGTGACC 21  
 |||||  
 Db 1 CTGTGTGCC 10  
 RESULT 186  
 AX152191  
 LOCUS AX152191 10 bp DNA linear PAT 22-JUN-2001  
 DEFINITION Sequence 106 from Patent WO0138577.  
 ACCESSION AX152191  
 VERSION AX152191.1 GI:14533842  
 KEYWORDS .  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.  
 TITLE Human transcriptomes  
 JOURNAL Patent: WO 0138577-A 106 31-MAY-2001;  
 The Johns Hopkins University (US)  
 FEATURES  
 source 1..10  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 Query Match 29.0%; Score 8.4; DB 1; Length 10;  
 Best Local Similarity 90.0%; Pred. No. 1.5e+02;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 12 CTGTGTGACC 21  
 |||||  
 Db 1 CTGTGTGTCC 10  
 RESULT 187  
 AX152676  
 LOCUS AX152676 10 bp DNA linear PAT 22-JUN-2001  
 DEFINITION Sequence 591 from Patent WO0138577.  
 ACCESSION AX152676  
 VERSION AX152676.1 GI:14534327  
 KEYWORDS .  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.  
 TITLE Human transcriptomes  
 JOURNAL Patent: WO 0138577-A 591 31-MAY-2001;  
 The Johns Hopkins University (US)  
 FEATURES  
 source 1..10  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 Query Match 29.0%; Score 8.4; DB 1; Length 10;  
 Best Local Similarity 90.0%; Pred. No. 1.5e+02;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 9 CTGCTGTGTG 18  
 |||||  
 Db 1 CTGCTATGTG 10  
 RESULT 189  
 AR051278  
 LOCUS AR051278 11 bp DNA linear PAT 29-SEP-1999  
 DEFINITION Sequence 15 from patent US 5830661.  
 ACCESSION AR051278  
 VERSION AR051278.1 GI:5974642  
 KEYWORDS .  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 UNCLASSIFIED  
 REFERENCE 1 (bases 1 to 11)  
 AUTHORS Sarfarazi,M.  
 TITLE Diagnosis and treatment of glaucoma  
 JOURNAL Patent: US 5830661-A 15 03-NOV-1998;  
 FEATURES  
 source 1..11  
 /organism="unknown"  
 /mol\_type="unassigned DNA"  
 Query Match 29.0%; Score 8.4; DB 1; Length 11;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 19 ACCTGCTAAA 28

|||||  
 Db 1 CTGCTGAGTG 10  
 RESULT 188  
 BD007884  
 LOCUS BD007884 10 bp DNA linear PAT 31-JAN-2002  
 DEFINITION LPS activated human monocyte expressing genes.  
 ACCESSION BD007884  
 VERSION BD007884.1 GI:18636257  
 KEYWORDS JP 2001069993-A/160.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 10)  
 AUTHORS Matsushima,K., Hashimoto,S. and Suzuki,T.  
 TITLE LPS activated human monocyte expressing genes  
 JOURNAL Patent: JP 2001069993-A 160 21-MAR-2001;  
 JAPAN SCIENCE AND TECHNOLOGY CORP  
 COMMENT OS Homo sapiens (human)  
 PN JP 2001069993-A/160  
 PD 21-MAR-2001  
 PF 28-APR-2000 JP 2000131079  
 PR KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC  
 C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC  
 A61P29/00,  
 PC A61P31/00,C12P21/08,C12N15/00  
 CC  
 FH Key Location/Qualifiers  
 FT source 1..10  
 FT /organism='Homo sapiens (human)'.  
 FEATURES  
 source 1..10  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 Query Match 29.0%; Score 8.4; DB 1; Length 10;  
 Best Local Similarity 90.0%; Pred. No. 1.5e+02;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 9 CTGCTGTGTG 18  
 |||||  
 Db 1 CTGCTATGTG 10  
 RESULT 189  
 AR051278  
 LOCUS AR051278 11 bp DNA linear PAT 29-SEP-1999  
 DEFINITION Sequence 15 from patent US 5830661.  
 ACCESSION AR051278  
 VERSION AR051278.1 GI:5974642  
 KEYWORDS .  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 UNCLASSIFIED  
 REFERENCE 1 (bases 1 to 11)  
 AUTHORS Sarfarazi,M.  
 TITLE Diagnosis and treatment of glaucoma  
 JOURNAL Patent: US 5830661-A 15 03-NOV-1998;  
 FEATURES  
 source 1..11  
 Location/Qualifiers  
 /organism="unknown"  
 /mol\_type="unassigned DNA"  
 Query Match 29.0%; Score 8.4; DB 1; Length 11;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 19 ACCTGCTAAA 28

Db 1 ACCAGGTAAA 10  
RESULT 190  
AR074507/c  
LOCUS AR074507 11 bp DNA linear PAT 28-AUG-2000  
DEFINITION Sequence 86 from patent US 5955075.  
ACCESSION AR074507  
VERSION AR074507.1 GI:10001262  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 11)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE Method of inhibiting tumor growth using antibodies to MN protein  
JOURNAL Patent: US 5955075-A 86 21-SEP-1999;  
FEATURES  
source Location/Qualifiers  
1..11  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 8 CCTGCTGTGT 17  
Db 10 CCTTCTGTGT 1  
RESULT 191  
AR077230  
LOCUS AR077230 11 bp DNA linear PAT 31-AUG-2000  
DEFINITION Sequence 15 from patent US 5962230.  
ACCESSION AR077230  
VERSION AR077230.1 GI:10003976  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 11)  
AUTHORS Sarfarazi,M.  
TITLE Diagnosis and treatment of glaucoma  
JOURNAL Patent: US 5962230-A 15 05-OCT-1999;  
FEATURES  
source Location/Qualifiers  
1..11  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 8 CCTGCTGTGT 17  
Db 10 CCTTCTGTGT 1  
RESULT 192  
AR081187/c  
LOCUS AR081187 11 bp DNA linear PAT 31-AUG-2000  
DEFINITION Sequence 86 from patent US 5972353.  
ACCESSION AR081187  
VERSION AR081187.1 GI:10007915  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 11)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE MN proteins, polypeptides, fusion proteins and fusion polypeptides

JOURNAL Patent: US 5972353-A 86 26-OCT-1999;  
FEATURES Location/Qualifiers  
source 1..11  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 8 CCTGCTGTGT 17  
Db 10 CCTTCTGTGT 1  
RESULT 193  
AR085384/c  
LOCUS AR085384 11 bp DNA linear PAT 01-SEP-2000  
DEFINITION Sequence 86 from patent US 5981711.  
ACCESSION AR085384  
VERSION AR085384.1 GI:10012153  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 11)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE MN-specific antibodies and hybridomas  
JOURNAL Patent: US 5981711-A 86 09-NOV-1999;  
FEATURES  
source Location/Qualifiers  
1..11  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 8 CCTGCTGTGT 17  
Db 10 CCTTCTGTGT 1  
RESULT 194  
AR088132/c  
LOCUS AR088132 11 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 86 from patent US 5989838.  
ACCESSION AR088132  
VERSION AR088132.1 GI:10014895  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 11)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE Immunological methods of detecting MN proteins and MN polypeptides  
JOURNAL Patent: US 5989838-A 86 23-NOV-1999;  
FEATURES  
source Location/Qualifiers  
1..11  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 8 CCTGCTGTGT 17  
Db 10 CCTTCTGTGT 1  
RESULT 195  
AR104291/c

```
LOCUS AR104291 11 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 86 from patent US 6093548.
ACCESSION AR104291
VERSION AR104291.1 GI:12816999
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE Detection and quantitation of MN-specific antibodies
JOURNAL Patent: US 6093548-A 86 25-JUL-2000;
FEATURES
    source
        1. .11
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGT 17
    ||| |||||
Db 10 CCTTCTGTGT 1

RESULT 196
AR143553/c
LOCUS AR143553 11 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 86 from patent US 6204370.
ACCESSION AR143553
VERSION AR143553.1 GI:15104839
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN gene and protein
JOURNAL Patent: US 6204370-A 86 20-MAR-2001;
FEATURES
    source
        1. .11
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGT 17
    ||| |||||
Db 10 CCTTCTGTGT 1

RESULT 196
AR143553/c
LOCUS AR143553 11 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 86 from patent US 6204370.
ACCESSION AR143553
VERSION AR143553.1 GI:15104839
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN gene and protein
JOURNAL Patent: US 6204370-A 86 20-MAR-2001;
FEATURES
    source
        1. .11
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGT 17
    ||| |||||
Db 10 CCTTCTGTGT 1

RESULT 197
AR171459/c
LOCUS AR171459 11 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 86 from patent US 6297041.
ACCESSION AR171459
VERSION AR171459.1 GI:17910409
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN gene and protein
JOURNAL Patent: US 6297041-A 86 02-OCT-2001;
FEATURES
    source
        1. .11
            /organism="unknown"
            /mol_type="unassigned DNA"
```

```
Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGT 17
    ||| |||||
Db 10 CCTTCTGTGT 1

RESULT 198
AR171630/c
LOCUS AR171630 11 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 86 from patent US 6297051.
ACCESSION AR171630
VERSION AR171630.1 GI:17910580
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN gene and protein
JOURNAL Patent: US 6297051-A 86 02-OCT-2001;
FEATURES
    source
        1. .11
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGT 17
    ||| |||||
Db 10 CCTTCTGTGT 1

RESULT 199
BD057177
LOCUS BD057177 11 bp DNA linear PAT 27-AUG-2002
DEFINITION Diagnosis and treatment of glaucoma.
ACCESSION BD057177
VERSION BD057177.1 GI:22602783
KEYWORDS JP 2001512969-A/15.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 11)
AUTHORS Sarfarazi,M.
TITLE Diagnosis and treatment of glaucoma
JOURNAL Patent: JP 2001512969-A 15 28-AUG-2001;
COMMENT THE UNIVERSITY OF CONNECTICUT
        PN JP 2001512969-A/15
        PD 28-AUG-2001
        PF 12-FEB-1998 JP 1998535963
        PR 13-FEB-1997 US 08/800036,10-SEP-1997 US 08/926492 PI
        MANSOOR SARFARAZI
        PC C12Q1/68,G01N33/50
        CC Strandedness: Single;
        CC Topology: Linear;
        FH Key Location/Qualifiers.
FEATURES
    source
        1. .11
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 19 ACCTGGTAAA 28
    ||| |||||
```

Db 1 ACCAGGTAAA 10

BD061634 11 bp DNA linear PAT 27-AUG-2002

LOCUS Human Lafora type epilepsy causal gene full-length sequence and use of mutation thereof.

DEFINITION BD061634

ACCESSION BD061634.1 GI:22607239

VERSION JP 2001299350-A/25.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 11)

AUTHORS Yamakawa,K. and Excweta,A.D.

TITLE Human Lafora type epilepsy causal gene full-length sequence and use of mutation thereof

JOURNAL Patent: JP 2001299350-A 25 30-OCT-2001;

COMMENT THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH

OS Homo sapiens (human)

PN JP 2001299350-A/25

PD 30-OCT-2001

PF 19-APR-2000 JP 2000118361

PI KAZUHIRO YAMAKAWA,ANTONIO DELGARD EXCWETA

PC C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC

FH Key Location/Qualifiers.

FEATURES

source 1. .11

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

Query Match 29.0%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 1.7e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 GTGACCTGGT 25

|||||

Db 2 GTGACTTGGT 11

RESULT 201

BD124282 11 bp DNA linear PAT 18-SEP-2002

LOCUS Compositions and method for healing wound.

DEFINITION BD124282

ACCESSION BD124282.1 GI:23219227

VERSION JP 2002503460-A/113.

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 11)

AUTHORS Katz,E.H.

TITLE Compositions and method for healing wound

JOURNAL Patent: JP 2002503460-A 113 05-FEB-2002;

COMMENT THE WISTAR INSTITUTE

OS Mus musculus (mouse)

PN JP 2002503460-A/113

PD 05-FEB-2002

PF 12-FEB-1999 JP 2000531545

PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR

28-SEP-1998 US 60/102051

PI ELLEN HEBER KATZ

PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC C12N5/00

CC Compositions and method for healing wound

FH Key Location/Qualifiers

FT source 1. .11

Query Match 29.0%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 1.7e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 GTGACCTGGT 25

|||||

Db 2 GTGACTTGGT 11

RESULT 201

BD124282 11 bp DNA linear PAT 18-SEP-2002

LOCUS Compositions and method for healing wound.

DEFINITION BD124282

ACCESSION BD124282.1 GI:23219227

VERSION JP 2002503460-A/113.

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 11)

AUTHORS Katz,E.H.

TITLE Compositions and method for healing wound

JOURNAL Patent: JP 2002503460-A 113 05-FEB-2002;

COMMENT THE WISTAR INSTITUTE

OS Mus musculus (mouse)

PN JP 2002503460-A/113

PD 05-FEB-2002

PF 12-FEB-1999 JP 2000531545

PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR

28-SEP-1998 US 60/102051

PI ELLEN HEBER KATZ

PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC C12N5/00

CC Compositions and method for healing wound

FH Key Location/Qualifiers

FT source 1. .11

FEATURES

source 1. .11

/organism="Mus musculus"

/mol\_type="genomic DNA"

/db\_xref="taxon:10090"

Query Match 29.0%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 1.7e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTGCTGTGTG 18

|||||

Db 1 CTGCTTTGTG 10

RESULT 202

BD124454 11 bp DNA linear PAT 18-SEP-2002

LOCUS Compositions and method for healing wound.

DEFINITION BD124454

ACCESSION BD124454.1 GI:23219399

VERSION JP 2002503460-A/285.

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 11)

AUTHORS Katz,E.H.

TITLE Compositions and method for healing wound

JOURNAL Patent: JP 2002503460-A 285 05-FEB-2002;

COMMENT THE WISTAR INSTITUTE

OS Mus musculus (mouse)

PN JP 2002503460-A/285

PD 05-FEB-2002

PF 12-FEB-1999 JP 2000531545

PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR

28-SEP-1998 US 60/102051

PI ELLEN HEBER KATZ

PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC C12N5/00

CC Compositions and method for healing wound

FH Key Location/Qualifiers

FT source 1. .11

/organism="Mus musculus (mouse)"

Query Match 29.0%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 1.7e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTGCTGTGTG 18

|||||

Db 1 CTGCTTTGTG 10

RESULT 203

BD243220/c 11 bp DNA linear PAT 17-JUL-2003

LOCUS MN gene and protein.

DEFINITION BD243220

ACCESSION BD243220.1 GI:33052990

VERSION JP 2002528085-A/69.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.





JOURNAL Patent: WO 2004059002-A 727 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 3 ATCCACCTGC 12  
| | | | | | | |  
Db 1 ACCCACCTGC 10  
  
RESULT 208  
CQ835321 11 bp DNA linear PAT 29-JUL-2004  
LOCUS  
DEFINITION Sequence 379 from Patent WO2004059001.  
ACCESSION CQ835321  
VERSION CQ835321.1 GI:50834855  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
Conradt,M. and Hofmann,K.  
TITLE Method for determining markers of human facial skin  
JOURNAL Patent: WO 2004059001-A 379 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 14 GTGTGACCTG 23  
| | | | | | | |  
Db 2 GTGAGACCTG 11  
  
RESULT 209  
CQ835588/c 11 bp DNA linear PAT 29-JUL-2004  
LOCUS  
DEFINITION Sequence 646 from Patent WO2004059001.  
ACCESSION CQ835588  
VERSION CQ835588.1 GI:50835122  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
Conradt,M. and Hofmann,K.  
TITLE Method for determining markers of human facial skin  
JOURNAL Patent: WO 2004059001-A 646 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 8 CCTGCTGTGT 17  
| | | | | | | |  
Db 11 CCTCCTGTGT 2  
  
RESULT 210  
CQ835701 11 bp DNA linear PAT 29-JUL-2004  
LOCUS  
DEFINITION Sequence 759 from Patent WO2004059001.  
ACCESSION CQ835701  
VERSION CQ835701.1 GI:50835235  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
Conradt,M. and Hofmann,K.  
TITLE Method for determining markers of human facial skin  
JOURNAL Patent: WO 2004059001-A 759 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 2 CATCCACCTG 11  
| | | | | | | |  
Db 1 CATCCATCTG 10  
  
RESULT 211  
CQ836236 11 bp DNA linear PAT 29-JUL-2004  
LOCUS  
DEFINITION Sequence 1294 from Patent WO2004059001.  
ACCESSION CQ836236  
VERSION CQ836236.1 GI:50835770  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
Conradt,M. and Hofmann,K.  
TITLE Method for determining markers of human facial skin  
JOURNAL Patent: WO 2004059001-A 1294 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 3 ATCCACCTGC 12  
| | | | | | | |



REFERENCE 1 Hominidae; Homo.  
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O., Conradt,M. and Hofmann,K.  
TITLE Method for determining markers of human facial skin  
JOURNAL Patent: WO 2004059001-A 2564 15-JUL-2004;  
FEATURES  
source Location/Qualifiers  
1 .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 4 TCCACCTGCT 13 11 bp DNA linear PAT 29-JUL-2004  
Db 11 TCCACCTCCT 2  
RESULT 217  
CQ837969/c  
LOCUS CQ837969 11 bp DNA linear PAT 29-JUL-2004  
DEFINITION Sequence 3027 from Patent WO2004059001.  
ACCESSION CQ837969  
VERSION CQ837969.1 GI:50837503  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O., Conradt,M. and Hofmann,K.  
TITLE Method for determining markers of human facial skin  
JOURNAL Patent: WO 2004059001-A 3027 15-JUL-2004;  
FEATURES  
source Location/Qualifiers  
1 .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 4 TCCACCTGCT 13 11 bp DNA linear PAT 13-APR-2005  
Db 11 TCCAGCTGCT 2  
RESULT 218  
CQ837969/c  
LOCUS CQ837969 11 bp DNA linear PAT 13-APR-2005  
DEFINITION Sequence 78 from Patent WO2005028671.  
ACCESSION CQ837969  
VERSION CQ837969.1 GI:62551133  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and Kessler-Becker,D.  
TITLE Method for determining hair cycle markers  
JOURNAL Patent: WO 2005028671-A 78 31-MAR-2005;  
FEATURES  
source Location/Qualifiers  
1 .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

FEATURES  
source Location/Qualifiers  
1 .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 3 ATCCACCTGC 12 11 bp DNA linear PAT 13-APR-2005  
Db 1 ATCCACCCGC 10  
RESULT 219  
CS058234/c  
LOCUS CS058234 11 bp DNA linear PAT 13-APR-2005  
DEFINITION Sequence 131 from Patent WO2005028671.  
ACCESSION CS058234  
VERSION CS058234.1 GI:62551417  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and Kessler-Becker,D.  
TITLE Method for determining hair cycle markers  
JOURNAL Patent: WO 2005028671-A 131 31-MAR-2005;  
FEATURES  
source Location/Qualifiers  
1 .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 4 TCCACCTGCT 13 11 bp DNA linear PAT 13-APR-2005  
Db 11 TCCAGCTGCT 2  
RESULT 220  
CS058596  
LOCUS CS058596 11 bp DNA linear PAT 13-APR-2005  
DEFINITION Sequence 493 from Patent WO2005028671.  
ACCESSION CS058596  
VERSION CS058596.1 GI:62551779  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and Kessler-Becker,D.  
TITLE Method for determining hair cycle markers  
JOURNAL Patent: WO 2005028671-A 493 31-MAR-2005;  
FEATURES  
source Location/Qualifiers  
1 .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 4 TCCACCTGCT 13 11 bp DNA linear PAT 13-APR-2005  
Db 11 TCCAGCTGCT 2  
RESULT 220  
CS058596  
LOCUS CS058596 11 bp DNA linear PAT 13-APR-2005  
DEFINITION Sequence 493 from Patent WO2005028671.  
ACCESSION CS058596  
VERSION CS058596.1 GI:62551779  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and Kessler-Becker,D.  
TITLE Method for determining hair cycle markers  
JOURNAL Patent: WO 2005028671-A 493 31-MAR-2005;  
FEATURES  
source Location/Qualifiers  
1 .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Best Local Similarity 90.0%; Pred. No. 1.7e+02; Mismatches 1; Indels 0; Gaps 0; Matches 9; Conservative 0;

QY 6 CACCTGCTGT 15  
Db |||||

2 CACTTGCTGT 11

RESULT 221

AR301532

LOCUS AR301532 11 bp DNA linear PAT 12-JUN-2003

DEFINITION Sequence 113 from patent US 6538173.

ACCESSION AR301532

VERSION AR301532.1 GI:31689334

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 11)

AUTHORS Heber-Katz,E.

TITLE Compositions and methods for wound healing

JOURNAL Patent: US 6538173-A 113 25-MAR-2003;

The Wistar Institute; Philadelphia, PA; WOX;

FEATURES

source Location/Qualifiers

1. .11

/organism="unknown"

/mol\_type="genomic DNA"

Query Match 29.0%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 1.7e+02; Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTGCTGTGTG 18  
Db |||||

1 CTGCTTTGTG 10

RESULT 222

AR301704

LOCUS AR301704 11 bp DNA linear PAT 12-JUN-2003

DEFINITION Sequence 285 from patent US 6538173.

ACCESSION AR301704

VERSION AR301704.1 GI:31689506

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 11)

AUTHORS Heber-Katz,E.

TITLE Compositions and methods for wound healing

JOURNAL Patent: US 6538173-A 285 25-MAR-2003;

The Wistar Institute; Philadelphia, PA; WOX;

FEATURES

source Location/Qualifiers

1. .11

/organism="unknown"

/mol\_type="genomic DNA"

Query Match 29.0%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 1.7e+02; Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTGCTGTGTG 18  
Db |||||

1 CTGCTTTGTG 10

RESULT 223

AR569658/c

LOCUS AR569658 11 bp DNA linear PAT 14-DEC-2004

DEFINITION Sequence 86 from patent US 6770438.

ACCESSION AR569658

VERSION AR569658.1 GI:56570287

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 11)

AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.

TITLE MN gene and protein

JOURNAL Patent: US 6770438-A 86 03-AUG-2004;

Institute of Virology, Slovak Academy of Sciences; Bratislava; CZX;

FEATURES

source Location/Qualifiers

1. .11

/organism="unknown"

/mol\_type="genomic DNA"

Query Match 29.0%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 1.7e+02; Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGT 17  
Db |||||

10 CCTTCTGTGT 1

RESULT 224

AX085766

LOCUS AX085766 11 bp DNA linear PAT 09-MAR-2001

DEFINITION Sequence 28 from Patent WO0112858.

ACCESSION AX085766

VERSION AX085766.1 GI:13275716

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS He,T.C., Kinzler,K.W. and Vogelstein,B.

TITLE ppar g(d) links apc to chemopreventive drugs

JOURNAL Patent: WO 0112858-A 28 22-FEB-2001;

The Johns Hopkins University (US)

FEATURES

source Location/Qualifiers

1. .11

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

Query Match 29.0%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 1.7e+02; Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 20 CCTGCTAAAT 29  
Db |||||

1 CCTGCTCAAT 10

RESULT 225

AX470852

LOCUS AX470852 11 bp DNA linear PAT 09-AUG-2002

DEFINITION Sequence 429 from Patent WO02053773.

ACCESSION AX470852

VERSION AX470852.1 GI:22205977

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.

TITLE Method for determining skin stress or skin ageing in vitro

JOURNAL Patent: WO 02053773-A 429 11-JUL-2002;



FEATURES  
source  
HENKEL KGAA (DE)  
Location/Qualifiers  
1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ATCCACCTGC 12  
|||||  
Db 1 ATCCACCCGC 10

RESULT 226  
AX470941/c  
LOCUS AX470941 11 bp DNA linear PAT 09-AUG-2002  
DEFINITION Sequence 518 from Patent WO02053773.  
ACCESSION AX470941  
VERSION AX470941.1 GI:22206066  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE Hofmann,K., Conradt,M. and Petersohn,D.  
AUTHORS Method for determining skin stress or skin ageing in vitro  
TITLE Patent: WO 02053773-A 518 11-JUL-2002;  
JOURNAL HENKEL KGAA (DE)  
FEATURES Location/Qualifiers  
source 1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGT 17  
|||||  
Db 11 CCTCCTGTGT 2

RESULT 227  
AX471016/c  
LOCUS AX471016 11 bp DNA linear PAT 09-AUG-2002  
DEFINITION Sequence 593 from Patent WO02053773.  
ACCESSION AX471016  
VERSION AX471016.1 GI:22206141  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE Hofmann,K., Conradt,M. and Petersohn,D.  
AUTHORS Method for determining skin stress or skin ageing in vitro  
TITLE Patent: WO 02053773-A 593 11-JUL-2002;  
JOURNAL HENKEL KGAA (DE)  
FEATURES Location/Qualifiers  
source 1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ATCCACCTGC 12  
|||||  
Db 10 ATCCAACTGC 1

RESULT 228  
AX471168  
LOCUS AX471168 11 bp DNA linear PAT 09-AUG-2002  
DEFINITION Sequence 745 from Patent WO02053773.  
ACCESSION AX471168  
VERSION AX471168.1 GI:22206293  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE Hofmann,K., Conradt,M. and Petersohn,D.  
AUTHORS Method for determining skin stress or skin ageing in vitro  
TITLE Patent: WO 02053773-A 745 11-JUL-2002;  
JOURNAL HENKEL KGAA (DE)  
FEATURES Location/Qualifiers  
source 1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ATCCACCTGC 12  
|||||  
Db 1 ATCCGCCTGC 10

RESULT 229  
AX471345/c  
LOCUS AX471345 11 bp DNA linear PAT 09-AUG-2002  
DEFINITION Sequence 922 from Patent WO02053773.  
ACCESSION AX471345  
VERSION AX471345.1 GI:22206470  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE Hofmann,K., Conradt,M. and Petersohn,D.  
AUTHORS Method for determining skin stress or skin ageing in vitro  
TITLE Patent: WO 02053773-A 922 11-JUL-2002;  
JOURNAL HENKEL KGAA (DE)  
FEATURES Location/Qualifiers  
source 1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 16 GTGACCTGGT 25  
|||||  
Db 10 GTGGCCTGGT 1

RESULT 230  
AX471608

LOCUS AX471608 11 bp DNA linear PAT 09-AUG-2002  
DEFINITION Sequence 1185 from Patent WO02053773.  
ACCESSION AX471608  
VERSION AX471608.1 GI:22206733  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.  
TITLE Method for determining skin stress or skin ageing in vitro  
JOURNAL Patent: WO 02053773-A 1185 11-JUL-2002;  
HENKEL KGAA (DE)  
FEATURES  
source Location/Qualifiers  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 4 TCCACCTGCT 13  
|||||  
Db 2 TCCAGCTGCT 11  
RESULT 231  
AX6233509/c  
LOCUS AX6233509 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 550 from Patent WO02053774.  
ACCESSION AX6233509  
VERSION AX6233509.1 GI:28451450  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 550 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source Location/Qualifiers  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 4 TCCACCTGCT 13  
|||||  
Db 11 TCCACCTCCT 2  
RESULT 232  
AX6233560/c  
LOCUS AX6233560 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 601 from Patent WO02053774.  
ACCESSION AX6233560  
VERSION AX6233560.1 GI:28451501  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 601 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source Location/Qualifiers  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 8 CCTGCTGTGT 17  
|||||  
Db 11 CCTCCTGTGT 2  
RESULT 233  
AX624060  
LOCUS AX624060 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 1101 from Patent WO02053774.  
ACCESSION AX624060  
VERSION AX624060.1 GI:28452001  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 1101 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source Location/Qualifiers  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 ATCCACCTGC 12  
|||||  
Db 1 ATCCGCCTGC 10  
RESULT 234  
AX624161/c  
LOCUS AX624161 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 1202 from Patent WO02053774.  
ACCESSION AX624161  
VERSION AX624161.1 GI:28452102  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 1202 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source Location/Qualifiers  
1. .11  
/organism="Homo sapiens"

/mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 Query Match 29.0%; Score 8.4; DB 1; Length 11;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 8 CCTGCTGTGT 17  
 | |||||  
 Db 10 CTTGCTGTGT 1  
 RESULT 235  
 AX624988/c  
 LOCUS AX624988 11 bp DNA PAT 21-FEB-2003  
 DEFINITION Sequence 2029 from Patent WO02053774.  
 ACCESSION AX624988  
 VERSION AX624988.1 GI:28452929  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
 TITLE Method for determining homeostasis of the skin  
 JOURNAL Patent: WO 02053774-A 2029 11-JUL-2002;  
 Henkel Kommanditgesellschaft auf Aktien (DE)  
 FEATURES  
 source Location/Qualifiers  
 1. .11  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 Query Match 29.0%; Score 8.4; DB 1; Length 11;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 ATCCACCTGC 12  
 | |||||  
 Db 10 ATCCAACATGC 1  
 RESULT 236  
 AX626149  
 LOCUS AX626149 11 bp DNA PAT 21-FEB-2003  
 DEFINITION Sequence 3190 from Patent WO02053774.  
 ACCESSION AX626149  
 VERSION AX626149.1 GI:28454187  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
 TITLE Method for determining homeostasis of the skin  
 JOURNAL Patent: WO 02053774-A 3190 11-JUL-2002;  
 Henkel Kommanditgesellschaft auf Aktien (DE)  
 FEATURES  
 source Location/Qualifiers  
 1. .11  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 Query Match 29.0%; Score 8.4; DB 1; Length 11;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 TCCACCTGCT 13  
 | |||||

Db 2 TCCAGCTGCT 11  
 RESULT 237  
 AX626748/c  
 LOCUS AX626748 11 bp DNA PAT 21-FEB-2003  
 DEFINITION Sequence 3789 from Patent WO02053774.  
 ACCESSION AX626748  
 VERSION AX626748.1 GI:28454786  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
 TITLE Method for determining homeostasis of the skin  
 JOURNAL Patent: WO 02053774-A 3789 11-JUL-2002;  
 Henkel Kommanditgesellschaft auf Aktien (DE)  
 FEATURES  
 source Location/Qualifiers  
 1. .11  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 Query Match 29.0%; Score 8.4; DB 1; Length 11;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 16 GTGACCTGGT 25  
 | || |||||  
 Db 10 GTGGCCTGGT 1  
 RESULT 238  
 AX626997/c  
 LOCUS AX626997 11 bp DNA PAT 21-FEB-2003  
 DEFINITION Sequence 4038 from Patent WO02053774.  
 ACCESSION AX626997  
 VERSION AX626997.1 GI:28455035  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
 TITLE Method for determining homeostasis of the skin  
 JOURNAL Patent: WO 02053774-A 4038 11-JUL-2002;  
 Henkel Kommanditgesellschaft auf Aktien (DE)  
 FEATURES  
 source Location/Qualifiers  
 1. .11  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 Query Match 29.0%; Score 8.4; DB 1; Length 11;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 7 ACCTGCTGTG 16  
 | |||||  
 Db 10 ACCTGCTGGG 1  
 RESULT 239  
 AX627183  
 LOCUS AX627183 11 bp DNA PAT 21-FEB-2003  
 DEFINITION Sequence 4224 from Patent WO02053774.  
 ACCESSION AX627183  
 VERSION AX627183.1 GI:28455221

KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 4224 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES Location/Qualifiers  
source 1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 9 CTGCTGTGTG 18  
|| |||||  
Db 1 CTTCTGTGTG 10  
RESULT 240  
AX627753  
LOCUS AX627753 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 4794 from Patent WO02053774.  
ACCESSION AX627753  
VERSION AX627753.1 GI:28455791  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 4794 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES Location/Qualifiers  
source 1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 3 ATCCACCTGC 12  
|||||  
Db 1 ATCCACCCGC 10  
RESULT 241  
AX627875/c  
LOCUS AX627875 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 4916 from Patent WO02053774.  
ACCESSION AX627875  
VERSION AX627875.1 GI:28455913  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin

JOURNAL Patent: WO 02053774-A 4916 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES Location/Qualifiers  
source 1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 4 TCCACCTGCT 13  
|||||  
Db 11 TCCACCTCCT 2  
RESULT 242  
AX627970  
LOCUS AX627970 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 5011 from Patent WO02053774.  
ACCESSION AX627970  
VERSION AX627970.1 GI:28456008  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 5011 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES Location/Qualifiers  
source 1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 3 ATCCACCTGC 12  
|||||  
Db 1 ACCCACCTGC 10  
RESULT 243  
AX628145/c  
LOCUS AX628145 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 5186 from Patent WO02053774.  
ACCESSION AX628145  
VERSION AX628145.1 GI:28456183  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 5186 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES Location/Qualifiers  
source 1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 29.0%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 1.7e+02; Mismatches 0; Indels 1; Gaps 0; Matches 9; Conservative 0; Gaps 0;

QY 4 TCCACCTGCT 13  
| | | | | | | |  
Db 11 TCCACCTGGT 2

RESULT 244  
AX628168  
LOCUS AX628168 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 5209 from Patent WO02053774.  
ACCESSION AX628168  
VERSION AX628168.1 GI:28456206  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 5209 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES  
source Location/Qualifiers  
1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02; Mismatches 0; Indels 1; Gaps 0; Matches 9; Conservative 0; Gaps 0;

QY 4 TCCACCTGCT 13  
| | | | | | | |  
Db 2 TCCACCTGGT 11

RESULT 245  
AX628220/c  
LOCUS AX628220 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 5261 from Patent WO02053774.  
ACCESSION AX628220  
VERSION AX628220.1 GI:28456258  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 5261 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES  
source Location/Qualifiers  
1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02; Mismatches 0; Indels 1; Gaps 0; Matches 9; Conservative 0; Gaps 0;

QY 17 TGACCTGGTA 26  
| | | | | | | |  
Db 11 TGACCTGGGA 2

RESULT 246

AX628331  
LOCUS AX628331 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 5372 from Patent WO02053774.  
ACCESSION AX628331  
VERSION AX628331.1 GI:28456369  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 5372 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES  
source Location/Qualifiers  
1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02; Mismatches 0; Indels 1; Gaps 0; Matches 9; Conservative 0; Gaps 0;

QY 14 GTGTGACCTG 23  
| | | | | | | |  
Db 2 GTGAGACCTG 11

RESULT 247  
AX628518/c  
LOCUS AX628518 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 5559 from Patent WO02053774.  
ACCESSION AX628518  
VERSION AX628518.1 GI:28456556  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 5559 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES  
source Location/Qualifiers  
1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02; Mismatches 0; Indels 1; Gaps 0; Matches 9; Conservative 0; Gaps 0;

QY 3 ATCCACCTGC 12  
| | | | | | | |  
Db 11 ATCCACCTTC 2

RESULT 248  
AX629299/c  
LOCUS AX629299 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 6340 from Patent WO02053774.  
ACCESSION AX629299  
VERSION AX629299.1 GI:28457337  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;



```

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1  Petersohn,D., Conradt,M. and Hofmann,K.
   TITLE  Method for determining homeostasis of the skin
   JOURNAL Patent: WO 02053774-A 6340 11-JUL-2002;
   FEATURES  Henkel Kommanditgesellschaft auf Aktien (DE)
            Location/Qualifiers
            source      1. .11
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"

Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCCACCTGCT 13
   ||||| |||||
Db 11 TCCAGCTGCT 2

RESULT 249
AX629728
LOCUS AX629728 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6769 from Patent WO02053774.
ACCESSION AX629728
VERSION AX629728.1 GI:28457766
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1  Petersohn,D., Conradt,M. and Hofmann,K.
   TITLE  Method for determining homeostasis of the skin
   JOURNAL Patent: WO 02053774-A 6769 11-JUL-2002;
   FEATURES  Henkel Kommanditgesellschaft auf Aktien (DE)
            Location/Qualifiers
            source      1. .11
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"

Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 TGTGTGACCT 22
   ||||| |||||
Db 1 TCTGTGACCT 10

RESULT 250
AX629959
LOCUS AX629959 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7000 from Patent WO02053774.
ACCESSION AX629959
VERSION AX629959.1 GI:28457997
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1  Petersohn,D., Conradt,M. and Hofmann,K.
   TITLE  Method for determining homeostasis of the skin
   JOURNAL Patent: WO 02053774-A 7000 11-JUL-2002;
   FEATURES  Henkel Kommanditgesellschaft auf Aktien (DE)
            Location/Qualifiers
            source      1. .11

```

```

/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 TGCTGTGTGA 19
   ||||| |||||
Db 2 TGCTGCGTGA 11

RESULT 251
AX630263/c
LOCUS AX630263 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7304 from Patent WO02053774.
ACCESSION AX630263
VERSION AX630263.1 GI:28458301
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1  Petersohn,D., Conradt,M. and Hofmann,K.
   TITLE  Method for determining homeostasis of the skin
   JOURNAL Patent: WO 02053774-A 7304 11-JUL-2002;
   FEATURES  Henkel Kommanditgesellschaft auf Aktien (DE)
            Location/Qualifiers
            source      1. .11
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"

Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATCCACCTGC 12
   ||||| |||||
Db 10 AACCACCTGC 1

RESULT 252
AX630930/c
LOCUS AX630930 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7971 from Patent WO02053774.
ACCESSION AX630930
VERSION AX630930.1 GI:28458972
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1  Petersohn,D., Conradt,M. and Hofmann,K.
   TITLE  Method for determining homeostasis of the skin
   JOURNAL Patent: WO 02053774-A 7971 11-JUL-2002;
   FEATURES  Henkel Kommanditgesellschaft auf Aktien (DE)
            Location/Qualifiers
            source      1. .11
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"

Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCCACCTGCT 13

```

Db 11 TCCACCTCCT 2

RESULT 253  
AX630981/c  
LOCUS AX630981 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 8022 from Patent WO02053774.  
ACCESSION AX630981  
VERSION AX630981.1 GI:28459023  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 8022 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGT 17  
| | | | | | | |  
Db 11 CCTCCTGTGT 2

RESULT 254  
AX631481  
LOCUS AX631481 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 8523 from Patent WO02053774.  
ACCESSION AX631481  
VERSION AX631481.1 GI:28459547  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 8523 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATCCACCTGC 12  
| | | | | | | |  
Db 1 ATCCGCCTGC 10

RESULT 255  
AX631582/c  
LOCUS AX631582 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 8624 from Patent WO02053774.  
ACCESSION AX631582

VERSION AX631582.1 GI:28459658  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 8624 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGT 17  
| | | | | | | |  
Db 10 CTGTGTGTGT 1

RESULT 256  
AX632409/c  
LOCUS AX632409 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 9451 from Patent WO02053774.  
ACCESSION AX632409  
VERSION AX632409.1 GI:28468024  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 9451 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 29.0%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATCCACCTGC 12  
| | | | | | | |  
Db 10 ATCCAACCTGC 1

RESULT 257  
HSPMLEX43  
LOCUS HSPMLEX43 11 bp DNA linear PRI 04-AUG-1992  
DEFINITION H.sapiens pml gene, exon 4.  
ACCESSION X63632  
VERSION X63632.1 GI:35538  
KEYWORDS PML gene; PML protein.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Pandolfi,P.P., Alcalay,M., Fagioli,M., Zangrilli,D., Mencarelli,A.,

Diverio,D., Biondi,A., Lo Coco,F., Rambaldi,A., Grignani,F.,
Rochette-Egly,C., Gaube,M.P., Chambon,P. and Pelicci,P.G.
Genomic variability and alternative splicing generate multiple
PML/RAR alpha transcripts that encode aberrant PML proteins and
PML/RAR alpha isoforms in acute promyelocytic leukaemia
EMBO J. 11 (4), 1397-1407 (1992)
1314166
2 (bases 1 to 11)
Fagioli,M., Alcalay,M., Pandolfi,P.P., Venturini,L., Mencarelli,A.,
Simeone,A., Acampora,D., Grignani,F. and Pelicci,P.G.
Alternative splicing of PML transcripts predicts coexpression of
several carboxy-terminally different protein isoforms
Oncogene 7 (6), 1083-1091 (1992)
1594241
3 (bases 1 to 11)
Pandolfi,P.P.
Direct Submission
Submitted (30-JAN-1992) P.P. Pandolfi, Istituto di Clinica Medica
I, University of Perugia, Policlinico Monteluce, 06100 Perugia,
ITALY
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol\_type="genomic DNA"
/db\_xref="taxon:9606"
/chromosome="15"
/map="15q24"
/cell\_line="WI38"
/clone\_lib="WI38 in lambda-FIX-II (Stratagene)"
1. .6
/gene="PML"
<1. .6
/gene="PML"
/product="PML (PML-EX4-3') "
/number=4
7. .>11
/number=4
gene
exon
intron
Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 18 GACCTGGTAA 27
|||||
Db 1 GACCTGGTGA 10
RESULT 258
A71560/c
LOCUS A71560 12 bp DNA linear PAT 07-MAY-1999
DEFINITION Sequence 119 from Patent WO9813521.
ACCESSION A71560
VERSION A71560.1 GI:4775172
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified sequences.
REFERENCE 1 (bases 1 to 12)
AUTHORS Fesce,R. and Consalez,G.
TITLE METHOD FOR THE DIFFERENTIAL SCREENING OF GENE EXPRESSION BY RANDOM
PRIMED REVERSE TRANSCRIPTION-POLYMERASE CHAIN REACTION
JOURNAL Patent: WO 9813521-A 119 02-APR-1998;
FESCE RICCARDO (IT)
FEATURES
source
Location/Qualifiers
1. .12
/organism="unidentified"
/mol\_type="unassigned DNA"
/db\_xref="taxon:32644"
Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCCACCT 10
|||||
Db 10 CCACCCACCT 1
RESULT 259
AR167777
LOCUS AR167777 12 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 141 from patent US 6287769.
ACCESSION AR167777
VERSION AR167777.1 GI:17903579
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Inoue,T.
TITLE Method of amplifying DNA fragment, apparatus for amplifying DNA
fragment, method of assaying microorganisms, method of analyzing
microorganisms and method of assaying contaminant
JOURNAL Patent: US 6287769-A 141 11-SEP-2001;
FEATURES
source
Location/Qualifiers
1. .12
/organism="unknown"
/mol\_type="unassigned DNA"
Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 CACCTGCTGT 15
|||||
Db 1 CTCCTGCTGT 10
RESULT 260
AR167827/c
LOCUS AR167827 12 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 191 from patent US 6287769.
ACCESSION AR167827
VERSION AR167827.1 GI:17903633
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Inoue,T.
TITLE Method of amplifying DNA fragment, apparatus for amplifying DNA
fragment, method of assaying microorganisms, method of analyzing
microorganisms and method of assaying contaminant
JOURNAL Patent: US 6287769-A 191 11-SEP-2001;
FEATURES
source
Location/Qualifiers
1. .12
/organism="unknown"
/mol\_type="unassigned DNA"
Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 CCACCTGCTG 14
|||||
Db 11 CCACCTCCTG 2
RESULT 261
BD143765/c
LOCUS BD143765 12 bp DNA linear PAT 17-JAN-2003
DEFINITION bZIP transcription factor controlling the expression of rice
storage protein.
ACCESSION BD143765
VERSION BD143765.1 GI:27849523
KEYWORDS JP 2002119282-A/12.

SOURCE  
ORGANISM  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 12)  
Takaiwa,F. and Onodera,Y.  
bZIP transcription factor controlling the expression of rice storage protein  
Patent: JP 2002119282-A 12 23-APR-2002;  
DIRECTOR GENERAL OF NATIONAL INSTITUTE OF AGROBIOLOGICAL RESOURCES  
MINISTRY OF AGRICULTURE FORESTRY AND FISHERIES, BIO ORIENTED TECHNOLOGY RESEARCH ADVANCEMENT INSTITUTION  
OS Oryza sativa (rice)  
PN JP 2002119282-A/12  
PD 23-APR-2002  
PF 11-OCT-2000 JP 2000311295  
PI FUMIO TAKAIWA, YASUYUKI ONODERA  
PC C12N15/09,A01H5/00,C07K14/415,C07K16/16,C12N1/15,C12N1/19, PC C12N1/21,  
PC C12N5/10,C12N5/10,C12N9/22,C12P21/02,C12P21/08//C12Q1/02, PC (C12N15/09,C12R1:91), (C12N5/10,C12R1:91), (C12P21/02,C12R1:91), PC C12N15/00,  
PC C12N5/00,C12N5/00, (C12N15/00,C12R1:91), (C12N5/00,C12R1:91) CC bZIP transcription factor controlling the expression of rice CC storage  
CC protein  
FH Key  
FT source  
FT Location/Qualifiers  
1..12  
/organism="Oryza sativa"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:4530"  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 15 TGTGACCTGG 24  
|||||  
Db 12 TGTGACGTGG 3  
RESULT 262  
BD168627/c  
LOCUS  
DEFINITION  
BZIP type transcriptional factor regulating the expression of rice reserve protein.  
ACCESSION  
BD168627.1 GI:27874439  
VERSION  
WO 0231154-A/12.  
KEYWORDS  
Oryza sativa  
SOURCE  
ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 12)  
Takaiwa,F. and Onodera,Y.  
bZIP type transcriptional factor regulating the expression of rice reserve protein  
Patent: WO 0231154-A 12 18-APR-2002;  
NATIONAL INSTITUTE OF AGROBIOLOGICAL SCIENCES, BIO ORIENTED TECHNOLOGY RESEARCH ADVANCEMENT INSTITUTION, FUMIO TAKAIWA, YASUYUKI ONODERA  
OS Oryza sativa (rice)  
PN WO 0231154-A/12  
PD 18-APR-2002  
PF 11-OCT-2001 WO 2001JP008936  
PR 11-OCT-2000 JP 00P 311295  
PI FUMIO TAKAIWA, YASUYUKI ONODERA  
PC C12N15/29,C12N5/14,C07K14/415,A01H5/00

CC BZIP type transcriptional factor regulating the expression of rice reserve  
CC protein  
FH Key  
FT source  
FT Location/Qualifiers  
1..12  
/organism="Oryza sativa (rice)".  
FEATURES  
source  
1..12  
/organism="Oryza sativa"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:4530"  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 15 TGTGACCTGG 24  
|||||  
Db 12 TGTGACGTGG 3  
RESULT 263  
CQ766277/c  
LOCUS  
DEFINITION  
Sequence 238 from Patent WO2004005547.  
ACCESSION  
CQ766277  
VERSION  
CQ766277.1 GI:44908537  
KEYWORDS  
synthetic construct  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
1  
AUTHORS  
Weinzierl,R.  
TITLE  
Method  
JOURNAL  
Patent: WO 2004005547-A 238 15-JAN-2004;  
IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)  
FEATURES  
source  
1..12  
Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="HS motif"  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 9 CTGCTGTGTG 18  
|||||  
Db 11 CTGCTGTGAG 2  
RESULT 264  
CQ828759/c  
LOCUS  
DEFINITION  
Sequence 477 from Patent WO2004053120.  
ACCESSION  
CQ828759  
VERSION  
CQ828759.1 GI:49732242  
KEYWORDS  
Mus musculus (house mouse)  
SOURCE  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
REFERENCE  
1  
AUTHORS  
Weihe,E., Bieller,A. and Schaefer,M.K.  
TITLE  
Regulatory elements in the 5' region of the vrl gene  
JOURNAL  
Patent: WO 2004053120-A 477 24-JUN-2004;  
Gruenthal GmbH (DE)  
FEATURES  
source  
1..12  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="unassigned DNA"





```
PC      C12N15/09,B09B3/00,C12Q1/00,C12Q1/68,C12N15/00,B09B3/00 CC
Strandedness: Single;
FH      Key      Location/Qualifiers
FT      source    1..12
                /organism='Unidentified'.

FEATURES             source
    source           1..12
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"

Query Match      29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 CCACCTGCTG 14
        |||||||
Db      11 CCACCTCCTG 2

RESULT 269
E38767
LOCUS      E38767      12 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION Method and device for amplifying DNA fragment.
ACCESSION  E38767
VERSION    E38767.1 GI:18621429
KEYWORDS   JP 2000270867-A/141.
SOURCE     unidentified
ORGANISM   unidentified
            unclassified.
REFERENCE  1 (bases 1 to 12)
AUTHORS   Inoue,K.
TITLE     Method and device for amplifying DNA fragment
JOURNAL   Patent: JP 2000270867-A 141 03-OCT-2000;
          SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
          FORESTRY AND FISHERIES

COMMENT    OS      Unidentified
           PN      JP 2000270867-A/141
           PD      03-OCT-2000
           PF      19-MAR-1999 JP 1999076844
           PR
           PI      KOICHI INOUE
           PC      C12N15/09,C12M1/00,C12Q1/68,C12N15/00
           CC      Strandedness: Single;
           CC      Topology: Linear;
           FH      Key      Location/Qualifiers
           FT      source    1..12
           FT      source    /organism='Unidentified'.

E38767
LOCUS      E38767      12 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION Method and device for amplifying DNA fragment
ACCESSION  E38767
VERSION    E38767.1 GI:18621429
KEYWORDS   JP 2000270867-A/141
SOURCE     unidentified
ORGANISM   unidentified
            unclassified.
REFERENCE  1 (bases 1 to 12)
AUTHORS   Inoue,K.
TITLE     Method and device for amplifying DNA fragment
JOURNAL   Patent: JP 2000270867-A 141 03-OCT-2000;
          SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
          FORESTRY AND FISHERIES

COMMENT    OS      Unidentified
           PN      JP 2000270867-A/141
           PD      03-OCT-2000
           PF      19-MAR-1999 JP 1999076844
           PR
           PI      KOICHI INOUE
           PC      C12N15/09,C12M1/00,C12Q1/68,C12N15/00
           CC      Strandedness: Single;
           CC      Topology: Linear;
           FH      Key      Location/Qualifiers
           FT      source    1..12
           FT      source    /organism='Unidentified'.

FEATURES             source
    source           1..12
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"

Query Match      29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 CACCTGCTGT 15
        |||||||
Db      1 CTCCTGCTGT 10

RESULT 270
E38817/c
LOCUS      E38817      12 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION Method and device for amplifying DNA fragment.
ACCESSION  E38817
VERSION    E38817.1 GI:18621479
KEYWORDS   JP 2000270867-A/191.
SOURCE     unidentified
ORGANISM   unidentified
            unclassified.

PC      C12N15/09,B09B3/00,C12Q1/00,C12Q1/68,C12N15/00,B09B3/00 CC
Strandedness: Single;
FH      Key      Location/Qualifiers
FT      source    1..12
                /organism='Unidentified'.

FEATURES             source
    source           1..12
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"

Query Match      29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 CACCTGCTGT 15
        |||||||
Db      1 CTCCTGCTGT 10

RESULT 270
E38817/c
LOCUS      E38817      12 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION Method and device for amplifying DNA fragment.
ACCESSION  E38817
VERSION    E38817.1 GI:18621479
KEYWORDS   JP 2000270867-A/191.
SOURCE     unidentified
ORGANISM   unidentified
            unclassified.
```

```
REFERENCE  1 (bases 1 to 12)
AUTHORS   Inoue,K.
TITLE     Method and device for amplifying DNA fragment
JOURNAL   Patent: JP 2000270867-A 191 03-OCT-2000;
          SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
          FORESTRY AND FISHERIES

COMMENT    OS      Unidentified
           PN      JP 2000270867-A/191
           PD      03-OCT-2000
           PF      19-MAR-1999 JP 1999076844
           PR
           PI      KOICHI INOUE
           PC      C12N15/09,C12M1/00,C12Q1/68,C12N15/00
           CC      Strandedness: Single;
           CC      Topology: Linear;
           FH      Key      Location/Qualifiers
           FT      source    1..12
           FT      source    /organism='Unidentified'.

FEATURES             source
    source           1..12
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"

Query Match      29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 CCACCTGCTG 14
        |||||||
Db      11 CCACCTCCTG 2

RESULT 271
E64193
LOCUS      E64193      12 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Method for amplifying DNA fragment, amplification apparatus of DNA
            fragment, method for assaying a group of microorganisms, method
            for analyzing a group of microorganisms, and method for assaying
            contaminating substance.
ACCESSION  E64193
VERSION    E64193.1 GI:13019597
KEYWORDS   JP 1999341989-A/141.
SOURCE     synthetic construct
ORGANISM   synthetic construct
            other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 12)
AUTHORS   Koichi,I.
TITLE     Method for amplifying DNA fragment, amplification apparatus of DNA
            fragment, method for assaying a group of microorganisms, method for
            analyzing a group of microorganisms, and method for assaying
            contaminating substance
JOURNAL   Patent: JP 1999341989-A 141 14-DEC-1999;
          SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
          FORESTRY AND FISHERIES

COMMENT    OS      Artificial Sequence
           PN      JP 1999341989-A/141
           PD      14-DEC-1999
           PF      16-MAR-1999 JP 1999069694
           PR
           PI      KOICHI INOUE
           PC      C12N15/09,C12M1/00,C12Q1/68,C12N15/00
           CC
           FH      Key      Location/Qualifiers
           FT      source    1..12
           FT      source    /organism='Artificial Sequence'.

FEATURES             source
    source           1..12
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"

Query Match      29.0%; Score 8.4; DB 1; Length 12;
```

```

Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CACCTGCTGT 15
Db ||||||
1 CTCCTGCTGT 10

RESULT 272
E64243/c
LOCUS E64243 12 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for amplifying DNA fragment, amplification apparatus of DNA
fragment, method for assaying a group of microorganisms, method
for analyzing a group of microorganisms, and method for assaying
contaminating substance.
E64243
ACCESSION E64243.1 GI:13019647
VERSION E64243.1 1999341989-A/191.
KEYWORDS JP 1999341989-A/191.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 12)
AUTHORS Koichi,I.
TITLE Method for amplifying DNA fragment, amplification apparatus of DNA
fragment, method for assaying a group of microorganisms, method for
analyzing a group of microorganisms, and method for assaying
contaminating substance
JOURNAL Patent: JP 1999341989-A 191 14-DEC-1999;
SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
FORESTRY AND FISHERIES
COMMENT OS Artificial Sequence
PN JP 1999341989-A/191
PD 14-DEC-1999
PF 16-MAR-1999 JP 1999069694
PR
PI KOICHI INOUE
PC C12N15/09,C12M1/00,C12Q1/68,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..12
FT /organism='Artificial Sequence'.

FEATURES
source
1..12
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTG 14
Db ||||||
11 CCACCTCCTG 2

RESULT 273
I34990/c
LOCUS I34990 12 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 76 from patent US 5599704.
ACCESSION I34990
VERSION I34990.1 GI:2087958
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Thompson,J.D. and Draper,K.G.
TITLE ErbB2/neu targeted ribozymes
JOURNAL Patent: US 5599704-A 76 04-FEB-1997;
FEATURES Location/Qualifiers
source
1..12
/organism="unknown"

Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTG 14
Db ||||||
11 CCACCTCCTG 2

RESULT 274
AR408074
LOCUS AR408074 12 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 167 from patent US 6632057.
ACCESSION AR408074
VERSION AR408074.1 GI:40158061
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Fauchet,C.R.J.
TITLE Fixing unit with an end imprint in a threaded terminal portion
JOURNAL Patent: US 6632057-A 167 14-OCT-2003;
GFI Aerospace; Paris;
FRX;

FEATURES Location/Qualifiers
source
1..12
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCCACCTGCT 13
Db ||||||
1 TCCACCAGCT 10

RESULT 275
AR630023
LOCUS AR630023 12 bp DNA linear PAT 14-FEB-2005
DEFINITION Sequence 77 from patent US 6838556.
ACCESSION AR630023
VERSION AR630023.1 GI:59762226
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
Sheppard,L.T., Kim,M.Y. and Bruice,T.W.
TITLE Promoters for regulated gene expression
JOURNAL Patent: US 6838556-A 77 04-JAN-2005;
Generabs Technologies, Inc.; Redwood City, CA

FEATURES Location/Qualifiers
source
1..12
/organism="unknown"
/mol_type="genomic DNA"

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 20 CCTGGTAAAT 29
Db ||||||
3 CCTGATAAAT 12

RESULT 276
```

```

/mol_type="unassigned DNA"

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCCACCT 10
Db ||||||
10 CCATCCACTT 1

RESULT 274
AR408074
LOCUS AR408074 12 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 167 from patent US 6632057.
ACCESSION AR408074
VERSION AR408074.1 GI:40158061
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Fauchet,C.R.J.
TITLE Fixing unit with an end imprint in a threaded terminal portion
JOURNAL Patent: US 6632057-A 167 14-OCT-2003;
GFI Aerospace; Paris;
FRX;

FEATURES Location/Qualifiers
source
1..12
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCCACCTGCT 13
Db ||||||
1 TCCACCAGCT 10

RESULT 275
AR630023
LOCUS AR630023 12 bp DNA linear PAT 14-FEB-2005
DEFINITION Sequence 77 from patent US 6838556.
ACCESSION AR630023
VERSION AR630023.1 GI:59762226
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
Sheppard,L.T., Kim,M.Y. and Bruice,T.W.
TITLE Promoters for regulated gene expression
JOURNAL Patent: US 6838556-A 77 04-JAN-2005;
Generabs Technologies, Inc.; Redwood City, CA

FEATURES Location/Qualifiers
source
1..12
/organism="unknown"
/mol_type="genomic DNA"

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 20 CCTGGTAAAT 29
Db ||||||
3 CCTGATAAAT 12

RESULT 276
```

AX097958/c  
LOCUS AX097958 12 bp DNA linear PAT 30-MAR-2001  
DEFINITION Sequence 26 from Patent WO0118048.  
ACCESSION AX097958  
VERSION AX097958.1 GI:13514713  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS van Eijs,G.J., Hateboer,G. and Havenga,M.J.  
TITLE Smooth muscle cell promoter and uses thereof  
JOURNAL Patent: WO 0118048-A 26 15-MAR-2001;  
Introgene B.V. (NL)  
FEATURES  
source Location/Qualifiers  
1..12  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="variant intron-exon splice recognition sequences"  
  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 ATCCACCTGC 12  
|||||  
Db 12 ATCCAGCTGC 3  
  
RESULT 277  
AX138534/c  
LOCUS AX138534 12 bp DNA linear PAT 30-MAY-2001  
DEFINITION Sequence 26 from Patent EP1083231.  
ACCESSION AX138534  
VERSION AX138534.1 GI:14274429  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Smooth muscle cell promoter and uses thereof  
TITLE Patent: EP 1083231-A 26 14-MAR-2001;  
JOURNAL Introgene B.V. (NL)  
FEATURES  
source Location/Qualifiers  
1..12  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="variant intron-exon splice recognition sequences"  
  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 ATCCACCTGC 12  
|||||  
Db 12 ATCCAGCTGC 3  
  
RESULT 278  
AX351125  
LOCUS AX351125 12 bp DNA linear PAT 06-FEB-2002  
DEFINITION Sequence 77 from Patent WO0194600.  
ACCESSION AX351125  
VERSION AX351125.1 GI:18616479  
KEYWORDS Escherichia coli  
SOURCE Escherichia coli  
ORGANISM Escherichia coli  
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
Enterobacteriaceae; Escherichia.  
REFERENCE 1

AUTHORS Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,  
Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,  
Sheppard,L.T., Lim,M.Y. and Bruice,T.W.  
TITLE Promoters for regulated gene expression  
JOURNAL Patent: WO 0194600-A 77 13-DEC-2001;  
GENELABS TECHNOLOGIES, INC. (US)  
FEATURES  
source Location/Qualifiers  
1..12  
/organism="Escherichia coli"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:562"  
  
Query Match 29.0%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 1.8e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 20 CCTGGTAAAT 29  
|||||  
Db 3 CCTGATAAAT 12  
  
RESULT 279  
AR071511  
LOCUS AR071511 10 bp DNA linear PAT 18-FEB-2000  
DEFINITION Sequence 11 from patent US 5911982.  
ACCESSION AR071511  
VERSION AR071511.1 GI:72223399  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Chao,Y.-C.  
TITLE HZ-1 virus persistence-associated-gene 1 (PAG1) promoter uses  
therefor, and compositions containing same or products therefrom  
JOURNAL Patent: US 5911982-A 11 15-JUN-1999;  
FEATURES  
source Location/Qualifiers  
1..10  
/organism="unknown"  
/mol\_type="unassigned DNA"  
  
Query Match 27.6%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 21 CTGGTAAA 28  
|||||  
Db 3 CTGGTAAA 10  
  
RESULT 280  
BD161300/c  
LOCUS BD161300 10 bp DNA linear PAT 17-JAN-2003  
DEFINITION Human activated Th1 and Th2 cell expression genes.  
ACCESSION BD161300  
VERSION BD161300.1 GI:27867058  
KEYWORDS JP 2002186482-A/122.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.  
TITLE Human activated Th1 and Th2 cell expression genes  
JOURNAL Patent: JP 2002186482-A 122 02-JUL-2002;  
JAPAN SCIENCE AND TECHNOLOGY CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002186482-A/122  
PD 02-JUL-2002  
PF 19-DEC-2000 JP 2000385816  
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC  
C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human









```
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT
OS Homo sapiens (human)
PN JP 2002534056-A/630
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.

FEATURES
source
1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TGACCTGG 24
|||||||
Db 2 TGACCTGG 9

RESULT 289
BD239785
LOCUS BD239785 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239785
VERSION BD239785.1 GI:33049555
KEYWORDS JP 2002534056-A/1203.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 10)
Roberts,B.L. and Shankara,S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 1203 15-OCT-2002;
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/1203
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT
OS Homo sapiens (human)
PN JP 2002534056-A/630
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
```

```
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 10)
Roberts,B.L. and Shankara,S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 630 15-OCT-2002;
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/630
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.

FEATURES
source
1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACCTGCTG 14
|||||||
Db 1 ACCTGCTG 8

RESULT 290
BD240273/c
LOCUS BD240273 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240273
VERSION BD240273.1 GI:33050043
KEYWORDS JP 2002534056-A/1691.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 10)
Roberts,B.L. and Shankara,S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 1691 15-OCT-2002;
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/1691
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/090077,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090079,19-JUN-1998 US 60/090045 PR
```

19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR  
08-DEC-1998 US 60/111715  
PI BRUCE L ROBERTS, SRINIVAS SHANKARA  
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC  
C12N1/19,  
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC  
G01N37/00,  
PC C12N15/00,C12N5/00,C12N15/00  
CC Preparation and use of superior vaccines  
FH Key Location/Qualifiers  
FT source 1..10  
FT /organism='Homo sapiens (human)'.  
  
FEATURES  
source Location/Qualifiers  
1..10  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
  
Query Match 27.6%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CCATCCAC 8  
|||||  
Db 8 CCATCCAC 1  
  
RESULT 291  
CQ766677  
LOCUS CQ766677 10 bp DNA linear PAT 03-MAR-2004  
DEFINITION Sequence 33 from Patent WO2004005541.  
ACCESSION CQ766677  
VERSION CQ766677.1 GI:44908907  
KEYWORDS .  
SOURCE synthetic construct  
ORGANISM synthetic constructs; artificial sequences.  
REFERENCE 1  
AUTHORS van Broeckhoven,C., de Jonghe,P., Timmerman,V. and Verhoeven,K.  
TITLE Diagnostic tests for the detection of peripheral neuropathy  
JOURNAL Patent: WO 2004005541-A 33 15-JAN-2004;  
Vlaams Interuniversitair Instituut voor Biotechnologie vz; w. (BE)  
  
FEATURES  
source Location/Qualifiers  
1..10  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="3-intron/exon, exon 3, gene ABTB1"  
  
Query Match 27.6%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 12 CTGTGTGA 19  
|||||  
Db 2 CTGTGTGA 9  
  
RESULT 292  
CQ766737/c  
LOCUS CQ766737 10 bp DNA linear PAT 03-MAR-2004  
DEFINITION Sequence 93 from Patent WO2004005541.  
ACCESSION CQ766737  
VERSION CQ766737.1 GI:44908967  
KEYWORDS .  
SOURCE synthetic construct  
ORGANISM synthetic constructs; artificial sequences.  
REFERENCE 1  
AUTHORS van Broeckhoven,C., de Jonghe,P., Timmerman,V. and Verhoeven,K.  
TITLE Diagnostic tests for the detection of peripheral neuropathy  
JOURNAL Patent: WO 2004005541-A 93 15-JAN-2004;  
Vlaams Interuniversitair Instituut voor Biotechnologie vz; w. (BE)

FEATURES  
source Location/Qualifiers  
1..10  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="3-intron/exon, exon 4"  
  
Query Match 27.6%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 CACCTGCT 13  
|||||  
Db 8 CACCTGCT 1  
  
RESULT 293  
CQ828565  
LOCUS CQ828565 10 bp DNA linear PAT 05-JUL-2004  
DEFINITION Sequence 283 from Patent WO2004053120.  
ACCESSION CQ828565  
VERSION CQ828565.1 GI:49732048  
KEYWORDS .  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchoptoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.  
REFERENCE 1  
AUTHORS Weihe,E., Bieller,A. and Schaefer,M.K.  
TITLE Regulatory elements in the 5' region of the vr1 gene  
JOURNAL Patent: WO 2004053120-A 283 24-JUN-2004;  
Gruenenthal GmbH (DE)  
  
FEATURES  
source Location/Qualifiers  
1..10  
/organism="Rattus norvegicus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10116"  
/note="V\$MYOD Q6"  
  
Query Match 27.6%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 CCACCTGC 12  
|||||  
Db 2 CCACCTGC 9  
  
RESULT 294  
CQ828675/c  
LOCUS CQ828675 10 bp DNA linear PAT 05-JUL-2004  
DEFINITION Sequence 393 from Patent WO2004053120.  
ACCESSION CQ828675  
VERSION CQ828675.1 GI:49732158  
KEYWORDS .  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchoptoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.  
REFERENCE 1  
AUTHORS Weihe,E., Bieller,A. and Schaefer,M.K.  
TITLE Regulatory elements in the 5' region of the vr1 gene  
JOURNAL Patent: WO 2004053120-A 393 24-JUN-2004;  
Gruenenthal GmbH (DE)  
  
FEATURES  
source Location/Qualifiers  
1..10  
/organism="Rattus norvegicus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10116"  
/note="V\$AP4 Q5"

Query Match 27.6%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTGCTGTG 16  
|||||  
Db 8 CTGCTGTG 1

RESULT 295  
CQ828736  
LOCUS 10 bp DNA linear PAT 05-JUL-2004  
DEFINITION Sequence 454 from Patent WO2004053120.  
ACCESSION CQ828736  
VERSION CQ828736.1 GI:49732219  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
REFERENCE 1  
AUTHORS Weihe,E., Bieller,A. and Schaefer,M.K.  
TITLE Regulatory elements in the 5' region of the vrl gene  
JOURNAL Patent: WO 2004053120-A 454 24-JUN-2004;  
Gruenenthal GmbH (DE)

FEATURES  
source Location/Qualifiers  
1..10  
/organism="Mus musculus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10090"  
/note="V\$MYOD Q6"

Query Match 27.6%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CACCTGCT 13  
|||||  
Db 3 CACCTGCT 10

RESULT 296  
CQ828850/c  
LOCUS 10 bp DNA linear PAT 05-JUL-2004  
DEFINITION Sequence 568 from Patent WO2004053120.  
ACCESSION CQ828850  
VERSION CQ828850.1 GI:49732333  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
REFERENCE 1  
AUTHORS Weihe,E., Bieller,A. and Schaefer,M.K.  
TITLE Regulatory elements in the 5' region of the vrl gene  
JOURNAL Patent: WO 2004053120-A 568 24-JUN-2004;  
Gruenenthal GmbH (DE)

FEATURES  
source Location/Qualifiers  
1..10  
/organism="Mus musculus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10090"  
/note="V\$AP4 Q5"

Query Match 27.6%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTGCTGTG 16  
|||||  
Db 8 CTGCTGTG 1

RESULT 297  
E16980/c  
LOCUS 10 bp DNA linear PAT 28-JUL-1999  
DEFINITION PCR primer for Acacia sp. genome.  
ACCESSION E16980  
VERSION E16980.1 GI:5711663  
KEYWORDS JP 1998229898-A/3.  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Hiono,T. and Koshiyama,J.  
TITLE EARLY DETECTION OF INTERSPECIFIC HYBRIDIZATION IN TROPICAL FAST GROWING TREE AND ITS PRIMER  
JOURNAL Patent: JP 1998229898-A 3 02-SEP-1998;  
NETSUTAIRIN SAISEI GIJUTSU KENKYU KUMIAI

COMMENT OS None  
OC Artificial sequences.  
PN JP 1998229898-A/3  
PD 02-SEP-1998  
PF 02-DEC-1997 JP 1997345724  
PR 17-DEC-1996 JP 96P 353354  
PI HIONO TAKASHI, KOSHIYAMA JUNKO  
PC C12Q1/68//C12N15/09;  
CC strandedness: Single;  
CC topology: Linear;  
FH Key Location/Qualifiers  
FT source 1..10  
FT /organism='Artificial sequences'.

FEATURES  
source Location/Qualifiers  
1..10  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

Query Match 27.6%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 GTGACCTG 23  
|||||  
Db 10 GTGACCTG 3

RESULT 298  
E28643  
LOCUS 10 bp DNA linear PAT 18-JUN-2001  
DEFINITION Microsatellite marker located in the vicinity of semi-dwarf gene and method for testing semi-dwarf gene therewith.  
ACCESSION E28643  
VERSION E28643.1 GI:13020808  
KEYWORDS JP 1999253167-A/3.  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Hiromori,A., Akiko,I. and Yumi,Y.  
TITLE Microsatellite marker located in the vicinity of semi-dwarf gene and method for testing semi-dwarf gene therewith  
JOURNAL Patent: JP 1999253167-A 3 21-SEP-1999;  
MITSUI CHEM INC

COMMENT OS Unidentified  
PN JP 1999253167-A/3  
PD 21-SEP-1999  
PF 13-MAR-1998 JP 1998063201  
PR HIROMORI AKAGI,AKIKO INAGAKI,YUMI YOKOZEKI  
PC C12N15/09,C12Q1/68,C12N15/00  
CC Strandedness: Single;  
CC Topology: Linear;

FH Key Location/Qualifiers
FT source 1..10
FT /organism='Unidentified'.

FEATURES
source
Location/Qualifiers
1..10
/organism="unidentified"
/mol\_type="genomic DNA"
/db\_xref="taxon:32644"

Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCTGCTG 14
|||||
Db 3 ACCTGCTG 10

RESULT 299
E64716/c
LOCUS E64716 10 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for distinguishing rice variety.
ACCESSION E64716
VERSION E64716.1 GI:18623011
KEYWORDS JP 2000287691-A/2.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Otsubo,K., Nakamura,S., Teshima,H., Okatome,H. and Kawasaki,S.
TITLE Method for distinguishing rice variety
JOURNAL Patent: JP 200287691-A 2 17-OCT-2000;
NATL FOOD RES INST,KENICHI OTSUBO,HIDECHIKA TESHIMA,HIROSHI OKATOME
OS Oryza sativa L. (rice)
PN JP 2000287691-A/2
PD 17-OCT-2000
PF 09-APR-1999 JP 1999102709
PR
PI KENICHI OTSUBO,SUMIKO NAKAMURA,HIDECHIKA TESHIMA, PI HIROSHI OKATOME,
PI SHINJI KAWASAKI
PC C12N15/09,C12Q1/68,G01N33/10,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Oryza sativa L. (rice)'.

FEATURES
source
Location/Qualifiers
1..10
/organism="unidentified"
/mol\_type="genomic DNA"
/db\_xref="taxon:32644"

Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CTGCTGTG 16
|||||
Db 9 CTGCTGTG 2

RESULT 300
AR241991/c
LOCUS AR241991 10 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 279 from patent US 6472154.
ACCESSION AR241991
VERSION AR241991.1 GI:27287803
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.

TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 279 29-OCT-2002;
Board of Regents, The University of Texas System; Austin, TX

FEATURES
source
Location/Qualifiers
1..10
/organism="unknown"
/mol\_type="genomic DNA"

Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCCAC 8
|||||
Db 8 CCATCCAC 1

RESULT 301
AR304497
LOCUS AR304497 10 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 122 from patent US 6544784.
ACCESSION AR304497
VERSION AR304497.1 GI:31693645
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Bullerdiek,J., Van de Ven,W.J.M., Schoenmakers,H.F.P.M. and Mols,R.
TITLE Multiple-tumor aberrant growth genes
JOURNAL Patent: US 6544784-A 122 08-APR-2003;
Vlaams Interuniversitair Instituut Voor Biotechnologie VZW;;
EPX;

FEATURES
source
Location/Qualifiers
1..10
/organism="unknown"
/mol\_type="genomic DNA"

Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCTGCTG 14
|||||
Db 3 ACCTGCTG 10

RESULT 302
AR306871/c
LOCUS AR306871 10 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 23 from patent US 6551476.
ACCESSION AR306871
VERSION AR306871.1 GI:31697271
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Scherba,E.S.
TITLE Noble-metal coated inert anode for aluminum production
JOURNAL Patent: US 6551476-A 23 22-APR-2003;

FEATURES
source
Location/Qualifiers
1..10
/organism="unknown"
/mol\_type="genomic DNA"

Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CTGCTGTG 16
|||||
Db 9 CTGCTGTG 2



RESULT 303  
AX152690  
LOCUS AX152690 10 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 605 from Patent WO0138577.  
ACCESSION AX152690  
VERSION AX152690.1 GI:14534341  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.  
TITLE Human transcriptomes  
JOURNAL Patent: WO 0138577-A 605 31-MAY-2001;  
The Johns Hopkins University (US)  
FEATURES  
source Location/Qualifiers  
1..10  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 27.6%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 9 CTGCTGTG 16  
|||||  
Db 1 CTGCTGTG 8  
RESULT 304  
AX152728  
LOCUS AX152728 10 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 643 from Patent WO0138577.  
ACCESSION AX152728  
VERSION AX152728.1 GI:14534379  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.  
TITLE Human transcriptomes  
JOURNAL Patent: WO 0138577-A 643 31-MAY-2001;  
The Johns Hopkins University (US)  
FEATURES  
source Location/Qualifiers  
1..10  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 27.6%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 11 GCTGTGTG 18  
|||||  
Db 3 GCTGTGTG 10  
RESULT 305  
AX152831  
LOCUS AX152831 10 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 746 from Patent WO0138577.  
ACCESSION AX152831  
VERSION AX152831.1 GI:14534482  
KEYWORDS

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.  
TITLE Human transcriptomes  
JOURNAL Patent: WO 0138577-A 746 31-MAY-2001;  
The Johns Hopkins University (US)  
FEATURES  
source Location/Qualifiers  
1..10  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 27.6%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 7 ACCTGCTG 14  
|||||  
Db 1 ACCTGCTG 8  
RESULT 306  
AX152911/c  
LOCUS AX152911 10 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 826 from Patent WO0138577.  
ACCESSION AX152911  
VERSION AX152911.1 GI:14534562  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.  
TITLE Human transcriptomes  
JOURNAL Patent: WO 0138577-A 826 31-MAY-2001;  
The Johns Hopkins University (US)  
FEATURES  
source Location/Qualifiers  
1..10  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 27.6%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 CATCCACC 9  
|||||  
Db 8 CATCCACC 1  
RESULT 307  
AX153356/c  
LOCUS AX153356 10 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 1271 from Patent WO0138577.  
ACCESSION AX153356  
VERSION AX153356.1 GI:14535007  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.  
TITLE Human transcriptomes  
JOURNAL Patent: WO 0138577-A 1271 31-MAY-2001;  
The Johns Hopkins University (US)

|                       |                                                                   |                                                                                 |                    |            |            |        |    |      |                 |  |
|-----------------------|-------------------------------------------------------------------|---------------------------------------------------------------------------------|--------------------|------------|------------|--------|----|------|-----------------|--|
| FEATURES              | The Johns Hopkins University (US)                                 |                                                                                 |                    |            |            |        |    |      |                 |  |
|                       | source                                                            | Location/Qualifiers                                                             |                    |            |            |        |    |      |                 |  |
|                       |                                                                   | 1. .10                                                                          |                    |            |            |        |    |      |                 |  |
|                       |                                                                   | /organism="Homo sapiens"<br>/mol_type="unassigned DNA"<br>/db_xref="taxon:9606" |                    |            |            |        |    |      |                 |  |
| Query Match           |                                                                   | 27.6%;                                                                          | Score 8;           | DB 1;      | Length 10; |        |    |      |                 |  |
| Best Local Similarity |                                                                   | 100.0%;                                                                         | Pred. No. 1.7e+02; |            |            |        |    |      |                 |  |
| Matches               | 8;                                                                | Conservative                                                                    | 0;                 | Mismatches | 0;         | Indels | 0; | Gaps | 0;              |  |
| QY                    | 6                                                                 | CACCTGCT                                                                        | 13                 |            |            |        |    |      |                 |  |
|                       |                                                                   |                                                                                 |                    |            |            |        |    |      |                 |  |
| Db                    | 10                                                                | CACCTGCT                                                                        | 3                  |            |            |        |    |      |                 |  |
| RESULT 308            |                                                                   |                                                                                 |                    |            |            |        |    |      |                 |  |
| AX301473              |                                                                   |                                                                                 |                    |            |            |        |    |      |                 |  |
| LOCUS                 | AX301473                                                          |                                                                                 |                    | 10 bp      | DNA        | linear |    |      | PAT 30-NOV-2001 |  |
| DEFINITION            | Sequence 187 from Patent WO0185941.                               |                                                                                 |                    |            |            |        |    |      |                 |  |
| ACCESSION             | AX301473                                                          |                                                                                 |                    |            |            |        |    |      |                 |  |
| VERSION               | AX301473.1                                                        | GI:17382556                                                                     |                    |            |            |        |    |      |                 |  |
| KEYWORDS              | .                                                                 |                                                                                 |                    |            |            |        |    |      |                 |  |
| SOURCE                | Homo sapiens (human)                                              |                                                                                 |                    |            |            |        |    |      |                 |  |
| ORGANISM              | Homo sapiens                                                      |                                                                                 |                    |            |            |        |    |      |                 |  |
|                       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |                                                                                 |                    |            |            |        |    |      |                 |  |
|                       | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;       |                                                                                 |                    |            |            |        |    |      |                 |  |
|                       | Hominidae; Homo.                                                  |                                                                                 |                    |            |            |        |    |      |                 |  |
| REFERENCE             | 1                                                                 |                                                                                 |                    |            |            |        |    |      |                 |  |
| AUTHORS               | Versteeg,R. and Caron,H.N.                                        |                                                                                 |                    |            |            |        |    |      |                 |  |
| TITLE                 | Myc targets                                                       |                                                                                 |                    |            |            |        |    |      |                 |  |
| JOURNAL               | Patent: WO 0185941-A 187 15-NOV-2001;                             |                                                                                 |                    |            |            |        |    |      |                 |  |
|                       | Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)      |                                                                                 |                    |            |            |        |    |      |                 |  |
| FEATURES              | Location/Qualifiers                                               |                                                                                 |                    |            |            |        |    |      |                 |  |
| source                | 1. .10                                                            |                                                                                 |                    |            |            |        |    |      |                 |  |
|                       | /organism="Homo sapiens"                                          |                                                                                 |                    |            |            |        |    |      |                 |  |
|                       | /mol_type="unassigned DNA"                                        |                                                                                 |                    |            |            |        |    |      |                 |  |
|                       | /db_xref="taxon:9606"                                             |                                                                                 |                    |            |            |        |    |      |                 |  |
| Query Match           |                                                                   | 27.6%;                                                                          | Score 8;           | DB 1;      | Length 10; |        |    |      |                 |  |
| Best Local Similarity |                                                                   | 100.0%;                                                                         | Pred. No. 1.7e+02; |            |            |        |    |      |                 |  |
| Matches               | 8;                                                                | Conservative                                                                    | 0;                 | Mismatches | 0;         | Indels | 0; | Gaps | 0;              |  |
| QY                    | 9                                                                 | CTGCTGTG                                                                        | 16                 |            |            |        |    |      |                 |  |
|                       |                                                                   |                                                                                 |                    |            |            |        |    |      |                 |  |
| Db                    | 1                                                                 | CTGCTGTG                                                                        | 8                  |            |            |        |    |      |                 |  |
| RESULT 309            |                                                                   |                                                                                 |                    |            |            |        |    |      |                 |  |
| AX301553              |                                                                   |                                                                                 |                    |            |            |        |    |      |                 |  |
| LOCUS                 | AX301553                                                          |                                                                                 |                    | 10 bp      | DNA        | linear |    |      | PAT 30-NOV-2001 |  |
| DEFINITION            | Sequence 267 from Patent WO0185941.                               |                                                                                 |                    |            |            |        |    |      |                 |  |
| ACCESSION             | AX301553                                                          |                                                                                 |                    |            |            |        |    |      |                 |  |
| VERSION               | AX301553.1                                                        | GI:17382636                                                                     |                    |            |            |        |    |      |                 |  |
| KEYWORDS              | .                                                                 |                                                                                 |                    |            |            |        |    |      |                 |  |
| SOURCE                | Homo sapiens (human)                                              |                                                                                 |                    |            |            |        |    |      |                 |  |
| ORGANISM              | Homo sapiens                                                      |                                                                                 |                    |            |            |        |    |      |                 |  |
|                       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |                                                                                 |                    |            |            |        |    |      |                 |  |
|                       | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;       |                                                                                 |                    |            |            |        |    |      |                 |  |
|                       | Hominidae; Homo.                                                  |                                                                                 |                    |            |            |        |    |      |                 |  |
| REFERENCE             | 1                                                                 |                                                                                 |                    |            |            |        |    |      |                 |  |
| AUTHORS               | Versteeg,R. and Caron,H.N.                                        |                                                                                 |                    |            |            |        |    |      |                 |  |
| TITLE                 | Myc targets                                                       |                                                                                 |                    |            |            |        |    |      |                 |  |
| JOURNAL               | Patent: WO 0185941-A 267 15-NOV-2001;                             |                                                                                 |                    |            |            |        |    |      |                 |  |
|                       | Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)      |                                                                                 |                    |            |            |        |    |      |                 |  |
| FEATURES              | Location/Qualifiers                                               |                                                                                 |                    |            |            |        |    |      |                 |  |
| source                | 1. .10                                                            |                                                                                 |                    |            |            |        |    |      |                 |  |
|                       | /organism="Homo sapiens"                                          |                                                                                 |                    |            |            |        |    |      |                 |  |
|                       | /mol_type="unassigned DNA"                                        |                                                                                 |                    |            |            |        |    |      |                 |  |
|                       | /db_xref="taxon:9606"                                             |                                                                                 |                    |            |            |        |    |      |                 |  |
| Query Match           |                                                                   | 27.6%;                                                                          | Score 8;           | DB 1;      | Length 10; |        |    |      |                 |  |
| Best Local Similarity |                                                                   | 100.0%;                                                                         | Pred. No. 1.7e+02; |            |            |        |    |      |                 |  |
| Matches               | 9;                                                                | Conservative                                                                    | 0;                 | Mismatches | 0;         | Indels | 0; | Gaps | 0;              |  |



LOCUS CQ832885 11 bp DNA linear PAT 29-JUL-2004  
DEFINITION Sequence 256 from Patent WO2004059002.  
ACCESSION CQ832885  
VERSION CQ832885.1 GI:50832492  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
AUTHORS Conradt,M. and Hofmann,K.  
TITLE Method for determining the homeostasis of hairy skin  
JOURNAL Patent: WO 2004059002-A 256 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES Location/Qualifiers  
source 1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 27.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCATCCAC 8  
|||||||  
Db 8 CCATCCAC 1  
RESULT 317  
CQ833280/c  
LOCUS CQ833280 11 bp DNA linear PAT 29-JUL-2004  
DEFINITION Sequence 651 from Patent WO2004059002.  
ACCESSION CQ833280  
VERSION CQ833280.1 GI:50832887  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
AUTHORS Conradt,M. and Hofmann,K.  
TITLE Method for determining the homeostasis of hairy skin  
JOURNAL Patent: WO 2004059002-A 651 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES Location/Qualifiers  
source 1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 27.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 22 TGGTAAAT 29  
|||||||  
Db 11 TGGTAAAT 4  
RESULT 318  
CQ835128  
LOCUS CQ835128 11 bp DNA linear PAT 29-JUL-2004  
DEFINITION Sequence 186 from Patent WO2004059001.  
ACCESSION CQ835128  
VERSION CQ835128.1 GI:50834662  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
AUTHORS Conradt,M. and Hofmann,K.  
TITLE Method for determining markers of human facial skin  
JOURNAL Patent: WO 2004059001-A 186 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES Location/Qualifiers  
source 1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 27.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 21 CTGGTAAA 28  
|||||||  
Db 2 CTGGTAAA 9  
RESULT 319  
CQ835562  
LOCUS CQ835562 11 bp DNA linear PAT 29-JUL-2004  
DEFINITION Sequence 620 from Patent WO2004059001.  
ACCESSION CQ835562  
VERSION CQ835562.1 GI:50835096  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
AUTHORS Conradt,M. and Hofmann,K.  
TITLE Method for determining markers of human facial skin  
JOURNAL Patent: WO 2004059001-A 620 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES Location/Qualifiers  
source 1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 27.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 10 TGCTGTGT 17  
|||||||  
Db 4 TGCTGTGT 11  
RESULT 320  
CQ835656/c  
LOCUS CQ835656 11 bp DNA linear PAT 29-JUL-2004  
DEFINITION Sequence 714 from Patent WO2004059001.  
ACCESSION CQ835656  
VERSION CQ835656.1 GI:50835190  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
AUTHORS Conradt,M. and Hofmann,K.  
TITLE Method for determining markers of human facial skin

JOURNAL Patent: WO 2004059001-A 714 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
  
Query Match 27.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CCATCCAC 8  
| | | | | | | |  
Db 8 CCATCCAC 1  
  
RESULT 321  
CQ836490 11 bp DNA linear PAT 29-JUL-2004  
LOCUS  
DEFINITION Sequence 1548 from Patent WO2004059001.  
ACCESSION CQ836490  
VERSION CQ836490.1 GI:50836024  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
Conradt,M. and Hofmann,K.  
TITLE Method for determining markers of human facial skin  
JOURNAL Patent: WO 2004059001-A 1548 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
  
Query Match 27.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 13 TGTGTGAC 20  
| | | | | | | |  
Db 3 TGTGTGAC 10  
  
RESULT 322  
CQ836499 11 bp DNA linear PAT 29-JUL-2004  
LOCUS  
DEFINITION Sequence 1557 from Patent WO2004059001.  
ACCESSION CQ836499  
VERSION CQ836499.1 GI:50836033  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
Conradt,M. and Hofmann,K.  
TITLE Method for determining markers of human facial skin  
JOURNAL Patent: WO 2004059001-A 1557 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 27.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 21 CTGGTAAA 28  
| | | | | | | |  
Db 2 CTGGTAAA 9  
  
RESULT 323  
CQ836747/c 11 bp DNA linear PAT 29-JUL-2004  
LOCUS  
DEFINITION Sequence 1805 from Patent WO2004059001.  
ACCESSION CQ836747  
VERSION CQ836747.1 GI:50836281  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
Conradt,M. and Hofmann,K.  
TITLE Method for determining markers of human facial skin  
JOURNAL Patent: WO 2004059001-A 1805 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
  
Query Match 27.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 6 CACCTGCT 13  
| | | | | | | |  
Db 10 CACCTGCT 3  
  
RESULT 324  
CQ836833 11 bp DNA linear PAT 29-JUL-2004  
LOCUS  
DEFINITION Sequence 1891 from Patent WO2004059001.  
ACCESSION CQ836833  
VERSION CQ836833.1 GI:50836367  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
Conradt,M. and Hofmann,K.  
TITLE Method for determining markers of human facial skin  
JOURNAL Patent: WO 2004059001-A 1891 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
  
Query Match 27.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 10 TGCTGTGT 17  
| | | | | | | |



Db 1 TGCTGTGT 8

RESULT 325

CQ837690

LOCUS CQ837690 11 bp DNA linear PAT 29-JUL-2004

DEFINITION Sequence 2748 from Patent WO2004059001.

ACCESSION CQ837690

VERSION CQ837690.1 GI:50837224

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O., Conradt,M. and Hofmann,K.

TITLE Method for determining markers of human facial skin

JOURNAL Patent: WO 2004059001-A 2748 15-JUL-2004;

FEATURES

source Location/Qualifiers

1. .11

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

Query Match 27.6%; Score 8; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCTGGTAA 27

|||||

Db 4 CCTGGTAA 11

RESULT 326

CQ837896

LOCUS CQ837896 11 bp DNA linear PAT 29-JUL-2004

DEFINITION Sequence 2954 from Patent WO2004059001.

ACCESSION CQ837896

VERSION CQ837896.1 GI:50837430

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O., Conradt,M. and Hofmann,K.

TITLE Method for determining markers of human facial skin

JOURNAL Patent: WO 2004059001-A 2954 15-JUL-2004;

FEATURES

source Location/Qualifiers

1. .11

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

Query Match 27.6%; Score 8; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GCTGTGTG 18

|||||

Db 2 GCTGTGTG 9

RESULT 327

CQ837956

LOCUS CQ837956 11 bp DNA linear PAT 29-JUL-2004

DEFINITION Sequence 3014 from Patent WO2004059001.

ACCESSION CQ837956

VERSION CQ837956.1 GI:50837490

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O., Conradt,M. and Hofmann,K.

TITLE Method for determining markers of human facial skin

JOURNAL Patent: WO 2004059001-A 3014 15-JUL-2004;

FEATURES

source Location/Qualifiers

1. .11

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

Query Match 27.6%; Score 8; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCTGCTG 14

|||||

Db 1 ACCTGCTG 8

RESULT 328

AR301525

LOCUS AR301525 11 bp DNA linear PAT 12-JUN-2003

DEFINITION Sequence 106 from patent US 6538173.

ACCESSION AR301525

VERSION AR301525.1 GI:31689327

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 11)

AUTHORS Heber-Katz,E.

TITLE Compositions and methods for wound healing

JOURNAL Patent: US 6538173-A 106 25-MAR-2003;

FEATURES

source Location/Qualifiers

1. .11

/organism="unknown"

/mol\_type="genomic DNA"

Query Match 27.6%; Score 8; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CTGTGTGA 19

|||||

Db 2 CTGTGTGA 9

RESULT 329

AR632418/c

LOCUS AR632418 11 bp DNA linear PAT 14-FEB-2005

DEFINITION Sequence 90 from patent US 6846623.

ACCESSION AR632418

VERSION AR632418.1 GI:59776728

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 11)

AUTHORS Beckmann,J. and Richard,I.

TITLE LGMD gene coding for a calcium dependent protease

JOURNAL Patent: US 6846623-A 90 25-JAN-2005;



LOCUS AX4711109 11 bp DNA linear PAT 09-AUG-2002  
DEFINITION Sequence 686 from Patent WO02053773.  
ACCESSION AX4711109  
VERSION AX4711109.1 GI:22206234  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.  
TITLE Method for determining skin stress or skin ageing in vitro  
JOURNAL Patent: WO 02053773-A 686 11-JUL-2002;  
HENKEL KGAA (DE)  
FEATURES  
source Location/Qualifiers  
1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 27.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 ACCTGCTG 14  
|||||  
Db 4 ACCTGCTG 11  
RESULT 335  
AX471236/c  
LOCUS AX471236 11 bp DNA linear PAT 09-AUG-2002  
DEFINITION Sequence 813 from Patent WO02053773.  
ACCESSION AX471236  
VERSION AX471236.1 GI:22206361  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.  
TITLE Method for determining skin stress or skin ageing in vitro  
JOURNAL Patent: WO 02053773-A 813 11-JUL-2002;  
HENKEL KGAA (DE)  
FEATURES  
source Location/Qualifiers  
1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 27.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCATCCAC 8  
|||||  
Db 8 CCATCCAC 1  
RESULT 336  
AX471465/c  
LOCUS AX471465 11 bp DNA linear PAT 09-AUG-2002  
DEFINITION Sequence 1042 from Patent WO02053773.  
ACCESSION AX471465  
VERSION AX471465.1 GI:22206590  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1  
Hominidae; Homo.  
1  
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.  
TITLE Method for determining skin stress or skin ageing in vitro  
JOURNAL Patent: WO 02053773-A 1042 11-JUL-2002;  
HENKEL KGAA (DE)  
FEATURES  
source Location/Qualifiers  
1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 27.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 18 GACCTGGT 25  
|||||  
Db 11 GACCTGGT 4  
RESULT 337  
AX471492  
LOCUS AX471492 11 bp DNA linear PAT 09-AUG-2002  
DEFINITION Sequence 1069 from Patent WO02053773.  
ACCESSION AX471492  
VERSION AX471492.1 GI:22206617  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.  
TITLE Method for determining skin stress or skin ageing in vitro  
JOURNAL Patent: WO 02053773-A 1069 11-JUL-2002;  
HENKEL KGAA (DE)  
FEATURES  
source Location/Qualifiers  
1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 27.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 13 TGTGTGAC 20  
|||||  
Db 3 TGTGTGAC 10  
RESULT 338  
AX482032  
LOCUS AX482032 11 bp DNA linear PAT 16-AUG-2002  
DEFINITION Sequence 9 from Patent EP1225233.  
ACCESSION AX482032  
VERSION AX482032.1 GI:22316754  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
1  
REFERENCE  
AUTHORS van der Kuyl,A.C. and Cornelissen,M.  
TITLE Means and methods for treatment evaluation  
JOURNAL Patent: EP 1225233-A 9 24-JUL-2002;  
Amsterdam Support Diagnostics B.V. (NL)  
FEATURES  
source Location/Qualifiers  
1..11  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

```
/note="TAG sequence Hs99923"

Query Match      27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 ACCTGCTG 14
        |||||
Db      4 ACCTGCTG 11

RESULT 339
AX511271
LOCUS      AX511271      11 bp      DNA      linear      PAT 27-SEP-2002
DEFINITION Sequence 9 from Patent WO02059558.
ACCESSION  AX511271
VERSION     AX511271.1 GI:23392148
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS     van der Kuy1,A.C. and Cornelissen,M.
TITLE       Means and methods for treatment evaluation
JOURNAL     Patent: WO 02059558-A 9 01-AUG-2002;
            Amsterdam Support Diagnostics B.V. (NL)
FEATURES    Location/Qualifiers
            source
            1..11
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="TAG sequence Hs99923"

Query Match      27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 ACCTGCTG 14
        |||||
Db      4 ACCTGCTG 11

RESULT 340
AX622962
LOCUS      AX622962      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 3 from Patent WO02053774.
ACCESSION  AX622962
VERSION     AX622962.1 GI:28450903
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 3 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 ACCTGCTG 14
        |||||
Db      4 ACCTGCTG 11

RESULT 343
AX511271
LOCUS      AX511271      11 bp      DNA      linear      PAT 27-SEP-2002
DEFINITION Sequence 9 from Patent WO02059558.
ACCESSION  AX511271
VERSION     AX511271.1 GI:23392148
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS     van der Kuy1,A.C. and Cornelissen,M.
TITLE       Means and methods for treatment evaluation
JOURNAL     Patent: WO 02059558-A 9 01-AUG-2002;
            Amsterdam Support Diagnostics B.V. (NL)
FEATURES    Location/Qualifiers
            source
            1..11
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="TAG sequence Hs99923"

Query Match      27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 ACCTGCTG 14
        |||||
Db      4 ACCTGCTG 11

RESULT 340
AX622962
LOCUS      AX622962      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 3 from Patent WO02053774.
ACCESSION  AX622962
VERSION     AX622962.1 GI:28450903
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 3 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 ACCTGCTG 14
        |||||
Db      4 ACCTGCTG 11

RESULT 343
AX511271
LOCUS      AX511271      11 bp      DNA      linear      PAT 27-SEP-2002
DEFINITION Sequence 9 from Patent WO02059558.
ACCESSION  AX511271
VERSION     AX511271.1 GI:23392148
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS     van der Kuy1,A.C. and Cornelissen,M.
TITLE       Means and methods for treatment evaluation
JOURNAL     Patent: WO 02059558-A 9 01-AUG-2002;
            Amsterdam Support Diagnostics B.V. (NL)
FEATURES    Location/Qualifiers
            source
            1..11
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="TAG sequence Hs99923"

Query Match      27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 ACCTGCTG 14
        |||||
Db      4 ACCTGCTG 11

RESULT 340
AX622962
LOCUS      AX622962      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 3 from Patent WO02053774.
ACCESSION  AX622962
VERSION     AX622962.1 GI:28450903
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 3 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 ACCTGCTG 14
        |||||
Db      4 ACCTGCTG 11

RESULT 343
AX511271
LOCUS      AX511271      11 bp      DNA      linear      PAT 27-SEP-2002
DEFINITION Sequence 9 from Patent WO02059558.
ACCESSION  AX511271
VERSION     AX511271.1 GI:23392148
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS     van der Kuy1,A.C. and Cornelissen,M.
TITLE       Means and methods for treatment evaluation
JOURNAL     Patent: WO 02059558-A 9 01-AUG-2002;
            Amsterdam Support Diagnostics B.V. (NL)
FEATURES    Location/Qualifiers
            source
            1..11
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="TAG sequence Hs99923"

Query Match      27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 ACCTGCTG 14
        |||||
Db      4 ACCTGCTG 11

RESULT 340
AX622962
LOCUS      AX622962      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 3 from Patent WO02053774.
ACCESSION  AX622962
VERSION     AX622962.1 GI:28450903
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 3 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 ACCTGCTG 14
        |||||
Db      4 ACCTGCTG 11

RESULT 343
AX511271
LOCUS      AX511271      11 bp      DNA      linear      PAT 27-SEP-2002
DEFINITION Sequence 9 from Patent WO02059558.
ACCESSION  AX511271
VERSION     AX511271.1 GI:23392148
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS     van der Kuy1,A.C. and Cornelissen,M.
TITLE       Means and methods for treatment evaluation
JOURNAL     Patent: WO 02059558-A 9 01-AUG-2002;
            Amsterdam Support Diagnostics B.V. (NL)
FEATURES    Location/Qualifiers
            source
            1..11
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="TAG sequence Hs99923"

Query Match      27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 ACCTGCTG 14
        |||||
Db      4 ACCTGCTG 11

RESULT 340
AX622962
LOCUS      AX622962      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 3 from Patent WO02053774.
ACCESSION  AX622962
VERSION     AX622962.1 GI:28450903
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 3 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 ACCTGCTG 14
        |||||
Db      4 ACCTGCTG 11

RESULT 343
AX511
```

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 1411 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES Location/Qualifiers  
source 1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
  
Query Match 27.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 CATCCACC 9  
| | | | | | | |  
Db 10 CATCCACC 3  
  
RESULT 344  
AX625507  
LOCUS AX625507 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 2548 from Patent WO02053774.  
ACCESSION AX625507  
VERSION AX625507.1 GI:28453448  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 2548 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES Location/Qualifiers  
source 1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
  
Query Match 27.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 15 TGTGACCT 22  
| | | | | | | |  
Db 1 TGTGACCT 8  
  
RESULT 345  
AX625837/c  
LOCUS AX625837 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 2878 from Patent WO02053774.  
ACCESSION AX625837  
VERSION AX625837.1 GI:28453778  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 2878 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES source Location/Qualifiers  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
  
Query Match 27.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 6 CACCTGCT 13  
| | | | | | | |  
Db 10 CACCTGCT 3  
  
RESULT 346  
AX626039/c  
LOCUS AX626039 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 3080 from Patent WO02053774.  
ACCESSION AX626039  
VERSION AX626039.1 GI:28454077  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 3080 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES Location/Qualifiers  
source 1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
  
Query Match 27.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 6 CACCTGCT 13  
| | | | | | | |  
Db 10 CACCTGCT 3  
  
RESULT 347  
AX626143/c  
LOCUS AX626143 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 3184 from Patent WO02053774.  
ACCESSION AX626143  
VERSION AX626143.1 GI:28454181  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 3184 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES Location/Qualifiers  
source 1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
  
Query Match 27.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 6 CACCTGCT 13  
| | | | | | | |  
Db 10 CACCTGCT 3  
  
RESULT 347  
AX626143/c  
LOCUS AX626143 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 3184 from Patent WO02053774.  
ACCESSION AX626143  
VERSION AX626143.1 GI:28454181  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 3184 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES Location/Qualifiers  
source 1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
  
Query Match 27.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 18 GACCTGGT 25  
Db | | | | | | | |  
11 GACCTGGT 4

RESULT 348  
AX626825  
LOCUS AX626825 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 3866 from Patent WO02053774.  
ACCESSION AX626825  
VERSION AX626825.1 GI:28454863  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 3866 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 27.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TGTGTGAC 20  
Db | | | | | | | |  
3 TGTGTGAC 10

RESULT 349  
AX627393/c  
LOCUS AX627393 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 4434 from Patent WO02053774.  
ACCESSION AX627393  
VERSION AX627393.1 GI:28455431  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 4434 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 27.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 CTGGTAAA 28  
Db | | | | | | | |  
11 CTGGTAAA 4

RESULT 350  
AX627828/c  
LOCUS AX627828 11 bp DNA linear PAT 21-FEB-2003

DEFINITION Sequence 4869 from Patent WO02053774.  
ACCESSION AX627828  
VERSION AX627828.1 GI:28455866  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 4869 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 27.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCCAC 8  
Db | | | | | | | |  
8 CCATCCAC 1

RESULT 351  
AX628284  
LOCUS AX628284 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 5325 from Patent WO02053774.  
ACCESSION AX628284  
VERSION AX628284.1 GI:28456322  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 5325 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 27.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TGTGACCT 22  
Db | | | | | | | |  
4 TGTGACCT 11

RESULT 352  
AX628336/c  
LOCUS AX628336 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 5377 from Patent WO02053774.  
ACCESSION AX628336  
VERSION AX628336.1 GI:28456374  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

```
REFERENCE 1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 5377 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source    Location/Qualifiers
          1. .11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATCCACC 9
    |||||||
Db 8 CATCCACC 1

RESULT 353
AX628472
LOCUS      AX628472                11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 5513 from Patent WO02053774.
ACCESSION  AX628472
VERSION     AX628472.1 GI:28456510
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE 1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 5513 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source    Location/Qualifiers
          1. .11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CTGTGTGA 19
    |||||||
Db 4 CTGTGTGA 11

RESULT 354
AX628654/c
LOCUS      AX628654                11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 5695 from Patent WO02053774.
ACCESSION  AX628654
VERSION     AX628654.1 GI:28456692
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE 1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 5695 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source    Location/Qualifiers
          1. .11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
```

```
            /db_xref="taxon:9606"

Query Match      27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GACCTGGT 25
    |||||||
Db 8 GACCTGGT 1

RESULT 355
AX628766
LOCUS      AX628766                11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 5807 from Patent WO02053774.
ACCESSION  AX628766
VERSION     AX628766.1 GI:28456804
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE 1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 5807 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source    Location/Qualifiers
          1. .11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCTGGTAA 27
    |||||||
Db 4 CCTGGTAA 11

RESULT 356
AX629030/c
LOCUS      AX629030                11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 6071 from Patent WO02053774.
ACCESSION  AX629030
VERSION     AX629030.1 GI:28457068
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE 1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 6071 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source    Location/Qualifiers
          1. .11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCTGCTGT 15
    |||||||
Db 11 CCTGCTGT 4
```

|                          |                                                                                                                                                |                                                |               |            |         |                 |
|--------------------------|------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------|---------------|------------|---------|-----------------|
| RESULT 357<br>AX629150/c | AX629150                                                                                                                                       | Sequence 6191 from Patent WO02053774.          | 11 bp         | DNA        | linear  | PAT 21-FEB-2003 |
| LOCUS                    | AX629150                                                                                                                                       | Sequence 6191 from Patent WO02053774.          |               |            |         |                 |
| DEFINITION               | AX629150                                                                                                                                       | Sequence 6191 from Patent WO02053774.          |               |            |         |                 |
| ACCESSION                | AX629150                                                                                                                                       | Sequence 6191 from Patent WO02053774.          |               |            |         |                 |
| VERSION                  | AX629150.1                                                                                                                                     | GI:28457188                                    |               |            |         |                 |
| KEYWORDS                 |                                                                                                                                                |                                                |               |            |         |                 |
| SOURCE                   | Homo sapiens (human)                                                                                                                           |                                                |               |            |         |                 |
| ORGANISM                 | Homo sapiens                                                                                                                                   |                                                |               |            |         |                 |
|                          | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. |                                                |               |            |         |                 |
| REFERENCE                | 1                                                                                                                                              | Petersohn,D., Conradt,M. and Hofmann,K.        |               |            |         |                 |
| AUTHORS                  |                                                                                                                                                | Method for determining homeostasis of the skin |               |            |         |                 |
| TITLE                    |                                                                                                                                                | Patent: WO 02053774-A 6191 11-JUL-2002;        |               |            |         |                 |
| JOURNAL                  |                                                                                                                                                | Henkel Kommanditgesellschaft auf Aktien (DE)   |               |            |         |                 |
| FEATURES                 | Location/Qualifiers                                                                                                                            |                                                |               |            |         |                 |
| source                   | 1..11                                                                                                                                          |                                                |               |            |         |                 |
|                          | /organism="Homo sapiens"                                                                                                                       |                                                |               |            |         |                 |
|                          | /mol_type="unassigned DNA"                                                                                                                     |                                                |               |            |         |                 |
|                          | /db_xref="taxon:9606"                                                                                                                          |                                                |               |            |         |                 |
| Query Match              | 27.6%;                                                                                                                                         | Score 8;                                       | DB 1;         | Length 11; |         |                 |
| Best Local Similarity    | 100.0%;                                                                                                                                        | Pred. No. 1.9e+02;                             |               |            |         |                 |
| Matches                  | 8;                                                                                                                                             | Conservative 0;                                | Mismatches 0; | Indels 0;  | Gaps 0; |                 |
| Qy                       | 2                                                                                                                                              | CATCCACC 9                                     |               |            |         |                 |
|                          |                                                                                                                                                |                                                |               |            |         |                 |
| Db                       | 11                                                                                                                                             | CATCCACC 4                                     |               |            |         |                 |
| RESULT 358<br>AX629152   | AX629152                                                                                                                                       | Sequence 6193 from Patent WO02053774.          | 11 bp         | DNA        | linear  | PAT 21-FEB-2003 |
| LOCUS                    | AX629152                                                                                                                                       | Sequence 6193 from Patent WO02053774.          |               |            |         |                 |
| DEFINITION               | AX629152                                                                                                                                       | Sequence 6193 from Patent WO02053774.          |               |            |         |                 |
| ACCESSION                | AX629152.1                                                                                                                                     | GI:28457190                                    |               |            |         |                 |
| VERSION                  | AX629152.1                                                                                                                                     | GI:28457190                                    |               |            |         |                 |
| KEYWORDS                 |                                                                                                                                                |                                                |               |            |         |                 |
| SOURCE                   | Homo sapiens (human)                                                                                                                           |                                                |               |            |         |                 |
| ORGANISM                 | Homo sapiens                                                                                                                                   |                                                |               |            |         |                 |
|                          | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. |                                                |               |            |         |                 |
| REFERENCE                | 1                                                                                                                                              | Petersohn,D., Conradt,M. and Hofmann,K.        |               |            |         |                 |
| AUTHORS                  |                                                                                                                                                | Method for determining homeostasis of the skin |               |            |         |                 |
| TITLE                    |                                                                                                                                                | Patent: WO 02053774-A 6193 11-JUL-2002;        |               |            |         |                 |
| JOURNAL                  |                                                                                                                                                | Henkel Kommanditgesellschaft auf Aktien (DE)   |               |            |         |                 |
| FEATURES                 | Location/Qualifiers                                                                                                                            |                                                |               |            |         |                 |
| source                   | 1..11                                                                                                                                          |                                                |               |            |         |                 |
|                          | /organism="Homo sapiens"                                                                                                                       |                                                |               |            |         |                 |
|                          | /mol_type="unassigned DNA"                                                                                                                     |                                                |               |            |         |                 |
|                          | /db_xref="taxon:9606"                                                                                                                          |                                                |               |            |         |                 |
| Query Match              | 27.6%;                                                                                                                                         | Score 8;                                       | DB 1;         | Length 11; |         |                 |
| Best Local Similarity    | 100.0%;                                                                                                                                        | Pred. No. 1.9e+02;                             |               |            |         |                 |
| Matches                  | 8;                                                                                                                                             | Conservative 0;                                | Mismatches 0; | Indels 0;  | Gaps 0; |                 |
| Qy                       | 2                                                                                                                                              | CATCCACC 9                                     |               |            |         |                 |
|                          |                                                                                                                                                |                                                |               |            |         |                 |
| Db                       | 11                                                                                                                                             | CATCCACC 4                                     |               |            |         |                 |
| RESULT 359<br>AX629352   | AX629352                                                                                                                                       | Sequence 6393 from Patent WO02053774.          | 11 bp         | DNA        | linear  | PAT 21-FEB-2003 |
| LOCUS                    | AX629352                                                                                                                                       | Sequence 6393 from Patent WO02053774.          |               |            |         |                 |
| DEFINITION               | AX629352                                                                                                                                       | Sequence 6393 from Patent WO02053774.          |               |            |         |                 |
| ACCESSION                | AX629352                                                                                                                                       | Sequence 6393 from Patent WO02053774.          |               |            |         |                 |
| VERSION                  | AX629352.1                                                                                                                                     | GI:28457390                                    |               |            |         |                 |
| KEYWORDS                 |                                                                                                                                                |                                                |               |            |         |                 |
| Qy                       | 7                                                                                                                                              | ACCTGCTG 14                                    |               |            |         |                 |
|                          |                                                                                                                                                |                                                |               |            |         |                 |
| Db                       | 1                                                                                                                                              | ACCTGCTG 8                                     |               |            |         |                 |
| RESULT 360<br>AX629742   | AX629742                                                                                                                                       | Sequence 6783 from Patent WO02053774.          | 11 bp         | DNA        | linear  | PAT 21-FEB-2003 |
| LOCUS                    | AX629742                                                                                                                                       | Sequence 6783 from Patent WO02053774.          |               |            |         |                 |
| DEFINITION               | AX629742                                                                                                                                       | Sequence 6783 from Patent WO02053774.          |               |            |         |                 |
| ACCESSION                | AX629742                                                                                                                                       | Sequence 6783 from Patent WO02053774.          |               |            |         |                 |
| VERSION                  | AX629742.1                                                                                                                                     | GI:28457780                                    |               |            |         |                 |
| KEYWORDS                 |                                                                                                                                                |                                                |               |            |         |                 |
| SOURCE                   | Homo sapiens (human)                                                                                                                           |                                                |               |            |         |                 |
| ORGANISM                 | Homo sapiens                                                                                                                                   |                                                |               |            |         |                 |
|                          | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. |                                                |               |            |         |                 |
| REFERENCE                | 1                                                                                                                                              | Petersohn,D., Conradt,M. and Hofmann,K.        |               |            |         |                 |
| AUTHORS                  |                                                                                                                                                | Method for determining homeostasis of the skin |               |            |         |                 |
| TITLE                    |                                                                                                                                                | Patent: WO 02053774-A 6783 11-JUL-2002;        |               |            |         |                 |
| JOURNAL                  |                                                                                                                                                | Henkel Kommanditgesellschaft auf Aktien (DE)   |               |            |         |                 |
| FEATURES                 | Location/Qualifiers                                                                                                                            |                                                |               |            |         |                 |
| source                   | 1..11                                                                                                                                          |                                                |               |            |         |                 |
|                          | /organism="Homo sapiens"                                                                                                                       |                                                |               |            |         |                 |
|                          | /mol_type="unassigned DNA"                                                                                                                     |                                                |               |            |         |                 |
|                          | /db_xref="taxon:9606"                                                                                                                          |                                                |               |            |         |                 |
| Query Match              | 27.6%;                                                                                                                                         | Score 8;                                       | DB 1;         | Length 11; |         |                 |
| Best Local Similarity    | 100.0%;                                                                                                                                        | Pred. No. 1.9e+02;                             |               |            |         |                 |
| Matches                  | 8;                                                                                                                                             | Conservative 0;                                | Mismatches 0; | Indels 0;  | Gaps 0; |                 |
| Qy                       | 11                                                                                                                                             | GCTGTGTG 18                                    |               |            |         |                 |
|                          |                                                                                                                                                |                                                |               |            |         |                 |
| Db                       | 3                                                                                                                                              | GCTGTGTG 10                                    |               |            |         |                 |
| RESULT 361<br>AX629813   | AX629813                                                                                                                                       | Sequence 6854 from Patent WO02053774.          | 11 bp         | DNA        | linear  | PAT 21-FEB-2003 |
| LOCUS                    | AX629813                                                                                                                                       | Sequence 6854 from Patent WO02053774.          |               |            |         |                 |
| DEFINITION               | AX629813                                                                                                                                       | Sequence 6854 from Patent WO02053774.          |               |            |         |                 |
| ACCESSION                | AX629813                                                                                                                                       | Sequence 6854 from Patent WO02053774.          |               |            |         |                 |
| VERSION                  | AX629813.1                                                                                                                                     | GI:28457851                                    |               |            |         |                 |
| KEYWORDS                 |                                                                                                                                                |                                                |               |            |         |                 |
| SOURCE                   | Homo sapiens (human)                                                                                                                           |                                                |               |            |         |                 |
| ORGANISM                 | Homo sapiens                                                                                                                                   |                                                |               |            |         |                 |
|                          | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. |                                                |               |            |         |                 |
| REFERENCE                | 1                                                                                                                                              | Petersohn,D., Conradt,M. and Hofmann,K.        |               |            |         |                 |
| AUTHORS                  |                                                                                                                                                | Method for determining homeostasis of the skin |               |            |         |                 |
| TITLE                    |                                                                                                                                                | Patent: WO 02053774-A 6854 11-JUL-2002;        |               |            |         |                 |
| JOURNAL                  |                                                                                                                                                | Henkel Kommanditgesellschaft auf Aktien (DE)   |               |            |         |                 |

|                       |  |                                                                   |                                         |    |            |     |        |                 |      |    |  |
|-----------------------|--|-------------------------------------------------------------------|-----------------------------------------|----|------------|-----|--------|-----------------|------|----|--|
| FEATURES              |  | Henkel Kommanditgesellschaft auf Aktien (DE)                      |                                         |    |            |     |        |                 |      |    |  |
| source                |  | Location/Qualifiers                                               |                                         |    |            |     |        |                 |      |    |  |
|                       |  | 1. .11                                                            |                                         |    |            |     |        |                 |      |    |  |
|                       |  | /organism="Homo sapiens"                                          |                                         |    |            |     |        |                 |      |    |  |
|                       |  | /mol_type="unassigned DNA"                                        |                                         |    |            |     |        |                 |      |    |  |
|                       |  | /db_xref="taxon:9606"                                             |                                         |    |            |     |        |                 |      |    |  |
| Query Match           |  | 27.6%; Score 8; DB 1; Length 11;                                  |                                         |    |            |     |        |                 |      |    |  |
| Best Local Similarity |  | 100.0%; Pred. No. 1.9e+02;                                        |                                         |    |            |     |        |                 |      |    |  |
| Matches               |  | 8;                                                                | Conservative                            | 0; | Mismatches | 0;  | Indels | 0;              | Gaps | 0; |  |
| QY                    |  | 10                                                                | TGCTGTGT 17                             |    |            |     |        |                 |      |    |  |
| Db                    |  | 4                                                                 | TGCTGTGT 11                             |    |            |     |        |                 |      |    |  |
| RESULT 362            |  |                                                                   |                                         |    |            |     |        |                 |      |    |  |
| AX629849/c            |  |                                                                   |                                         |    |            |     |        |                 |      |    |  |
| LOCUS                 |  | AX629849                                                          | Sequence 6890 from Patent WO02053774.   |    | 11 bp      | DNA | linear | PAT 21-FEB-2003 |      |    |  |
| DEFINITION            |  | AX629849                                                          |                                         |    |            |     |        |                 |      |    |  |
| ACCESSION             |  | AX629849.1                                                        | GI:28457887                             |    |            |     |        |                 |      |    |  |
| VERSION               |  |                                                                   |                                         |    |            |     |        |                 |      |    |  |
| KEYWORDS              |  | Homo sapiens (human)                                              |                                         |    |            |     |        |                 |      |    |  |
| SOURCE                |  | Homo sapiens                                                      |                                         |    |            |     |        |                 |      |    |  |
| ORGANISM              |  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |                                         |    |            |     |        |                 |      |    |  |
|                       |  | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;       |                                         |    |            |     |        |                 |      |    |  |
|                       |  | Hominidae; Homo.                                                  |                                         |    |            |     |        |                 |      |    |  |
| REFERENCE             |  | 1                                                                 | Petersohn,D., Conradt,M. and Hofmann,K. |    |            |     |        |                 |      |    |  |
| AUTHORS               |  | Method for determining homeostasis of the skin                    |                                         |    |            |     |        |                 |      |    |  |
| TITLE                 |  | Patent: WO 02053774-A 6890 11-JUL-2002;                           |                                         |    |            |     |        |                 |      |    |  |
| JOURNAL               |  | Henkel Kommanditgesellschaft auf Aktien (DE)                      |                                         |    |            |     |        |                 |      |    |  |
| FEATURES              |  | Location/Qualifiers                                               |                                         |    |            |     |        |                 |      |    |  |
| source                |  | 1. .11                                                            |                                         |    |            |     |        |                 |      |    |  |
|                       |  | /organism="Homo sapiens"                                          |                                         |    |            |     |        |                 |      |    |  |
|                       |  | /mol_type="unassigned DNA"                                        |                                         |    |            |     |        |                 |      |    |  |
|                       |  | /db_xref="taxon:9606"                                             |                                         |    |            |     |        |                 |      |    |  |
| Query Match           |  | 27.6%; Score 8; DB 1; Length 11;                                  |                                         |    |            |     |        |                 |      |    |  |
| Best Local Similarity |  | 100.0%; Pred. No. 1.9e+02;                                        |                                         |    |            |     |        |                 |      |    |  |
| Matches               |  | 8;                                                                | Conservative                            | 0; | Mismatches | 0;  | Indels | 0;              | Gaps | 0; |  |
| QY                    |  | 4                                                                 | TCCACCTG 11                             |    |            |     |        |                 |      |    |  |
| Db                    |  | 10                                                                | TCCACCTG 3                              |    |            |     |        |                 |      |    |  |
| RESULT 363            |  |                                                                   |                                         |    |            |     |        |                 |      |    |  |
| AX630339              |  |                                                                   |                                         |    |            |     |        |                 |      |    |  |
| LOCUS                 |  | AX630339                                                          | Sequence 7380 from Patent WO02053774.   |    | 11 bp      | DNA | linear | PAT 21-FEB-2003 |      |    |  |
| DEFINITION            |  | AX630339                                                          |                                         |    |            |     |        |                 |      |    |  |
| ACCESSION             |  | AX630339.1                                                        | GI:28458377                             |    |            |     |        |                 |      |    |  |
| VERSION               |  |                                                                   |                                         |    |            |     |        |                 |      |    |  |
| KEYWORDS              |  | Homo sapiens (human)                                              |                                         |    |            |     |        |                 |      |    |  |
| SOURCE                |  | Homo sapiens                                                      |                                         |    |            |     |        |                 |      |    |  |
| ORGANISM              |  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |                                         |    |            |     |        |                 |      |    |  |
|                       |  | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;       |                                         |    |            |     |        |                 |      |    |  |
|                       |  | Hominidae; Homo.                                                  |                                         |    |            |     |        |                 |      |    |  |
| REFERENCE             |  | 1                                                                 | Petersohn,D., Conradt,M. and Hofmann,K. |    |            |     |        |                 |      |    |  |
| AUTHORS               |  | Method for determining homeostasis of the skin                    |                                         |    |            |     |        |                 |      |    |  |
| TITLE                 |  | Patent: WO 02053774-A 7380 11-JUL-2002;                           |                                         |    |            |     |        |                 |      |    |  |
| JOURNAL               |  | Henkel Kommanditgesellschaft auf Aktien (DE)                      |                                         |    |            |     |        |                 |      |    |  |
| FEATURES              |  | Location/Qualifiers                                               |                                         |    |            |     |        |                 |      |    |  |
| source                |  | 1. .11                                                            |                                         |    |            |     |        |                 |      |    |  |
|                       |  | /organism="Homo sapiens"                                          |                                         |    |            |     |        |                 |      |    |  |
|                       |  | /mol_type="unassigned DNA"                                        |                                         |    |            |     |        |                 |      |    |  |
|                       |  | /db_xref="taxon:9606"                                             |                                         |    |            |     |        |                 |      |    |  |
| Query Match           |  | 27.6%; Score 8; DB 1; Length 11;                                  |                                         |    |            |     |        |                 |      |    |  |
| Best Local Similarity |  | 100.0%; Pred. No. 1.9e+02;                                        |                                         |    |            |     |        |                 |      |    |  |
| Matches               |  | 8;                                                                | Conservative                            | 0; | Mismatches | 0;  | Indels | 0;              | Gaps | 0; |  |
| QY                    |  | 11                                                                | GCTGTGTG 18                             |    |            |     |        |                 |      |    |  |
| Db                    |  | 11                                                                | GCTGTGTG 4                              |    |            |     |        |                 |      |    |  |
| RESULT 366            |  |                                                                   |                                         |    |            |     |        |                 |      |    |  |
| AX630649/c            |  |                                                                   |                                         |    |            |     |        |                 |      |    |  |

|                       |                                                                                                                                                |                                       |    |            |     |        |                 |      |    |
|-----------------------|------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------|----|------------|-----|--------|-----------------|------|----|
| Matches               | 8;                                                                                                                                             | Conservative                          | 0; | Mismatches | 0;  | Indels | 0;              | Gaps | 0; |
| Qy                    | 21                                                                                                                                             | CTGGTAAA 28                           |    |            |     |        |                 |      |    |
| Db                    | 2                                                                                                                                              | CTGGTAAA 9                            |    |            |     |        |                 |      |    |
| RESULT 364            |                                                                                                                                                |                                       |    |            |     |        |                 |      |    |
| AX630383              |                                                                                                                                                |                                       |    |            |     |        |                 |      |    |
| LOCUS                 | AX630383                                                                                                                                       | Sequence 7424 from Patent WO02053774. |    | 11 bp      | DNA | linear | PAT 21-FEB-2003 |      |    |
| DEFINITION            | AX630383                                                                                                                                       |                                       |    |            |     |        |                 |      |    |
| ACCESSION             | AX630383.1                                                                                                                                     | GI:28458421                           |    |            |     |        |                 |      |    |
| VERSION               |                                                                                                                                                |                                       |    |            |     |        |                 |      |    |
| KEYWORDS              | Homo sapiens (human)                                                                                                                           |                                       |    |            |     |        |                 |      |    |
| SOURCE                | Homo sapiens                                                                                                                                   |                                       |    |            |     |        |                 |      |    |
| ORGANISM              | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. |                                       |    |            |     |        |                 |      |    |
| REFERENCE             | 1                                                                                                                                              |                                       |    |            |     |        |                 |      |    |
| AUTHORS               | Petersohn,D., Conradt,M. and Hofmann,K.                                                                                                        |                                       |    |            |     |        |                 |      |    |
| TITLE                 | Method for determining homeostasis of the skin                                                                                                 |                                       |    |            |     |        |                 |      |    |
| JOURNAL               | Patent: WO 02053774-A 7424 11-JUL-2002;                                                                                                        |                                       |    |            |     |        |                 |      |    |
|                       | Henkel Kommanditgesellschaft auf Aktien (DE)                                                                                                   |                                       |    |            |     |        |                 |      |    |
| FEATURES              | Location/Qualifiers                                                                                                                            |                                       |    |            |     |        |                 |      |    |
| source                | 1. .11                                                                                                                                         |                                       |    |            |     |        |                 |      |    |
|                       | /organism="Homo sapiens"                                                                                                                       |                                       |    |            |     |        |                 |      |    |
|                       | /mol_type="unassigned DNA"                                                                                                                     |                                       |    |            |     |        |                 |      |    |
|                       | /db_xref="taxon:9606"                                                                                                                          |                                       |    |            |     |        |                 |      |    |
| Query Match           | 27.6%; Score 8; DB 1; Length 11;                                                                                                               |                                       |    |            |     |        |                 |      |    |
| Best Local Similarity | 100.0%; Pred. No. 1.9e+02;                                                                                                                     |                                       |    |            |     |        |                 |      |    |
| Matches               | 8;                                                                                                                                             | Conservative                          | 0; | Mismatches | 0;  | Indels | 0;              | Gaps | 0; |
| Qy                    | 7                                                                                                                                              | ACCTGCTG 14                           |    |            |     |        |                 |      |    |
| Db                    | 4                                                                                                                                              | ACCTGCTG 11                           |    |            |     |        |                 |      |    |
| RESULT 365            |                                                                                                                                                |                                       |    |            |     |        |                 |      |    |
| AX630504/c            |                                                                                                                                                |                                       |    |            |     |        |                 |      |    |
| LOCUS                 | AX630504                                                                                                                                       | Sequence 7545 from Patent WO02053774. |    | 11 bp      | DNA | linear | PAT 21-FEB-2003 |      |    |
| DEFINITION            | AX630504                                                                                                                                       |                                       |    |            |     |        |                 |      |    |
| ACCESSION             | AX630504.1                                                                                                                                     | GI:28458542                           |    |            |     |        |                 |      |    |
| VERSION               |                                                                                                                                                |                                       |    |            |     |        |                 |      |    |
| KEYWORDS              | Homo sapiens (human)                                                                                                                           |                                       |    |            |     |        |                 |      |    |
| SOURCE                | Homo sapiens                                                                                                                                   |                                       |    |            |     |        |                 |      |    |
| ORGANISM              | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. |                                       |    |            |     |        |                 |      |    |
| REFERENCE             | 1                                                                                                                                              |                                       |    |            |     |        |                 |      |    |
| AUTHORS               | Petersohn,D., Conradt,M. and Hofmann,K.                                                                                                        |                                       |    |            |     |        |                 |      |    |
| TITLE                 | Method for determining homeostasis of the skin                                                                                                 |                                       |    |            |     |        |                 |      |    |
| JOURNAL               | Patent: WO 02053774-A 7545 11-JUL-2002;                                                                                                        |                                       |    |            |     |        |                 |      |    |
|                       | Henkel Kommanditgesellschaft auf Aktien (DE)                                                                                                   |                                       |    |            |     |        |                 |      |    |
| FEATURES              | Location/Qualifiers                                                                                                                            |                                       |    |            |     |        |                 |      |    |
| source                | 1. .11                                                                                                                                         |                                       |    |            |     |        |                 |      |    |
|                       | /organism="Homo sapiens"                                                                                                                       |                                       |    |            |     |        |                 |      |    |
|                       | /mol_type="unassigned DNA"                                                                                                                     |                                       |    |            |     |        |                 |      |    |
|                       | /db_xref="taxon:9606"                                                                                                                          |                                       |    |            |     |        |                 |      |    |
| Query Match           | 27.6%; Score 8; DB 1; Length 11;                                                                                                               |                                       |    |            |     |        |                 |      |    |
| Best Local Similarity | 100.0%; Pred. No. 1.9e+02;                                                                                                                     |                                       |    |            |     |        |                 |      |    |
| Matches               | 8;                                                                                                                                             | Conservative                          | 0; | Mismatches | 0;  | Indels | 0;              | Gaps | 0; |
| Qy                    | 11                                                                                                                                             | GCTGTGTG 18                           |    |            |     |        |                 |      |    |
| Db                    | 11                                                                                                                                             | GCTGTGTG 4                            |    |            |     |        |                 |      |    |
| RESULT 366            |                                                                                                                                                |                                       |    |            |     |        |                 |      |    |
| AX630649/c            |                                                                                                                                                |                                       |    |            |     |        |                 |      |    |

LOCUS AX630649 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 7690 from Patent WO02053774.  
ACCESSION AX630649  
VERSION AX630649.1 GI:28458687  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 7690 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source Location/Qualifiers  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 27.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 21 CTGGTAAA 28  
|||||  
Db 11 CTGGTAAA 4  
RESULT 367  
AX631791/c  
LOCUS AX631791 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 8833 from Patent WO02053774.  
ACCESSION AX631791  
VERSION AX631791.1 GI:28459898  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 8833 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source Location/Qualifiers  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 27.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 CATCCACC 9  
|||||  
Db 10 CATCCACC 3  
RESULT 368  
AX924272  
LOCUS AX924272 11 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 57 from Patent EP1350841.  
ACCESSION AX924272  
VERSION AX924272.1 GI:40217196  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
1  
REFERENCE

AUTHORS Schoenbrunner,N.J., Myers,T.W. and Gelfland,D.H.  
TITLE Thermostable or thermoactive DNA polymerase with attenuated  
3'-5'exonuclease activity  
JOURNAL Patent: EP 1350841-A 57 08-OCT-2003;  
Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)  
FEATURES  
source Location/Qualifiers  
1. .11  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
Query Match 27.6%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 17 TGACCTGG 24  
|||||  
Db 1 TGACCTGG 8  
RESULT 369  
A36701/c  
LOCUS A36701 11 bp DNA linear PAT 05-MAR-1997  
DEFINITION Sequence 3 from Patent EP0590721.  
ACCESSION A36701  
VERSION A36701.1 GI:2293973  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
unclassified sequences.  
REFERENCE  
1 (bases 1 to 11)  
AUTHORS Ficca,A.G.  
TITLE Method for expressing receptors of the human nervous system in the  
yeast Schizosaccharomyces pombe  
JOURNAL Patent: EP 0590721-A 3 06-APR-1994;  
ENICHEM SPA (IT)  
COMMENT Other publication AT 140484T 960815  
Other publication DE 69303685D 960822  
Other publication IT 1255697 951110.  
FEATURES  
source Location/Qualifiers  
1. .11  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
Query Match 26.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 2.1e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 12 CTGTGTGACCT 22  
|||||  
Db 11 CTGCGTGACGT 1  
RESULT 370  
BD095127/c  
LOCUS BD095127 11 bp DNA linear PAT 27-AUG-2002  
DEFINITION A polynucleotide encoding mouse histidine decarboxylase.  
ACCESSION BD095127  
VERSION BD095127.1 GI:22640715  
KEYWORDS WO 0132892-A/20.  
SOURCE Mus sp.  
ORGANISM Mus sp.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 11)  
AUTHORS Otsu,H.  
TITLE A polynucleotide encoding mouse histidine decarboxylase  
JOURNAL Patent: WO 0132892-A 20 10-MAY-2001;  
JAPAN SCIENCE AND TECHNOLOGY CORP,HIROSHI OTSU  
COMMENT OS Mus sp. (mouse)  
PN WO 0132892-A/20



PD 10-MAY-2001  
PF 01-NOV-2000 WO 2000JP007689  
PR 02-NOV-1999 JP 99P 312559,23-MAR-2000 JP 00P 082953 PI  
HIROSHI OTSU  
PC C12N15/60,C12N9/88  
CC A polynucleotide encoding mouse histidine decarboxylase FH  
Key Location/Qualifiers  
FT source 1..11  
FT /organism='Mus sp. (mouse)'.  
Location/Qualifiers  
1..11  
/organism="Mus sp."  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10095"  
Query Match 26.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 2.1e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 16 GTGACCTGGTA 26 11 bp DNA linear PAT 05-JUL-2004  
| | | | | | | |  
Db 11 GTGCCCTGGAA 1  
RESULT 371  
CQ828950/c  
LOCUS CQ828950 11 bp DNA linear PAT 05-JUL-2004  
DEFINITION Sequence 668 from Patent WO2004053120.  
ACCESSION CQ828950  
VERSION CQ828950.1 GI:49732433  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Weihe,E., Bieller,A. and Schaefer,M.K.  
TITLE Regulatory elements in the 5' region of the vr1 gene  
JOURNAL Patent: WO 2004053120-A 668 24-JUN-2004;  
Gruenenthal GmbH (DE)  
FEATURES  
source Location/Qualifiers  
1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="V\$AP1FJ Q2"  
Query Match 26.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 2.1e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 13 TGTGTGACCTG 23 11 bp DNA linear PAT 29-JUL-2004  
| | | | | | | |  
Db 11 TGTGTGTCATG 1  
RESULT 372  
CQ832704/c  
LOCUS CQ832704 11 bp DNA linear PAT 29-JUL-2004  
DEFINITION Sequence 75 from Patent WO2004059002.  
ACCESSION CQ832704  
VERSION CQ832704.1 GI:50832311  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
Conradt,M. and Hofmann,K.  
TITLE Method for determining the homeostasis of hairy skin  
JOURNAL Patent: WO 2004053120-A 668 24-JUN-2004;  
Gruenenthal GmbH (DE)  
FEATURES  
source Location/Qualifiers  
1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

JOURNAL Patent: WO 2004059002-A 75 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source Location/Qualifiers  
1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 26.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 2.1e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 CATCCACCTGC 12 11 bp DNA linear PAT 29-JUL-2004  
| | | | | | | |  
Db 11 CCTCCACCTCC 1  
RESULT 373  
CQ832725  
LOCUS CQ832725 11 bp DNA linear PAT 29-JUL-2004  
DEFINITION Sequence 96 from Patent WO2004059002.  
ACCESSION CQ832725  
VERSION CQ832725.1 GI:50832332  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
Conradt,M. and Hofmann,K.  
TITLE Method for determining the homeostasis of hairy skin  
JOURNAL Patent: WO 2004059002-A 96 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source Location/Qualifiers  
1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 26.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 2.1e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 CATCCACCTGC 12 11 bp DNA linear PAT 29-JUL-2004  
| | | | | | | |  
Db 1 CATCTGCTGC 11  
RESULT 374  
CQ833139  
LOCUS CQ833139 11 bp DNA linear PAT 29-JUL-2004  
DEFINITION Sequence 510 from Patent WO2004059002.  
ACCESSION CQ833139  
VERSION CQ833139.1 GI:50832746  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
Conradt,M. and Hofmann,K.  
TITLE Method for determining the homeostasis of hairy skin  
JOURNAL Patent: WO 2004059002-A 510 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source Location/Qualifiers  
1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 26.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 2.1e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 GTGTGACCTGG 24  
| | | | | | | | |  
Db 1 GTGAACCTGG 11

RESULT 375  
CQ833700  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE  
1  
AUTHORS  
Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
Conrad,M. and Hofmann,K.  
TITLE  
JOURNAL  
Method for determining the homeostasis of hairy skin  
Patent: WO 2004059002-A 1071 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES  
source  
1 .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 26.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 2.1e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 TGTGTGACCTG 23  
| | | | | | | | |  
Db 1 TTTGAGACCTG 11

RESULT 376  
CQ833823/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE  
1  
AUTHORS  
Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
Conrad,M. and Hofmann,K.  
TITLE  
JOURNAL  
Method for determining the homeostasis of hairy skin  
Patent: WO 2004059002-A 1194 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES  
source  
1 .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 26.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 2.1e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 CTGTGTGACCT 22  
| | | | | | | | |

Db 11 CTGTGTTATCT 1

RESULT 377  
CQ833936  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE  
1  
AUTHORS  
Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
Conrad,M. and Hofmann,K.  
TITLE  
JOURNAL  
Method for determining the homeostasis of hairy skin  
Patent: WO 2004059002-A 1307 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES  
Location/Qualifiers  
1 .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 26.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 2.1e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCCACCTG 11  
| | | | | | | | |  
Db 1 CCATTCTCCTG 11

RESULT 378  
CQ835054/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE  
1  
AUTHORS  
Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
Conrad,M. and Hofmann,K.  
TITLE  
JOURNAL  
Method for determining markers of human facial skin  
Patent: WO 2004059001-A 112 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES  
Location/Qualifiers  
1 .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 26.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 2.1e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 GCTGTGTGACC 21  
| | | | | | | | |  
Db 11 GCTCTGTCACC 1

RESULT 379  
CQ836644  
LOCUS  
DEFINITION  
Sequence 1702 from Patent WO2004059001.

ACCESSION CQ836644  
VERSION CQ836644.1 GI:50836178  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
Conradt,M. and Hofmann,K.  
TITLE Method for determining markers of human facial skin  
JOURNAL Patent: WO 2004059001-A 1702 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 26.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 2.1e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 18 GACCTGGTAA 28  
| | | | | | | | | |  
Db 1 GCCTTGGTAA 11  
RESULT 380  
CQ837342  
LOCUS CQ837342 11 bp DNA linear PAT 29-JUL-2004  
DEFINITION Sequence 2400 from Patent WO2004059001.  
ACCESSION CQ837342  
VERSION CQ837342.1 GI:50836876  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
Conradt,M. and Hofmann,K.  
TITLE Method for determining markers of human facial skin  
JOURNAL Patent: WO 2004059001-A 2400 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 26.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 2.1e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 19 ACCTGGTAAAT 29  
| | | | | | | | | |  
Db 1 ACTTGATAAT 11  
RESULT 381  
CQ837591  
LOCUS CQ837591 11 bp DNA linear PAT 29-JUL-2004  
DEFINITION Sequence 2649 from Patent WO2004059001.  
ACCESSION CQ837591  
VERSION CQ837591.1 GI:50837125  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
Conradt,M. and Hofmann,K.  
TITLE Method for determining markers of human facial skin  
JOURNAL Patent: WO 2004059001-A 2649 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 26.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 2.1e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 7 ACCTGCTGTGT 17  
| | | | | | | | | |  
Db 1 ACCTGCTGTCT 11  
RESULT 382  
CQ837743/c  
LOCUS CQ837743 11 bp DNA linear PAT 29-JUL-2004  
DEFINITION Sequence 2801 from Patent WO2004059001.  
ACCESSION CQ837743  
VERSION CQ837743.1 GI:50837277  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
Conradt,M. and Hofmann,K.  
TITLE Method for determining markers of human facial skin  
JOURNAL Patent: WO 2004059001-A 2801 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 26.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 2.1e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 18 GACCTGGTAAA 28  
| | | | | | | | | |  
Db 1 GCCCTGGTGAA 1  
RESULT 383  
CQ838096  
LOCUS CQ838096 11 bp DNA linear PAT 29-JUL-2004  
DEFINITION Sequence 3154 from Patent WO2004059001.  
ACCESSION CQ838096  
VERSION CQ838096.1 GI:50837630  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
Conradt,M. and Hofmann,K.  
TITLE Method for determining markers of human facial skin  
JOURNAL Patent: WO 2004059001-A 3154 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES source Location/Qualifiers  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 26.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 2.1e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ATCCACCTGCT 13  
||| |||||  
Db 1 ATTTACCTGCT 11

RESULT 384  
CQ838096/c  
LOCUS CQ838096 11 bp DNA linear PAT 29-JUL-2004  
DEFINITION Sequence 3154 from Patent WO2004059001.  
ACCESSION CQ838096  
VERSION CQ838096.1 GI:50837630  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
Conradt,M. and Hofmann,K.  
TITLE Method for determining markers of human facial skin  
JOURNAL Patent: WO 2004059001-A 3154 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES source Location/Qualifiers  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 26.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 2.1e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 19 ACCTGGTAAAT 29  
||| |||||  
Db 11 AGCAGGTAAT 1

RESULT 385  
CS058269  
LOCUS CS058269 11 bp DNA linear PAT 13-APR-2005  
DEFINITION Sequence 166 from Patent WO2005028671.  
ACCESSION CS058269  
VERSION CS058269.1 GI:62551452  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and  
Kessler-Becker,D.  
TITLE Method for determining hair cycle markers  
JOURNAL Patent: WO 2005028671-A 166 31-MAR-2005;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES source Location/Qualifiers  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 26.9%; Score 7.8; DB 1; Length 11;

Best Local Similarity 81.8%; Pred. No. 2.1e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 13 TGTGTGACCTG 23  
||| |||||  
Db 1 TTTGAGACCTG 11

RESULT 386  
AR364168/c  
LOCUS AR364168 11 bp DNA linear PAT 03-SEP-2003  
DEFINITION Sequence 12 from patent US 5256558.  
ACCESSION AR364168  
VERSION AR364168.1 GI:34426497  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 11)  
AUTHORS Coruzzi,G.M. and Tsai,F.-Y.  
TITLE Gene encoding plant asparagine synthetase  
JOURNAL Patent: US 5256558-A 12 26-OCT-1993;  
The Trustees of Rockefeller University; New York, NY

FEATURES source Location/Qualifiers  
1. .11  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 26.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 2.1e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGT 15  
||| |||||  
Db 11 CTACGTGCTGT 1

RESULT 387  
AX470620  
LOCUS AX470620 11 bp DNA linear PAT 09-AUG-2002  
DEFINITION Sequence 197 from Patent WO20053773.  
ACCESSION AX470620  
VERSION AX470620.1 GI:22205745  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.  
TITLE Method for determining skin stress or skin ageing in vitro  
JOURNAL Patent: WO 02053773-A 197 11-JUL-2002;  
HENKEL KGAA (DE)

FEATURES source Location/Qualifiers  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 26.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 2.1e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TCCACCTGCTG 14  
||| |||||  
Db 1 TCCATCTGTTG 11

RESULT 388  
AX470911  
LOCUS AX470911 11 bp DNA linear PAT 09-AUG-2002  
DEFINITION Sequence 488 from Patent WO20053773.

```
ACCESSION      AX470911
VERSION        AX470911.1  GI:22206036
KEYWORDS
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE      1
AUTHORS        Hofmann,K., Conradt,M. and Petersohn,D.
TITLE          Method for determining skin stress or skin ageing in vitro
JOURNAL        Patent: WO 02053773-A 488 11-JUL-2002;
               HENKEL KGAA (DE)
FEATURES       Location/Qualifiers
               source
               1..11
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match    26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      18  GACCTGGTAA 28
        |||||||
Db      1  GAGCTGGTGAA 11

RESULT 389
AX471463
LOCUS        AX471463                11 bp  DNA          linear    PAT 09-AUG-2002
DEFINITION   Sequence 1040 from Patent WO02053773.
ACCESSION    AX471463
VERSION      AX471463.1  GI:22206588
KEYWORDS     .
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE     1
AUTHORS       Hofmann,K., Conradt,M. and Petersohn,D.
TITLE         Method for determining skin stress or skin ageing in vitro
JOURNAL       Patent: WO 02053773-A 1040 11-JUL-2002;
               HENKEL KGAA (DE)
FEATURES      Location/Qualifiers
               source
               1..11
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match    26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2  CATCCACCTGC 12
        |||||
Db      1  CATCCTGCTGC 11

RESULT 390
AX471815
LOCUS        AX471815                11 bp  DNA          linear    PAT 09-AUG-2002
DEFINITION   Sequence 1392 from Patent WO02053773.
ACCESSION    AX471815
VERSION      AX471815.1  GI:22206940
KEYWORDS     .
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE     1
```

```
AUTHORS        Hofmann,K., Conradt,M. and Petersohn,D.
TITLE          Method for determining skin stress or skin ageing in vitro
JOURNAL        Patent: WO 02053773-A 1392 11-JUL-2002;
               HENKEL KGAA (DE)
FEATURES       Location/Qualifiers
               source
               1..11
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match    26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      19  ACCTGGTAAAT 29
        |||||
Db      1  ACTTGATAAAT 11

RESULT 391
AX623055
LOCUS        AX623055                11 bp  DNA          linear    PAT 21-FEB-2003
DEFINITION   Sequence 96 from Patent WO02053774.
ACCESSION    AX623055
VERSION      AX623055.1  GI:28450996
KEYWORDS     .
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE     1
AUTHORS       Petersohn,D., Conradt,M. and Hofmann,K.
TITLE         Method for determining homeostasis of the skin
JOURNAL       Patent: WO 02053774-A 96 11-JUL-2002;
               Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES      Location/Qualifiers
               source
               1..11
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match    26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      10  TGTGTGTGAC 20
        |||||||
Db      1  TTCTGTGTGCC 11

RESULT 392
AX623372/c
LOCUS        AX623372                11 bp  DNA          linear    PAT 21-FEB-2003
DEFINITION   Sequence 413 from Patent WO02053774.
ACCESSION    AX623372
VERSION      AX623372.1  GI:28451313
KEYWORDS     .
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE     1
AUTHORS       Petersohn,D., Conradt,M. and Hofmann,K.
TITLE         Method for determining homeostasis of the skin
JOURNAL       Patent: WO 02053774-A 413 11-JUL-2002;
               Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES      Location/Qualifiers
               source
               1..11
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"
```



|                       |                                                                   |                    |       |            |                      |
|-----------------------|-------------------------------------------------------------------|--------------------|-------|------------|----------------------|
| Query Match           | 26.9%;                                                            | Score 7.8;         | DB 1; | Length 11; |                      |
| Best Local Similarity | 81.8%;                                                            | Pred. No. 2.1e+02; |       |            |                      |
| Matches               | 9;                                                                | Conservative       | 0;    | Mismatches | 2; Indels 0; Gaps 0; |
| QY                    | 6                                                                 | CACCTGCTGTG 16     |       |            |                      |
| Db                    | 11                                                                | CTCCTGCTGAG 1      |       |            |                      |
| RESULT 393            |                                                                   |                    |       |            |                      |
| AX623975              |                                                                   |                    |       |            |                      |
| LOCUS                 | AX623975                                                          | 11 bp              | DNA   | linear     | PAT 21-FEB-2003      |
| DEFINITION            | Sequence 1016 from Patent WO02053774.                             |                    |       |            |                      |
| ACCESSION             | AX623975                                                          |                    |       |            |                      |
| VERSION               | AX623975.1 GI:28451916                                            |                    |       |            |                      |
| KEYWORDS              | .                                                                 |                    |       |            |                      |
| SOURCE                | Homo sapiens (human)                                              |                    |       |            |                      |
| ORGANISM              | Homo sapiens                                                      |                    |       |            |                      |
|                       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |                    |       |            |                      |
|                       | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;       |                    |       |            |                      |
|                       | Hominidae; Homo.                                                  |                    |       |            |                      |
| REFERENCE             | 1                                                                 |                    |       |            |                      |
| AUTHORS               | Petersohn,D., Conradt,M. and Hofmann,K.                           |                    |       |            |                      |
| TITLE                 | Method for determining homeostasis of the skin                    |                    |       |            |                      |
| JOURNAL               | Patent: WO 02053774-A 1016 11-JUL-2002;                           |                    |       |            |                      |
|                       | Henkel Kommanditgesellschaft auf Aktien (DE)                      |                    |       |            |                      |
| FEATURES              | Location/Qualifiers                                               |                    |       |            |                      |
| source                | 1. .11                                                            |                    |       |            |                      |
|                       | /organism="Homo sapiens"                                          |                    |       |            |                      |
|                       | /mol_type="unassigned DNA"                                        |                    |       |            |                      |
|                       | /db_xref="taxon:9606"                                             |                    |       |            |                      |
| Query Match           | 26.9%;                                                            | Score 7.8;         | DB 1; | Length 11; |                      |
| Best Local Similarity | 81.8%;                                                            | Pred. No. 2.1e+02; |       |            |                      |
| Matches               | 9;                                                                | Conservative       | 0;    | Mismatches | 2; Indels 0; Gaps 0; |
| QY                    | 1                                                                 | CCATCCACCTG 11     |       |            |                      |
| Db                    | 1                                                                 | CAATCCTCCTG 11     |       |            |                      |
| RESULT 394            |                                                                   |                    |       |            |                      |
| AX624312              |                                                                   |                    |       |            |                      |
| LOCUS                 | AX624312                                                          | 11 bp              | DNA   | linear     | PAT 21-FEB-2003      |
| DEFINITION            | Sequence 1353 from Patent WO02053774.                             |                    |       |            |                      |
| ACCESSION             | AX624312                                                          |                    |       |            |                      |
| VERSION               | AX624312.1 GI:28452253                                            |                    |       |            |                      |
| KEYWORDS              | .                                                                 |                    |       |            |                      |
| SOURCE                | Homo sapiens (human)                                              |                    |       |            |                      |
| ORGANISM              | Homo sapiens                                                      |                    |       |            |                      |
|                       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |                    |       |            |                      |
|                       | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;       |                    |       |            |                      |
|                       | Hominidae; Homo.                                                  |                    |       |            |                      |
| REFERENCE             | 1                                                                 |                    |       |            |                      |
| AUTHORS               | Petersohn,D., Conradt,M. and Hofmann,K.                           |                    |       |            |                      |
| TITLE                 | Method for determining homeostasis of the skin                    |                    |       |            |                      |
| JOURNAL               | Patent: WO 02053774-A 1353 11-JUL-2002;                           |                    |       |            |                      |
|                       | Henkel Kommanditgesellschaft auf Aktien (DE)                      |                    |       |            |                      |
| FEATURES              | Location/Qualifiers                                               |                    |       |            |                      |
| source                | 1. .11                                                            |                    |       |            |                      |
|                       | /organism="Homo sapiens"                                          |                    |       |            |                      |
|                       | /mol_type="unassigned DNA"                                        |                    |       |            |                      |
|                       | /db_xref="taxon:9606"                                             |                    |       |            |                      |
| Query Match           | 26.9%;                                                            | Score 7.8;         | DB 1; | Length 11; |                      |
| Best Local Similarity | 81.8%;                                                            | Pred. No. 2.1e+02; |       |            |                      |
| Matches               | 9;                                                                | Conservative       | 0;    | Mismatches | 2; Indels 0; Gaps 0; |
| QY                    | 14                                                                | GTGTGACCTGG 24     |       |            |                      |
| Db                    | 1                                                                 | GTGAGACCTCG 11     |       |            |                      |

|            |          |            |            |                                       |       |     |        |                 |
|------------|----------|------------|------------|---------------------------------------|-------|-----|--------|-----------------|
| RESULT 395 | AX625384 | LOCUS      | AX625384   | Sequence 2425 from Patent WO02053774. | 11 bp | DNA | linear | PAT 21-FEB-2003 |
|            |          | DEFINITION | AX625384   |                                       |       |     |        |                 |
|            |          | ACCESSION  | AX625384   |                                       |       |     |        |                 |
|            |          | VERSION    | AX625384.1 | GI:28453325                           |       |     |        |                 |
|            |          | KEYWORDS   |            |                                       |       |     |        |                 |
|            |          | SOURCE     |            |                                       |       |     |        |                 |
|            |          | ORGANISM   |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |
|            |          |            |            |                                       |       |     |        |                 |

```

ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 3330 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       Location/Qualifiers
              1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      12 CTGTGTGACCT 22
        |||||
Db      11 CTGTGTTATCT 1

RESULT 398
AX626533/c
LOCUS      AX626533      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 3574 from Patent WO02053774.
ACCESSION  AX626533
VERSION     AX626533.1 GI:28454571
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 3574 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       Location/Qualifiers
              1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CATCCACCTGC 12
        |||||
Db      11 CATCCACAGC 1

RESULT 399
AX627698/c
LOCUS      AX627698      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4739 from Patent WO02053774.
ACCESSION  AX627698
VERSION     AX627698.1 GI:28455736
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 4739 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)

```

```

FEATURES
source       Location/Qualifiers
              1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      17 TGACCTGGTAA 27
        ||| |||||
Db      11 TGATATGTAA 1

RESULT 400
AX627752
LOCUS      AX627752      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4793 from Patent WO02053774.
ACCESSION  AX627752
VERSION     AX627752.1 GI:28455790
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 4793 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       Location/Qualifiers
              1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 TCCACCTGCTG 14
        |||||
Db      1 TCCATCTGTTG 11

RESULT 401
AX628274
LOCUS      AX628274      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 5315 from Patent WO02053774.
ACCESSION  AX628274
VERSION     AX628274.1 GI:28456312
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 5315 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       Location/Qualifiers
              1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 TCCACCTGCTG 14
        |||||
Db      1 TCCATCTGTTG 11

RESULT 401
AX628274
LOCUS      AX628274      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 5315 from Patent WO02053774.
ACCESSION  AX628274
VERSION     AX628274.1 GI:28456312
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 5315 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       Location/Qualifiers
              1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Qy 7 ACCTGCTGTGT 17  
|||||  
Db 1 ACCTGGTGCT 11

RESULT 402  
AX628612  
LOCUS AX628612 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 5653 from Patent WO02053774.  
ACCESSION AX628612  
VERSION AX628612.1 GI:28456650  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 5653 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 26.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 2.1e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 10 TGCTGTGTGAC 20  
|||||  
Db 1 TGATGTTTGAC 11

RESULT 403  
AX628674/c  
LOCUS AX628674 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 5715 from Patent WO02053774.  
ACCESSION AX628674  
VERSION AX628674.1 GI:28456712  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 5715 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 26.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 2.1e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTGA 19  
|||||  
Db 11 CTGCTGGGTTA 1

RESULT 404  
AX629060/c  
LOCUS AX629060 11 bp DNA linear PAT 21-FEB-2003

DEFINITION Sequence 6101 from Patent WO02053774.  
ACCESSION AX629060  
VERSION AX629060.1 GI:28457098  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 6101 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 26.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 2.1e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 18 GACCTGGTAAA 28  
|  
Db 11 GCCCTGGTGAA 1

RESULT 405  
AX629446  
LOCUS AX629446 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 6487 from Patent WO02053774.  
ACCESSION AX629446  
VERSION AX629446.1 GI:28457484  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 6487 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 26.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 2.1e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGTG 18  
|  
Db 1 CCCGGTGTGTG 11

RESULT 406  
AX629919  
LOCUS AX629919 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 6960 from Patent WO02053774.  
ACCESSION AX629919  
VERSION AX629919.1 GI:28457957  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

```

1
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 6960 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       Location/Qualifiers
              1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches          9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      12 CTGTGTGACCT 22
        |||||
Db      1 CTGTGTAAGCT 11

RESULT 407
AX630160
LOCUS      AX630160
DEFINITION Sequence 7201 from Patent WO02053774.
ACCESSION AX630160
VERSION   AX630160.1 GI:28458198
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.

REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 7201 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       Location/Qualifiers
              1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches          9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      10 TGCTGTGTGAC 20
        | |||||
Db      1 TTCTGTGTCTAC 11

RESULT 408
AX630234
LOCUS      AX630234
DEFINITION Sequence 7275 from Patent WO02053774.
ACCESSION AX630234
VERSION   AX630234.1 GI:28458272
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.

REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 7275 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       Location/Qualifiers
              1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"

```

RESULT 411  
AX631396  
LOCUS AX631396 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 8438 from Patent WO02053774.  
ACCESSION AX631396  
VERSION AX631396.1 GI:28459462  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 8438 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source Location/Qualifiers  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 26.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 2.1e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CCATCCACCTG 11  
| |||| ||||  
Db 1 CAATCCTCCTG 11

RESULT 412  
AX631733  
LOCUS AX631733 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 8775 from Patent WO02053774.  
ACCESSION AX631733  
VERSION AX631733.1 GI:28459840  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 8775 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source Location/Qualifiers  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 26.9%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 2.1e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 14 GTGTGACCTGG 24  
||| ||||| |  
Db 1 GTGAGACCTCG 11



This Page Blank (uspto)